



# 1<sup>st</sup> National Conference on Plant Genetic Resources Management

November 22-24, 2022

National Agricultural Science Centre  
Pusa Campus, New Delhi

# ABSTRACT BOOK

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## **Abstract Book**

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## **PREFACE**

We are delighted to present the Abstract Book of the 1<sup>st</sup> National Conference on Plant Genetic Resources Management (NCPGRM), 2022. The 1<sup>st</sup> NCPGRM-2022, spanning three days, is comprises one plenary session, five technical sessions, one panel discussion and one valedictory session with more than 71 oral presentations and > 150 posters.

This publication is unique as it carries abstracts based on the research and development in conservation and use of plant genetic resources (PGR). The abstracts included here offer a cross-sectional view of the ongoing work in the area of management of PGR. Organizers acknowledge the contributors who submitted the abstracts in camera ready form and the editors for compiling the publication by racing against the time.

**Date: November 20, 2022**

**Technical Program Committee**



## **ACKNOWLEDGEMENTS**

NCPGRM-2022 is a great opportunity for us, as both organizers and participants, to share mutual experience in such an important field of plant genetic resources management. NCPGRM-2022 would be attended by nearly 300 delegates from National Agricultural Research System (NARS) including ICAR institutes, agricultural universities, private stakeholders, farmers etc., besides participation from CSIR and overseas.

We would like to express our deepest gratitude to Dr. R.S. Paroda, President ISPGR for extended discussions and valuable suggestions. Contributions by Dr. Himanshu Pathak, Secretary-DARE and DG-ICAR, Dr. Trilochan Mohapatra, President NAAS and Dr. K.V. Prabhu, Chairman, PPV&FRA are greatly acknowledged. We sincerely thank for the excellent technical and administrative support provided by the Bioversity International Country Director and the Director, ICAR-NBPGR.

We place on record the guidance received from various committees such as Local Organizing Committee, Registration cum Invitation Committee, Stage and Hall Arrangement Committee, Food and Refreshment Committee, Accommodation and Transport Committee, Abstract Screening Committee, Souvenir Committee, Poster Session Committee, Resource Generation Committee and Cultural Program Committee for the smooth conduct of the Conference.

NCPGRM-2022 is projected to be a mega-event in recent times to deliberate on science, technology, policy and partnership driving the PGR management. An event of this scale and of national importance cannot be successful without financial support from our organizing partners, co-organizers and sponsors. We express our sincere appreciation to institutional and industry partners for joining hands with us in this endeavor.

We draw our strength from the support of colleagues from different participating institutes in this conference. A confluence of people involved in PGR management would not have been possible without the cooperation of many government and scientific institutions. We thank each one of them for their role in organizational steps.

**Date: November 20, 2022**

**Editors**



# **ABSTRACTS**



## 101 (P-101)

### Genetic divergence analysis in rice (*Oryza sativa L.*) genotypes for yield and quality traits

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Total forty-two rice genotypes excluding six checks comprising traditional landraces and released varieties from IGKV was evaluated for 18 quantitative and quality traits by principal component analysis and cluster analysis for determining the pattern of variation, relationship among individuals and their characteristics. Principal component analysis (PCA) was utilized to examine the variation and to estimate the relative contribution of various traits for total variability. Using PCA, we found that kernel length after cooking, Decorticated grain l:b ratio, grain yield/plant, decorticated length of grain, decorticated breadth of grain, Head rice recovery percentage, hundred grain weight have the most substantial contribution. Six principal components exhibit in excess of 1 Eigen value and explain as a minimum 5% of disparity beside with 74.60% cumulative variability amongst the characters considered. However, the seven PCs were agreed due to its consequence for further explained. The PC1 was show 26.93% while PC2, PC3, PC4 PC5, PC6 and PC7 presented 16.26, 9.25, 8.74, 7.28 and 6.13% variability among the traits. PCA revealed principal discriminatory characteristics *e.g.* kernel length after cooking, Decorticated grain l:b ratio, grain yield/plant, Decorticated length of grain, Decorticated breadth of grain, head rice recovery percentage, hundred grain weight and milling percentage respectively. Forty-two rice accessions were used for UPGMA cluster analysis and these accessions were grouped in eight clusters. The uppermost numbers of genotypes were found in cluster VII, which consist 9 genotypes followed by cluster V having 7 genotypes with cluster VI with 7 genotypes with one check TN1 and cluster IV with of 4 genotypes; while cluster II and III contain 3 genotypes each. Although cluster VIII having 5 check varieties *viz.* Annada, IR64, Pusa Basmati-1, Swarna and PTB 33 representing the imminence of these genotypes with the above checks as well as the relatedness among the checks themselves.

**Keywords:** Principal Component Analysis, Cluster analysis, Genotypes, Rice, Quality traits

## 102 (P-102)

### Augmentation of vegetative growth of small cardamom by co-cultivation with *Piriformospora indica*

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Small cardamom (*Elettaria cardamomum* Maton) is an economically valuable spice crop. The objectives of this study were to evaluate vegetative growth performance of cardamom after co-cultivation with *Piriformospora indica*-a root-colonizing endophytic fungus and to identify differentially expressed transcripts in cardamom responding to the root colonization for elucidation of molecular basis of growth and development. *In vitro* raised cardamom plantlets were hardened and co-cultivated in polybags under greenhouse conditions with *P. indica*. Growth parameters of control and *P. indica* colonized plantlets were observed for three months at an interval of 15 days. Various physiological, morphological, and molecular traits were assessed during this period. *P. indica* colonization resulted in a significant increase in the morpho-physiological traits of the host plant. There was a significant increase ( $p<0.05$ ) in the number and length of leaves, height of the plant and chlorophyll content in *P. indica* colonized plants compared to non-colonized controlled plants. In addition to this, the expression levels of auxin (AUX), nitrate reductase (NR), vegetative storage protein (VSP) and phosphate transporter (PHT) genes were upregulated by 3.45, 3.26, 1.62 and 1.19 folds respectively by the co-cultivation of *P. indica* in cardamom plantlets. The findings obtained from this study can be used as a foundation for future lines of research related to rational improvement of cardamom plants under different environmental conditions.

**Keywords:** Cardamom, *Piriformospora indica*, Co-cultivation, Root colonization, Gene expression, Real-time PCR

### 103 (P-103)

#### **Conservation of *kharchialandrace* of wheat: socio-ecological resilience in saline agroecosystems of arid climate**

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Crop genetic resources have long been crucial to agricultural production, and the second half of the last century saw considerable efforts in collecting, characterizing, and conserving this diversity in seed banks (*ex-situ* conservation). The diversity of traditional varieties sustained by farmers around the world is increasingly valuable for adaptation as climate changes, particularly as modern agriculture relies on a very limited number of crops and varieties. salt, pest and disease tolerance. This suggests the need to support initiatives such as local landrace conservation, community seed banks, and community-based conservation and adaptation. Keeping the above facts in view, research was conducted in Pali district of Rajasthan, India to evaluate the farmers perception about conservation and propagation of *Kharchia* wheat in saline belt of semi-arid zone of Rajasthan. The results showed that most of the farmers (92%) feel that growing *Kharchialandrace* of wheat is inevitable because this is the only variety which can adapt to harsh local conditions of saline soil, saline water and high temperature and can still give some yield even in thebad situation. Another reason of inevitability of *Kharchiawheat* is that it can be grown underconserved soil moisture as rainfed crop



which is not possible with the improved varieties of wheat. In Palidistrict, most of the farmers are resource poor who do not have irrigation facility while those having wells, irrigating crop is impossible due to high ground water salinity. Hence there is simply no other choice almost for entire farming community as they don't want to take risk by growing new varieties. For farmers who do not believe that growing *Kharchi* wheat is inevitable for better adaptation to harsh local conditions, they consider that the failure of the *Kharchi* wheat may be because it is not productive enough and having lack of tolerance to disease and susceptible to lodging. Majority of the farmers (94%) grow this landrace as the seed viability is very high and can be cultivated for years together without any decline in yield. Besides other characteristics, 93% of the farmers are of the opinion that in addition to the grain yield, the fodder yield is also high as liked most by the cattle. In arid zone, its fodder is also a valuable resource hence makes this variety inevitable for farmers.

**Keywords:** *Kharchi* landrace, Saline agroecosystems, Seed viability, Wheat

**104 (P-104)**

### **Identification and characterization of niche specific Rajmash landraces and farmers varieties from Kashmir valley**

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Common bean (*Phaseolus vulgaris* L.) is considered one of the most important pulse worldwide. Because of its great variability in terms of plant physiology and architecture, the common bean cultivation spans a wide range of cropping systems and environments. More specifically the study was envisioned as developing common bean varieties with increased levels of yield in farmers' preferred grain types. The experiment was carried out during Rabi season of 2021-2022 to estimate the morphological variability in 15 common bean varieties collected from different areas of Kashmir valley using 22 morphological traits (20 visual and 01 measurable). The varieties PPR-6 and PPR-7 showed circular to elliptic, PPR-1, PPR-10, PPR-11 and PPR-14 showed elliptic, and rest 9 varieties showed kidney shaped seed whereas, none of the variety had round seed shape. The study revealed that flower color and hypocotyl pigmentation could be used as critical morphological characters for ascertaining varietal distinctiveness amongst genotypes. Of the 15 genotypes, few were utterly unique as they could be distinguished based on a single trait while most of the genotypes were very close to each other. Thus, results suggest that the characterization of these varieties were done in order to use them as reference varieties for protection of other new varieties under PPV&FR Rules, 2001. The database generated may be useful for the selection of suitable varieties to compare against the candidate varieties and can be analysed at molecular level for various traits. This investigation may also be helpful to the researchers with respect to breeding of common bean varieties for particular trait. Moreover, farmers can also be benefited by selecting suitable varieties of their interest.



**Keywords:** Characterization, Common bean, Morphology

### 105 (P-105)

#### **Yield based selection indices for water stress tolerance evaluation in Common Bean (*Phaseolus vulgaris* L.) varieties under temperate conditions of Kashmir valley**

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Common bean (*Phaseolus vulgaris* L.) known as rajmash is the most important summer season pulse crop of Kashmir valley. Given that abiotic stresses (drought, high temperature) are pervasive, often strong, and occur practically every year, reported to cause larger yield loss. Drought stress indices are quantitative measures characterizing water stress response by yield data from one or several environments based on timing, duration and intensity of stress. For the present study, material comprised of 20 breeding lines including three released varieties were used and shown in a randomized block design with two replications each for drought and irrigated treatments. Data was analysed using XLSTAT software. A number of response indices such as stress susceptibility index (SSI), tolerance index (TOL), mean productivity (MP), geometric mean productivity (GMP) and stress tolerance index (STI) were used to identify genotypes with higher productive potential and resilience to water stress. The indices had varying ranks, emphasizing the need to create a more relevant index. Two new indices resilience and production capacity indices were used to elucidate differential genotypic response in terms of adaptability, under stress and non-stress environments and were found to be efficient in genotypic screening based on resilience and productivity.

**Keywords:** Productivity, Resilience, Water stress

### 106 (P-106)

#### **Morpho-molecular diversity intraditional rice varieties of northern Kerala**

**Nisha SK<sup>1\*</sup>, Vaijyanthi PV<sup>1</sup> and Sujatha R<sup>1</sup>**

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Traditional rice varieties (TRVs) have a reputation for adaptation to specific ecosystems and are valuable resources for trait/gene discovery. Kerala, being one of the hotspots for rice diversity, a study was undertaken to characterize and evaluate 50 TRVs as per the DUS descriptor of rice. Substantial polymorphism for qualitative traits and genetic variability for quantitative traits among TRVs were evident. Analysis of Variance



(ANOVA) suggested highly significant mean squares for important yield contributing traits except for grain width. Traits such as plant height, tillers plant<sup>-1</sup>, spikelet panicle<sup>-1</sup>, 1000 seed weight, and grain length showed high heritability coupled with high genetic advance indicating predominance of additive gene action and effectiveness of selection. Genetic variability was further confirmed by genotyping with 30 genome-wide SSR markers. Among these, RM 413 and OSR 13 showed the highest PIC values of 0.559 and 0.594, respectively. The cluster analysis indicated six major clusters and the TRV Mallinatta showed maximum divergence. Diversity among TRVs offers a possibility to use it as a priority resource for trait/gene/allele mining.

**Keywords:** Traditional rice varieties, Diversity, Genetic variability

## 107 (0-25)

### **Preservation of central India's forest genetic resources through the establishment of a seed gene bank at Tropical Forest Research Institute, Jabalpur, Madhya Pradesh**

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Forest Genetic Resources (FGR) are considered as a crucial element of biodiversity. These serve as the starting point for the development of improved varieties, clones, and a hybrid, so protecting them is essential to continuing the tree improvement program. This crucial portion of the biodiversity must be highlighted, accurately documented, and sustainably preserved for both its own sake and for the benefit of mankind. Unlike agricultural and horticultural species, the germplasm of FGR is either dispersed across the country in the form of scattered populations or is restricted to extremely specific locations, making research difficult. Unlike ICAR, there is currently no custodian of FGRs at the national level. A 10-year program (2018-2028) to be completed in two phases (Phase I 2018-2023; Phase II 2023-2028) is developed at ICFRE for carrying out FGR documentation, collection, seed conservation, characterization, and construction of field gene bank through CAMPA funding. The list of 65 priority species has been finalized as part of the project at the Tropical Forest Research Institute, Jabalpur. Majority of these belong to RET species occurring in central India (Madhya Pradesh, Maharashtra, and Chhattisgarh state), which have socio-economic and ecological importance. Distribution maps of the identified species are being generated, and seed source populations are being identified for seed collection and conservation based on Relative Density (RD) values. Both medium-term and long-term cold storage facilities for active and base collections have been constructed for seed conservation. Under the current scenario of a drastic decrease in forest diversity due to climate change and changes in land use patterns, this entire activity will assist in the preparation of a comprehensive inventory of the FGRs of central India and the conservation of seed germplasm diversity of important FGR species.

**Keywords:** Biodiversity, Forest genetic resources, Seed bank, Relative density



## 108 (P-108)

### Assessment of genetic diversity among wild and cultivated brinjal genotypes employing SSR markers

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Brinjal (*Solanum melongena* L.) stands as one of the most economically popular vegetables in the world and carries a wide range of genetic diversity at the species level. However, because of the existence of a high level of genetic diversity, the huge morphological data has led to ambiguous interpretations. A key approach to overcome this issue is to study diversity at the allelic level, using molecular markers to detect polymorphisms at the DNA level. A study has been conducted using 10 SSR markers to assess the genetic diversity among 30 genotypes of brinjal which includes local genotypes from North Kerala, accessions from NBPGR, the weedy form *Solanum insanum*, and wild progenitor *Solanum incanum*. The SSR characterization revealed the size of amplified products ranged from 200 to 400 base pairs with an average of 253.68 bp. A total of 19 alleles were amplified using 10 SSR primers across the brinjal genotypes and revealed an average of 1.9 alleles per primer. The Polymorphic Information Content (PIC) ranged from 0.249 to 0.527 with an average PIC value of 0.300. The Unweighed Pair Group Method with Arithmetic Means (UPGMA) cluster tree analysis led to the grouping of entire set of genotypes into 3 major clusters and the genotypes that are derivatives of genetically similar type form cluster together with Jaccard's similarity coefficient ranging from 0.60 to 1.00 with maximum brinjal genotypes included in cluster III. However, further studies involving more number of genotypes and primers need to be conducted to get more precise information relating to molecular characterization of other solanaceous crops.

**Keywords:** Brinjal, Characterization, Genetic diversity, SSR

## 109 (P-109)

### Molecular characterization of senna (*Cassia angustifolia* Vahl.) using non-genic random amplification of polymorphic DNA (RAPD) and inter simple sequence repeat (ISSR) based sequence characterized amplified region (SCAR) markers

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The leaves and pods of senna (*Cassia angustifolia* Vahl.), an important species of family Fabaceae, yields sennosides and rhein based laxative. Adulteration of senna with related species such as *C. fistula*, *C. occidentalis*, *C. sophera*, *C. tora* etc. at gross morphology is a



serious issue with true-to-type identification and authentication of senna accessions. Molecular marker based authentication of herbal drugs, as senna in this case, strives to establish unmatched unique identity of an individual against a score of such adulterants. The present investigation seeks to develop species-specific random amplified polymorphic DNA (RAPD) and inter simple sequence repeat (ISSR) based sequence characterised amplified region (SCAR) markers for the identification and authentication of true-to-type senna and adulterant *Cassia* species. Both RAPD and ISSR are non-genic, random, multi-locus, dominant, and sequence independent markers. Thus, the information generated through use of these markers is faithfully converted to single-locus, highly reproducible and sequence based SCAR markers. In this investigation, genomic DNA extracted from the accessions (44 in all) of senna and its adulterants (4 in all) were subjected to RAPD and ISSR PCRs. The polymorphic bands were identified, eluted, ligated (with pGEM-T Easy vector) and transformed into competent *E. coli* DH5  $\alpha$  strain by heat shock method. The transformed recombinant plasmid clones were confirmed by PCR, restriction analysis and DNA sequencing. Post-sequencing, a pair of SCAR primers was designed to validate and address the issue of true-to-type identity of senna accessions against other adulterant *Cassia* species.

**Keywords:** Characterization, ISSR, Senna, SCAR, SSR

## 110 (P-110)

### **DNA barcoding: important tool for identification of closely related species of *Curcuma***

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DNA barcode, one of the major points is that the genetic data is an important factor to improve the biodiversity conservation, identification strategies and in fact at the different level of analysis in conservation biology and molecular techniques. The aim of this research is to assess the DNA barcoding in *Curcuma* genus identification in molecular level. In this study two chloroplast regions of barcoding primer *rbcL* and *trnL* were applied to assess the genetic relationships of *Curcuma* species, which are difficult to distinguish from morphology. The PCR and sequence success rate were high in *trnL* (95.7%) and *rbcL* (90%) regions. The Maximum Parsimony tree was conducted by Kimura 2 p model with MEGA 11. The results showed that candidate chloroplast barcoding regions (*rbcL*, and *trnL*) were closely related to *Curcuma angustifolia* and *Curcuma caesia*.

**Keywords:** *Curcuma*, DNA barcode, Identification

111 (P-111)

**Genetic diversity studies using morpho-molecular markers in peach (*Prunus persica* (L.) Batsch)**

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The rising interest in the stone fruits due to their high nutritive value and market demand initiated this investigation about genetic diversity study in peach (*Prunus persica*). The great Himalayas possess the natural wealth of temperate fruit germplasm including peach (*Prunus persica*), belong to family Rosaceae. Different markers *viz.*, biochemical, morphological and molecular can be used to study the genetic diversity of peach, among which morphological characterization forms the preliminary step. However genetic diversity cannot be revealed only based on morphological data, so molecular characterization should also be done to avoid environmental variation and limited polymorphism. Total of twelve varieties of peach grown in Himachal Pradesh have been characterized using morpho-molecular markers. Molecular characterization using RAPD markers showed high heritability in fruit length, yield, fruit weight, leaf breadth, stone width and leaf length while moderate heritability was observed in TSS, stone length, fruit width and stone weight. Stone weight had high phenotypic coefficient of variation (PCV) and moderate genetic coefficient of variation (GCV) followed by yield. Genetic gain was observed high in yield, fruit length and stone weight. Genetic and phenotypic correlation study showed that yield had positive and significant correlation with fruit length, fruit weight, fruit width, stone width and leaf width. Yield had negative and significant correlation with TSS at genotypic level while at phenotypic level yield had negative and non significant correlation with TSS, stone length, stone weight, and leaf length. Genetic diversity among twelve cultivars of peach was estimated with fifty-two primers. Twenty-two primers found informative which resulted into sixty six polymorphic bands and thirteen unique bands. High polymorphism was observed among twelve cultivars of peach i.e. 83.54%. The similarity coefficient in twelve genotypes ranged from 0.090 to 0.667. Maximum similarity index was observed in Earligrande and Shan-i-Punjab (0.667) while minimum was observed in Pratap and Royal Paradelux (0.090).

**Keywords:** Heritability, Polymorphism, Phenotypic correlation coefficient, Genotyping correlation coefficient



112 (P-112)

**Collection, conservation and bioprospecting of crop germplasm from Eastern Uttar Pradesh: efforts of PRDF Gorakhpur**

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As a region, eastern Uttar Pradesh is one the richest yet unexplored centres of plant genetic diversity. PRDF collected germplasm of *Dioscorea* sp. (5); *Echinochloa* sp. (60); *Eleusine* sp. (62); *Eruca sativa* (28); barley (232); *Lathyrus sativus* (28); *Linum* sp. (168); *Oryza sativa* (927, including 587 Boro, 90 scented and 250 Kalanamak); *Paspalum* sp. (69); *Pisum sativum* (258); *Sesbania* sp. (7) and *Setaria italica* (109) germplasm. Most of these were collected under UNDP funded project through ICAR - NBPGR New Delhi. Out of these, Kalanamak rice landrace with a 3,000 year old history was chosen for bioprospecting. It contains high protein, iron, and zinc. Besides, it is sugar free and has Vitamin A as beta Carotene. Kalanamak was registered under PPV & FRA and also has been assigned Geographical Indication (GI) tag until March 2030. Four improved varieties namely Kalanamak KN3, Bauna Kalanamak 101, Bauna Kalanamak 102 and Kalanamak Kiran were developed using Kalanamak landrace and notified in 2010, 2016, 2017 and 2019 respectively. Market price of Kala namak landrace ranges between Rs. 3,500/- to Rs. 4,500/- per quintal contrary to Rs. 1,950 MSP. Summarily comparing to Rs. 28,000 per ha net profit from common HYV rice; common normal Kalanamak variety earns Rs. 78,500 and organic Kalanamak earns Rs. 99,000 net profit per ha. Farmers are assured of local and export market defying the proverb "Paddy and poverty go together". Formation of FPOs, ODOP, CFC and opening of Kushinagar international airport are added conduit for its organised marketing. About 55 tons to Singapore and 10 tons to other countries were exported within the last 2 years. This is win win situation for farmers, marketers and consumers alike.

**Keywords:** Germplasm, PRDF, Kalanamak rice, Geographical Indication, Bioprospecting

113 (P-113)

**On-farm crop diversity management in rainfed agro-ecosystem of Jaunsar-Bawar, Jaunpur and Ranwain areas of Uttarakhand, India: a case study**

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Conservation of traditional crop diversity on-farm and its sustainable cultivation for livelihood has been a part of socio-economic and religious culture being practiced by Indian farming communities since ancient times. Such diversity has been recognized with unique



cooking quality, taste, resistance to biotic and abiotic traits. In the present study, crop diversity in a hill agro-ecosystem covering Jaunsar-Bawar (Dehradun), Jaunpur (Tehri) and Ranwain (Uttarkashi) area of Uttarakhand, India was assessed on-farm, and factors responsible for erosion and changes in cropping systems thereof were identified. The entire area is immensely rich in floristic and crop diversity and coupled with rich cultural and ethnic diversity. About 55 crop taxa reported under cultivation three decades ago have presently shrunken to 40-45. Analysis of data showed that among the selected areas, farming community of Jaunpur area are still maintaining maximum crop taxa (23 crops) on-farm as compared to other two sites. Maximum erosion in crop diversity was recorded in Rawain area (34.47%), followed by Jaunpur (19.24%) and Jaunsar-Bawar (11.24%). Among the traditional crop landraces, *halmunji* and *sankull* landraces of rice from Jaunsar-Bawar; *ramjawan* and *utawalif* from Rawain and *safeddhan* from Jaunpur; *kathiyu*, *kisala* and *meshre* landraces of wheat from Jaunsar-Bawar and Rawain areas were observed to have completely been eroded. Among the crop landraces, erosion in rice landraces was assessed above 80%, in wheat above 90% and in millets above 70%. Study has also revealed that three decades ago fifteen cropping patterns/crop rotations used to follow, now have left with seven only. Drastic reduction in on-farm crop diversity was observed mainly due to impact of climate change, irregular and erratic rainfall pattern, change in cropping pattern, introduction and adoption of new crops/high yielding varieties, low crop productivity (soil low fertility, damage by cattle, birds and wild animals), non-availability of seeds of traditional landraces, changing food habits and reduction in family size (due to migration).

**Keywords:** Agro-ecosystem, Jaunsar-Bawar, On-farm crop diversity, Landraces

## 114 (P-114)

### **Expedition in unexplored diversity rich mountainous agro-ecosystem of Cachar Hills of Assam, India**

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The Dema Hasao district, earlier called North Cachar Hills district in Assam, India endowed with rich agri-horticultural diversity. Inadequate *ex-situ* conservation of plant genetic resources (PGR) from the area coupled with anthropogenic pressure and climate change has necessitated systematic collection of PGR wealth from these hilly areas. Three explorations were executed during 2011, 2020 & 2021, resulted into the collection of 178 accessions belonging to cereals, minor millets, pseudo-cereals, legumes, oilseeds, vegetables, and crop wild relative (CWR) with remarkable variability. Of the 28 taxa belonging to CWR and other minor economic plants, *Cajanus scarabaeoides*, *Calopogon mucunoides*, *Dysolobium pilosum*, *Rhynchosia beddomei*, *Sesbania bispinosa*, *Trichosanthes dunniana*, *Vigna angularis* var. *nipponensis*, etc. were among the first time collected species. Out of 33 rice landraces, 18 were collected with rich variability for the first time include *Khoi beroin*, *Gandiberoin*, *Kalasahi*, *Paniberoin*,



*Sembra, Bairang, Aizong, Changbem, Changbin Meu, Kalajiri, Kba-prinkhmuj, Sasurchi, and Sa-toi-sen*. Other crop landraces like soft, sticky and sweet types in maize; pumpkin with variability in size (300-5000g); and aroma rich ash guard were among interesting collections. Several species having food and medicinal value like *Begonia, Centella, Clerodendrum, Corchorus, Phlogocanthus, Rhynchotechum, Spilanthes, Hibiscus, Lasiacare* under cultivation in jhums and kitchen garden, while also found to occur in wild habitats. The entire hills are inhabited by ethnic groups like Dimasas, Hmar, Zemes, who have an inseparable relation with forest in their daily life. A local liquor 'Ju-dima/Judima' prepared from rice landrace- *Bairang* by Dimasasis considered good for health, consumed frequently. The consumption of wild plants is one of the strategies, adopted by the local people for sustenance.

**Keywords:** Bairang, Cachar Hills, Crop wild relative, Judima, Landraces

115 (P-115)

### **Deciphering Genetic Diversity of varied flesh colored *Cucumis sativus* L.**

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Cucumber (*Cucumis sativus* L.) is among the most widely cultivated and consumed cucurbitaceous vegetable crops. India is the origin of *Cucumis* species and is known to be a treasure of cucumber germplasm. Commonly cultivated cucumber is green/white fleshed with low carotenoid content. However, orange fleshed cucumber is a rich source of carotenoids that is nutraceutically rich. In order to decipher genetic diversity amongst varied flesh color cucumber germplasm, a total of 35 accessions with varied flesh colour from green/white-fleshed to orange/yellow was used profiled with 46 simple sequence repeat (SSR) markers. A sum of 125 alleles was detected from 46 polymorphic markers with an average of 2.71 alleles per locus. Observed heterozygosity had a mean of 0.4 across the genotypes and the highest observed heterozygosity was in marker 2 (SSR20705) with a value of 0.8 and lowest was with marker 25 (SSR14268). The polymorphic information content (PIC) of the markers had an average of 0.36. Marker 39 (SSR16472) revealed the highest PIC of 0.72, while marker 25 (SSR14268) had the lowest PIC. Genetic distance calculated by Nei's 1983 showed the highest diversity between accession IC 371617 and INGR18029. The mean major allele frequency was 0.61 and the dendrogram grouped 35 genotypes into 5 distinct clusters based on flesh colour—orange, white and green. All the orange fleshed cucumber grouped together in cluster B and E. Cluster A, C and D consisted only green and white flesh genotypes. This study suggests that India has a good diversity in carotenoid rich germplasm which could be utilized in breeding nutrition rich cucumber varieties.

**Keywords:** Cucumber; orange flesh colour; genetic diversity; molecular markers



## 116 (P-116)

### **Phenotyping of Brassica germplasm for discovery of resistant sources against white rust (*Albugo candida*)**

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White rust, a serious foliar disease caused by the oomycete, *Albugo candida* is one of the most destructive disease of oilseeds and vegetable Brassica resulting yield losses ranging from 17-60% in India. Keeping potential threat in view the present study was aimed with an objective to identify resistant sources against White rust. Field screening of 62 accessions of *Brassica* under natural epiphytotic conditions of Delhi revealed that five accessions, viz., IC265495, EC206642, EC766193, NDN 125, NDN 126, NDN 128 and one introgressed line, i.e., RBJ 40 were identified as immune to white rust disease. Only three resistant accessions, namely IC313380, EC766136 and EC766164 showed per cent disease intensity (PDI) ranging from 5.00 to 7.50 per cent. Artificial screening of the same accessions under controlled environment was done using inocula i.e., *Ab-Del* (Delhi isolate) and *Ab-Png* (Pantnagar isolate) of *A. candida*. After 8-12 days of incubation, symptoms were observed and disease severity was recorded. More or less similar patterns were observed with some deviations at both the crop stages against both the isolates. Out of 62 accessions, five were observed with resistant reaction at cotyledonary stage showed PDI ranging from 2.50 to 10.00 and 5.00 and 10.00 per cent against *Ab-Del* and *Ab-Png* isolates, respectively. Whereas, PDI at true leaf stage ranged between 5.00 and 10.00 per cent against both the isolates. Since developing resistant varieties is the most effective and economically viable strategy for disease management. Therefore, all the accession identified as immune/ resistant could be utilized as resistant donor in crop improvement programme for developing resistant/high yielding varieties and also for mapping and tagging resistance genes against *A. candida*.



**117 (P-117)**

### **Mainstreaming of Potential Crops in India under National Coordinated Network**

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Globally, humanity depends on a very narrow range of crops to meet its food and other requirements. Presently, only 30 crops are reported to feed the world, of which 10 crops provide 75% of the total plant derived energy (calories) intake and rice, wheat and maize provide 60% of the total food requirement. Realizing the significance of the underutilized crops in diversifying agriculture under different strategic situations, an AICRN on Under Utilized and Under Exploited Plants was initiated during 1982 by ICAR and recently rechristened as AICRN on Potential Crops. The network is conducting research on 16 crops through 16 main, 9 cooperating and 10 voluntary centres in India. During the last 39 years, a germplasm holding of over 13,000 accessions of prioritized plant species has been collected/introduced, characterized and conserved in the National Gene Bank. Multi-location evaluation of germplasm/breeding lines has led to identification/release of 52 varieties of 12 Potential Crops and standardization of their cultivation practices for different regions of India. Grain amaranth is replacing wheat and potato in view of water scarcity in Gujarat and area estimated around 12000 ha. The grain market at Palanpur in Gujarat receives about ten thousand tones grains annually. Future strategies are proposed for their popularization for enhanced utilization, to sustain the productivity of fragile and marginal lands, to sustain man's food and his multifarious requirements as well as generate a support system for small and marginal farmers for their livelihood in the times to come.

**Keywords:** All India Coordinated Research Network (AICRN), Genetic resource, Germplasm, Potential crops, Underutilized plants

**118 (P-118)**

### **Evaluation and diversity analysis of Sponge Gourd genotypes**

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Twenty-three diverse genotypes of sponge gourd (*Luffa cylindrica*) were evaluated to assess the genetic variation and diversity for yield and yield attributing characters. Analysis of variation revealed significant differences for all the twelve characters among the genotypes. Highest fruit yield /plant was recorded in the genotype AAUSG7 (2.85 kg/plant) followed by AAUSG5 (2.78 kg/plant), AAUSG9 (2.71 kg/plant) and AAUSG13 (2.61 kg/plant) which was significantly higher than the check variety PusaChikni(1.58kg/plant). Maximum genotypic coefficient of variation was observed for fruit yield per plant (38.05%) followed by node of appearance of first female flower (32.23%), fruit length (22.88%), seeds per fruit (21.96%) and average weight of matured fruit (21.59%). High heritability in broad sense and genetic advance was observed for fruit yield per plant (89.85%, 74.31%) followed by node of appearance of first female flower (89.77%,62.91%) and average weight of matured fruit (88.69%, 41.89%). Path coefficient analysis revealed that average weight of matured fruit followed by days to flowering and fruits per plant exhibited high direct effect on fruit yield per plant. From diversity analysis based on Mahalanobis D<sup>2</sup> statistics, the genotypes were grouped into six clusters. Highest inter-cluster distance was between cluster II and III (629.23) followed by cluster III and V (617.34). Intra-cluster distance was highest for cluster IV (95.60). In this study, the contribution of each of twelve characters to the total divergence was worked out using method suggested by Singh (1981). The characters node of appearance of first female flower (26.7%) showed maximum contribution to diversity followed by fruit yield per plant (17.6%), seeds per fruit (14.8%) and fruit length (10.7%).

**Keywords:** Evaluation, Diversity analysis, Sponge gourd genotypes

## 119 (0-09)

**Inter-specific hybridisation followed by mutation to improve the yield potential of cultivated emmer or Khapli wheat (*Triticum dicoccum* Schrank ex Schubl.).**

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Cultivated emmer wheat (*Triticum dicoccum*), a tetraploid species, known as Khapli in India is gaining importance as functional/therapeutic food because of the low glycaemic index (<55), slow digestibility, high satiety value coupled with resistant starch, high protein (16%) and fibre. These quality attributes are considered vital for the dietary management of diabetes and cardiovascular risks. Traditional varieties/landraces of



emmer wheat are tall, susceptible to lodging and low yielding with high quality, while the modern semi dwarf cultivars are high yielding with low quality. Most of the currently cultivated semi dwarf *dicoccum* cultivars derived their dwarfing genes from *Triticum durum* (cultivated tetraploid species) and has strong linkage drag in altering the quality traits. This necessitates the need to search for new sources to create variability among the emmer wheat gene pool using wild/related species. *Triticum carthlicum*, a wild tetraploid species with comparable quality traits of emmer wheat utilized to create variability. Tall transgressive segregants for yield and quality traits obtained from the progenies of *T. dicoccum* X *T. carthlicum* was subjected to mutation for reduction of height. Inter-specific derived lines were treated with gamma rays (250, 300 and 350 Gy) (Cobalt 60) and 250 Gy electron beam (electron accelerator). Electron beam treatment had thrown three semi dwarf mutant lines which were high yielding with superior quality. Mutant lines were stabilized at M6 generation. Significant reduction in plant height (up to 38% reduction) over the parent combined with an increase in grain yield/m<sup>2</sup> (up to 13% increase) over the check was observed in the mutant lines. Quality analysis of mutant lines revealed a grain protein (17%), iron (45 ppm) and zinc (43 ppm) content which were higher than the check. Present study signifies the relevance of wide hybridisation and artificial mutagenesis to create genetic variation for improvement in crop species.

**Keywords:** Hybridisation, Khapli wheat, Mutation, Quality

## 120 (P-120)

### **Phenotyping of cotton (*Gossypium hirsutum*) accessions and assessment of genetic variability for yield and fiber quality parameters through multivariate analysis**

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Cotton has manifold merits; it is used as fibre, lint for making clothes, food, feed, and cotton seed oil. In India *G. hirsutum* cotton occupies more than 90 (%) of total cotton cultivated area. Identification of appropriate germplasm accessions and a trait-directed approach could ensure development of varieties and hybrids with higher productivity and fibre quality. A field experiment in three replications was conducted to ascertain genetic variability of 393 *G. hirsutum* accessions for yield and fiber quality traits at ICAR-CICR, RS, Sirsa. Principle component analysis (PCA) for yield attributing traits extracted a total of eight principal components (PCs) accounting for about 100% variability of which PC<sub>1</sub> and PC<sub>2</sub> contributed more than 51 (%) of the total genetic variability. The PCA biplot test showed a close association of single plant yield with plant height (cm), number of sympods and boll weight (g). The Pearson correlation analysis showed a significant positive correlation among single plant yield and number of sympods ( $r=0.57^*$ ) and boll weight ( $r=0.365^*$ ). Cluster analysis using Ward's method grouped the accessions in 17 clusters for yield attributing traits and into 16 clusters for fiber quality traits indicating the presence of high levels of genetic variability among the germplasm accessions. Among 17 clusters, cluster no. 16 consisted of four accessions viz.



NCPGRM

EC 138570(101.67g), EXO-37 (106.33g), EC138572cc (95g) and EC618300 (113.93g) having highest mean single plant yield(g) and cluster no. 4 consisted of 3 accessions viz. EC170340 (36.67 %), EC134389 (37.5 %) and IC 291694 (40%) having highest mean GOT (%). Among 16 clusters for fiber quality traits cluster no. 13 consisted of 2 genotypes EC128578 (29.3 mm, 29.8 g/tex) and EC344451 (31.5mm, 30.4g/tex) showed highest mean UHML (mm) as well as fiber strength (g/tex). These identified genotypes may prove a valuable resource to fuel the breeding efforts for not only broadening the genetic base of the newly developed material but can also add synergy to various cotton genomic projects for specific trait-transfer.

**Keywords:** Germplasm, *Gossypium hirsutum*, PCA, Cluster analysis, GOT (%)

**121(P-121)**

### **Introduction and establishment of nine Wild species of *Gossypium* from USDA, USA**

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The genus *Gossypium* to which cotton belongs has more than 50 well-established species, only 4 of which are cultivated. In terms of fiber production and quality, the wild cotton relatives are relatively inferior compared to the cultivated species. Despite this, the wild *Gossypium* germplasm serves as a rich reservoir of novel alleles that can be utilized to improve trait performance in cultivated cotton. Efforts were made to import accessions of wild species of *Gossypium* to enrich the collection at the Central Institute for Cotton Research, Nagpur and 21 accessions of 9 wild species namely *G. areysianum*, *G. costulatum*, *G. darwinii*, *G. gossypoides*, *G. incanum*, *G. mustelinum*, *G. nobile*, *G. sturtianum*, and *G. tomentosum*. of *Gossypium* have been introduced and established at the ICAR-CICR, Nagpur from United States Department of Agriculture (USDA), USA. Further evaluation of these wild species has showed that they are free from exotic seed-borne/ germplasm-borne viruses/ pathogens / pests namely: Fungi-*Colletotricum gossypii* var. *cephalosporioides* (Witches broom), Bacteria -*Xanthomonas campestris pv malvecearum* - African strain (Bacterial Blight) and Insects - *Anthonomus grandis*, *Anthonomus* spp, *Amblycerus* spp., *Megacerus* spp. and *Spermophagus* spp. Utilisation of these wild species in interspecific hybridization to broaden the genetic base of the existing cultivars would be important in utilizing the abundant genetic variation for improvement of cultivated cotton. Wild or exotic germplasm constitutes an important resource that can provide novel genetic diversity in cultivated cotton. Utilization of naturally occurring genetic variation from wild relatives of crops has been generally perceived as a better option (as opposed to artificial variation) in plant breeding because of the certain selective pressures that has already acted on the fitness of the organism.

**Keywords:** Germplasm, *Gossypium*, Introduction, USDA



**122 (P-122)**

**Marker trait association analysis of seedling establishment traits in the wheat (*Triticum aestivum* L.) accessions conserved in National Genebank**

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Seedling establishment traits for wheat like seed weight, coleoptile length, root length, root angle, root number and plant height are very important for better plant establishment. These traits are also relevant in the context of conservation agriculture and in crop improvement for climate resilience. Hence, a genome wide association study was conducted to identify genomic regions associated with these traits by using 145 wheat germplasm accessions which were conserved in NGB and multiplied at 3 locations – Delhi, Ludhiana and Pune. IC252790 (K-9323- conserved in 1999) is a promising accession having higher CL and lower plant height along with other desirable traits for seedling establishment. Genotyping was done with Axiom® bread wheat 35K array and a total of high quality 19090 SNPs were used for GWAS in a subset of 104 accessions. In the marker-trait association analysis for seed weight trait, four significant MTAs with regards to seed weight were identified. The MTA identified on chromosome 7D (TraesCS7D02G48900) is a novel locus governing seed weight. A significant association was observed in the case of 7D SNP, 129.5Kb upstream of SNP, and the potential candidate gene TraesCS3B02G333400 was identified. In the case of root angle, a significant MTA marker-trait association involving SNP AX-94414610 was identified. TraesCS6A02G405800 which is 245Kb upstream from the SNP is the potential candidate gene with major role in root angle. For CL, on chromosome 4B, a significant MTA (SNP AX-94735690) was identified. For 4B SNP, TraesCS4B02G051400 and TraesCS4B02G051600 are the potential candidate genes involved in trait expression. For plant height, a highly stable marker-trait association was identified in all three locations (SNP AX-94547615) and TraesCS4D02G032700 gene (TaNFYA-1) which is 7.8Kb downstream from SNP is the potential gene with a major role in plant height. The information generated in this study could be of potential value for conservation agriculture, resilience breeding and for improving the genetic base of seedling establishment traits in wheat.

**Keywords:** Genebank, GWAS, IC252790, Seedling establishment traits, Wheat

**123 (P-123)**

**Population structure and variability studies of Guava (*Psidium guajava* L.) in cultivated and wild habitats in the mid-hills of Uttarakhand**

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The present study was undertaken in 10 villages of Thal tehsil having cultivated and naturalized guava population in wild habitat along Ramganga valley of district Pithoragarh of Uttarakhand. In this study the phytosociology, population structure, diversity distribution pattern and fruit variability of guava among the sites were analysed. Quadrat method was used to record quantitative data on guava population and associate species in 50 hectares of total sampled area, consisting sample plots dispersed at varied altitudes (600m - 1400m amsl). In sampled sites, 19 species of higher plants consisting 15 trees and four shrub species were observed. Various ecological formulae were used to analyse the quantitative data namely frequency, density, abundance and A/F ratio of different species. Maximum density (2.2 trees/100m<sup>2</sup>) of guava was found in an abandoned site at Murthi village, while minimum density (0.6 trees/100m<sup>2</sup>) of guava was found in cultivated field at Gaina village. Guava trees showed contagious distribution (>0.05 values) as compared to other species. The Importance value index (IVI) of the cultivated guava among the sites varied from 19.94 (Barla village, a cultivated site) to 103.59 (Murthi village, which is an abandoned site) was observed. Among 19 species, the highest Shannon diversity (H=0.367) values of guava was found at Pipaltar village. Variability was recorded for fruit colour (pale yellow, dark yellow, pink and whitish), fruit shape (long, round to pear-shaped), fruit length (34.35-80.7mm), fruit diameter (34.05-70.78 mm), fruit weight (34.45- 79.78g), pulp colour (white to pink), fruit maturity (September to late December) and total soluble solids (TSS) content (7.2- 12.2 degree brix) of fruits sampled from different sites. The cluster analysis of quantitative traits of guava fruits has grouped the populations into two main clusters followed by each into two sub-clusters. Population of maximum similarities and divergence were categorized. Planning for *in-situ* conservation, management strategies and utilization is also discussed.

**Keywords:** Guava, Importance value index, Population structure, Survey, Uttarakhand

## 124 (P-124)

### **Allelic test and validation of linked molecular markers in white rust resistant Indian mustard [*Brassica juncea* (L.) Czern&Coss] germplasm accessions**

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The white rust (WR) caused by *Albugo candida* is one of the major disease in Indian mustard (causes 23–89.9% yield loss). As majority of our native germplasm are highly susceptible to WR, while the Indian breeding program for rust resistance is mainly relied



on East European resistant donors like Heera and Donskaja. Overdependence on only these two exotic sources for WR resistance further increases the risk of resistance breakdown and disease outbreak. Hence, the present investigation was aimed at identifying new WR resistance source using available Indian mustard germplasm (5950 accessions). After repeated screening, the numbers of accessions were narrowed down to 90 WR resistant lines. Which on further rigorous screening along with 7 checks for 11 seasons (2016-2022) under natural hotspot for diseases at ICAR-IARI, RS, Wellington, 7 accessions have shown consistency as well as complete resistance. These seven resistant accessions were crossed with East European resistant donors' viz., Heera and Donskaja with resistant loci AcB1.4.1 and AcB1.5.1 respectively, to test the allelism in F<sub>2</sub> population. The allelism test revealed the presence of "New Resistant Locus" in one of the seven accessions namely WRW28 apart from the two earlier reported loci. The molecular characterization of 90 accessions and seven checks using previously reported linked/genetic markers (BjuA015829 - linked to AcB1.4.1; WR-DIV and WR-360 - linked to AcB1.5.1; WR-Tumida - linked to AcB1.6.1) also indicated that the accession WRW28 may contain "New Resistant Locus" conferring resistance to WR at Wellington. Moreover, the molecular analysis discovered the presence of resistant allele of locus AcB1.4.1, AcB1.5.1 and AcB1.6.1 in 10, 10 and 14 accessions, respectively. Furthermore, three accessions were observed to possess resistant alleles of both loci AcB1.4.1 and AcB1.5.1 and two accessions possess of both AcB1.5.1 and AcB1.6.1. However, no accessions were found to possess resistant alleles of all the three loci together. Most importantly, the WRW28, including 13 other accessions, did not contain any resistant alleles of these three loci, indicating the presence of "New Resistant Locus" conferring resistance to WR at Wellington. Thus, the identified accession WRW28 will pave the way for mapping of newer genes for WR resistance and facilitate breeding Indian mustard varieties with broad based resistance to *A. candida* variants prevailing in different regions of India.

**Keywords:** Indian mustard, White rust, Hotspot, Genepool, Broad based resistance

## 125 (P-125)

### **Assessment of Genetic Diversity and Differential Reaction of Cowpea (*Vigna unguiculata*) Germplasm to Pulse Beetle *Callosobruchus chinensis***

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Accessions were evaluated for their reaction to pulse beetles under no choice artificial infestation conditions to determine their differential reaction to *Callosobruchus chinensis* to identify the sources of resistance followed by their genetic diversity assessment. Both inter and intraspecific variations among the accessions were observed for various parameters viz., oviposition, development period, adult emergence, number of emergence holes, weight loss and growth index (GI). The GI ranged from 0.149 to 4.768, and based on GI, accessions were categorized as highly resistant (4 accessions, GI=0.149-



1.249), resistant (16 accessions, GI=1.249-2.349), moderately resistant (39 accessions, GI=2.349-3.449), moderately susceptible (19 accessions, GI=3.449-4.549), susceptible (5 accessions, GI=4.549-5.649) to attack of *C. chinensis*. Based on GI, the species were arranged in the order of their resistance to *C. chinensis*. *V. stipulacea* > *V. trilobata* > *V. unguiculata* i.e., wild species *V. stipulacea* was more resistant when compared to cultivated species *V. unguiculata*. Further, genetic diversity was assessed in 62 accessions of cowpea using SSR markers. The collection included accessions of cultivated species, *V. unguiculata* from five countries viz., India, Philippines, Nigeria, USA and Brazil. Of the primers tested, primers VR016, VR108, VM24 and VR015 were found to be most informative for assessing diversity of *V. unguiculata* as shown by their high PIC values when compared to others. The molecular marker data and cluster analysis showed a clear separation of all the three *Vigna* species, with three major clusters. Cluster 1 includes four 80 accessions from India, Nigeria, Philippines and USA which indicates that although these were derived from different parts of the world, they show some kind of similarity and clustered together. Two accessions one each from USA and Nigeria found moderately resistant and one each accession from India and Philippines found resistant to bruchids clustered together. Hence, Cluster-1 contains both resistant and moderately resistant accessions but did not have any susceptible accessions. As in Cluster-1 there are accessions from different countries are having resistance to bruchid attack, there is no clear-cut indication on geographic origin specific resistant/ susceptible genotypes. Cluster 2 comprised four accessions, two from India, one from USA and one from Nigeria. Cluster-3 comprised 54 accessions from five different countries and also included both resistant and susceptible genotypes. Thus, a clear-cut indication of any geographic origin specific resistant/ susceptible genotypes is not evident.

**Keywords:** Legume, CWR, bruchid resistance, variability, clustering

**126 (P-126)**

### **Delineation of diversity in early maturing pigeonpea based on DUS traits**

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Every crop improvement programme begins with the identification of better performing genotypes through its characterization. Development of core and composite collections from the available germplasm facilitates their utilization in crop improvement programmes. Core collections developed from the thousands of pigeonpea accessions around the world based on the qualitative traits have aided in the breeding programme. The qualitative traits are stable and can be used as molecular markers (not clear) in characterization and evaluation of genotypes. The characterization of cultivated species or genotypes aids in varietal description which can be used to maintain genetic purity. Characterization of released varieties, hybrids, essentially derived varieties (EDVs),



variety of common knowledge (VCK) and farmer's variety using DUS descriptors aids in their protection under Protection of Plant Varieties and Farmers Right Act, 2001 hence, characterization of the crop germplasm is essential. The present deals with the morphological characterization of pigeonpea genotypes conducted at the Department of Pulses, Tamil Nadu Agricultural University during *kharif*, 2019 and *rabi*, 2019-2020. The germplasm was sown in randomized complete block design with two replications. Total 68 short duration pigeonpea genotypes were characterized for 17 qualitative traits. The morphological characterization revealed that variation was observed for various traits *viz.*, pattern of streaks on standard petal, plant height, seed colour, seed shape and seed size. Entire genotypes were subjected to cluster analysis and grouped into four major clusters with an average similarity of 80%. The similarity coefficient ranged from 0.65 to 1.00. The cluster I consisted of 60 genotypes, which were grouped into two sub-groups. The sub-group I had 59 genotypes at 84 per cent similarity, whereas the sub-group II consisted of the genotype ICPL19050. Cluster II contains six genotypes, which was also grouped into two sub-groups at 84 per cent similarity. Clusters III and IV were solitary clusters, each with a single genotype. The characterization of genotypes with specific traits can be used to identify the genotypes, maintenance of genetic purity and to utilize in future breeding programmes.

**Keywords:** Diversity, DUS, Early maturity, Pigeonpea

## 127 (S-02)

### Unique plant germplasm collections from diverse agro-ecological regions of India

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The Indian gene centre belonging to four of the global biodiversity hot-spots, holds rich plant wealth. In recent-past, the rapid changing climatic conditions have posed serious threats to it, leading to extinction of crop landraces, genetic erosion and loss of various useful plant genetic resources (PGR). Hence, to counteract these imminent threats, there is urgency for collecting trait-specific and climate resilient germplasm, besides other PGRs. Since inception of ICAR-NBPGR in 1976, germplasm of over 2,000 taxa including over 10% notable/unique collections have been assembled. Though a significantly high number of unique germplasm have been collected, however in present paper recently compiled 75 unique plant germplasm, assembled along with various agri-horticultural crops through vigorous efforts by ICAR-NBPGR in collaborative mode have been discussed. These unique plant germplasm belong to trait-specific germplasm (12) *viz.* *Aegilops tauschii*, *Flemingia procumbes*, *Brassica tournefortii*, *Cucumis melo* var. *alwarensis*, etc., which have been validated through field and laboratory experiments; new species (19) collected, described and reported *viz.* *Abelmoschus enbeepegearense*, *Allium negianum*, *Vigna konkanensis*, *Herpetospermum operculatum*, *Trichosanthes dunniana* subsp. *clarkei* etc.; species recorded from new areas of distribution (24) *viz.* *Tubocapsicum anomalum*, *Vigna angularis* var. *nipponensis*, *Momordica subangulata* subsp. *subangulata*, *Juglans sigillata*, etc. Besides, potential crops/species (20)



are being consumed/grown by the local inhabitants, considered nutritionally rich and locally adapted including crop wild relatives *viz. Crotalaria tetragona, Bidens pilosa, Blumea lacera, Arivela viscosa, Hodgsonia heteroclita, etc.* also presented. Despite this, still there are gaps in representation of wild/less-cultivated taxa; areas unattended in some agro-ecological zones. Many taxa which have been reported from new areas of distribution; could not be conserved sufficiently, needs to be studied and recollected for the purpose. Further research/study on different aspects like enrichment, validation of trait-specific germplasm and popularization of less-known potential germplasm through networking; conducting especial exploration missions, etc. are required for their effective utilization and management.

**Keywords:** Collections, Indian gene center, New species, Landraces, Unique germplasm

## 128 (P-128)

### **Genetic resources of wild edible plants in high altitude of Chamoli district of Uttarakhand**

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The wild edible fruits are the key source of essential minerals for native community of Indian Himalaya. They possess good knowledge on uses of wild edible plants, and are an integral part of their daily life as well as culture. Chamoli district is located in the north western part of Uttarakhand, has a unique climatic and topographic condition, which supports occurrence of rich diversity of wild edible plants. Keeping this in view, survey was conducted in high altitude area of Chamoli to undertake study on ethnobotany, diversity distribution, threat status and domestication and marketing potentials of wild edibles. A total of 61 species of wild edible plants belonging to 35 genera were recorded from surveyed areas. It has been observed that most of the wild edible species are extensively exploited by the native community and consumed as a raw or as a value-added product. In the case of wild apricot, sweet kernels are used as a substitute of almond, however bitter kernels for oil extraction. Oil of apricot (chuli oil) is widely used for cooking purpose and also for body massages; and an alcoholic drink is also prepared from fruit pulp. At high altitudes, wild *Allium* species like *Allium stracheyi*, *Allium negianum*, *Allium wallichii* are found to grow, are commonly used as a seasoning material during cooking. Among the collections, about 12 wild edibles species were found to be facing threat due to anthropogenic activity and excessive harvesting.

**Keywords:** *Allium* species, Genetic resource, Ethnobotanical uses, Wild edibles

## 129 (P-129)



## Principal component analysis for assessment of genetic diversity in Indian kharif sorghum [*Sorghum bicolor* (L.) Moench] landraces

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*Sorghum* (*Sorghum bicolor* L. Moench) known as Great Millet, is the fifth most important nutritious cereal crop. Landraces are usually the major sources of genetic variation defined as variable plant populations adapted to local agro-climatic conditions. Because of its importance, protection and utilization are essential. During the Kharif 2021, 90 sorghum landraces along with 6 checks viz., CSV 15, CSV 20, CSV 27, CSV 17, CSV 21F and CSV 24SS were planted in Alpha Lattice Design in experimental field at ICAR-Indian Institute of Millets Research, Hyderabad. The data collected on twenty quantitative traits were subjected to principal component analysis to determine the variability and to estimate the relative contribution of various traits for total variability. The PCA analysis indicated that seven components (PC1 to PC7) exhibited more than 1.0 Eigen value and showed about 72.34% of the total variation among traits. The variance in the Eigen values was the greatest for PC1 (4.67) followed by PC2 (2.23) and PC3 (2.06). The traits contributing maximum towards the existing variability were plant height, stem diameter, leaf length, leaf width, 100-seed weight, grain yield/plant, Stem juice Brix, Number of internodes, Internode length, Total number of tillers per plant, Potential tillers per plant, Green fodder yield and Dry fodder yield. The results revealed that vast genetic variation exists among Kharif sorghum landraces for which the agro-morphological traits are immensely contributing to their variation. We need to exploit the potential trait-specific Kharif landraces for sorghum improvement.

**Keywords:** Genetic diversity, Principal component analysis, Sorghum landraces, Trait specific germplasm

### 130 (P-130)

#### Development and optimization of NIRS prediction models for simultaneous multi-trait assessment in diverse cowpea germplasm

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Cowpea is one such legume that can facilitate to achieve sustainable nutrition and climate change goals. Assessing nutritional traits conventionally can be laborious and time-consuming. NIRS is a technique which is rapidly used to determine biochemical parameters for large germplasm. NIRS prediction models were developed to assess protein, starch, TDF, phenols, and phytic acid based on MPLS regression. Higher RSQ external values were obtained for different traits viz., protein (0.903), starch (0.997), TDF (0.901), phenols (0.706) & phytic acid (0.955) in “2,4,6,1”, “2,8,8,1”, “2,4,4,1”, “3,4,4,1” and “2,8,8,1” mathematical treatments respectively. Models for all the traits displayed RPD values of >2.5 except phenolics (1.78) and low SEP indicating the excellent prediction of models. Paired t-test and reliability analysis were used to determine the difference in the mean of analytical and predicted values. For all the traits worked, p value $\geq$ 0.05 implied the accuracy and reliability score>0.8 (except phenol) ensured the applicability of the models. The developed models will facilitate high throughput screening of cowpea germplasm conserved in the national gene bank at ICAR-NBPGR, New Delhi, for identifying traits specific germplasm and selecting desirable chemotypes.

**Keywords:** Cowpea, NIR, Prediction model, Trait specific Germplasm

**131 (P-131)**

### **Agro-morphological characterization of proso millet germplasm**

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Proso millet (*Panicum miliaceum*) is one of the oldest crops domesticated by humankind. In India, proso millet is cultivated in Tamil Nadu, Maharashtra, Karnataka, Andhra Pradesh, Bihar, Madhya Pradesh and Uttar Pradesh in 0.41 lakh hectares, producing 0.22 lakh tonnes of grains. Due to presence of higher protein content, antioxidants and beneficial secondary metabolites in the grains, it is increasingly becoming part of healthy diets. Proso millet can be harvested just in 60-65 days therefore can fit into any major cropping system. The lack of information on characterization of proso millet accession for yield and agronomic and quality traits limit its use and utility. In this study, 634 proso millet accessions were characterized for agronomic traits to identify trait specific germplasm. The data were recorded on 11 quantitative traits viz., number of basal tillers, days to 50% flowering (days), flag leaf bladelength (cm), flag leaf blade width (cm), peduncle length (cm), panicle length (cm), panicle width (cm), plant height (cm), days to maturity (days), grain yield (g/plan) and 100-seed weight (g) as per descriptors developed. The data was subjected to Shannon–Waver diversity index and principal component analysis (PCA). The first three PCs explained 60% of the variation in the germplasm. The variable loading plot of PCA showed that the days to flowering, days to maturity and panicle width have relatively less correlation with other yield related traits. Grain yield, plant height and panicle length were having greater contribution to PC1 while, days to flowering and maturity were contributing greatly to PC2. 21 acc. were identified



with multi-trait specific germplasm for 3-6 traits. The identified multiple trait donor germplasm may act as potential trait donors for use in proso millet improvement programmes.

**Keywords:** Agro-morphological characterization, Germplasm, Proso millet, Shannon-Weaver diversity index

### **132(P-132)**

#### **Agro-morphological diversity of barnyard millet germplasm**

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Millets due to their inherent climate resilience and rich in micro nutrients makes them the most sought-after health foods. In the present study a set of 515 genebank accessions of barnyard millet [*Echinochloa frumentacea* (Roxb.)] were characterized for agro-morphological traits using augmented block design. The data on eleven quantitative traits were subjected to ANOVA followed by Principal component analysis (PCA) to study the diversity and group the genotypes based on PCA. Descriptive statistics and ANOVA indicated presence of wide range of variability. The Shannon diversity index revealed that 100-seed weight was having a maximum value of 8.12. The PCA results indicated that, the first four principal components together explained 60.1 % of the variation and individually the variations in PC1 (29.4 %), PC2 (11.4%), PC3 (10.1 %) and PC4 (9.2 %) was also observed. Days to 50% flowering (days), flag leaf blade length (cm), flag leaf blade width (cm), peduncle length (cm), panicle length (cm) and panicle width (cm) were the important traits contributing to the PC1. Grain yield (g/plant) and 100-seed weight (g) along with panicle length, panicle width, number of basal tillers were contributing maximum to the PC2. The grouping of principal components based on state of origin indicated that the accessions from Karnataka and Tamil Nadu may be selected for improvement of yield attributing traits whereas, the accessions from state of Andhra Pradesh had higher number of basal tillers. The study also identified several superior accessions which could serve as trait donors for important traits.

**Keywords:** Agro-morphological characterization, Germplasm, Barnyard millet, Shannon-Weaver diversity index

### **133(P-133)**

#### **Identification of trait-specific multi-whorled finger millet [*Eleusine coracana* (L.) Gaertn.] accessions**

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Finger millet or ragi (*Eleusine coracana* L. Gaertn.), being healthy grain rich in calcium is the most important crop among small millets and other cereals. High yielding varieties having more stability in performance and wider range of adaptability over the environments are necessary for sustaining the production levels in finger millet crop. Environment plays a vital role in exploiting the genetic potential of the genotype to the maximum extent. In this study, a multi-location evaluation of stability and genotype x environmental interaction of 57 accessions of multi-whorled finger millet germplasm was conducted during Kharif 2021. The experiment was conducted in randomized complete block design at five locations under AICRP on small millets. Data on eight quantitative traits viz., days to 50% flowering (days), days to maturity (days), number of basal tillers (number), plant height (cm), finger number (cm), finger length (cm), grain yield (kg ha<sup>-1</sup>) and fodder yield (kg ha<sup>-1</sup>) were recorded. The data was subjected to genotype plus genotype-by-environment (GGE) analysis to identify stable genotypes across locations. The results indicated that, wide variability was observed among the germplasm for all the grain yield and related traits. From GGE biplots, the 1st two principal components captured 64.8 % of the total variation as explained by the genotypes. The accessions IC0473493, IC0474052, IC 0478766 were identified as stable genotypes with higher grain yield as they recorded shorter vector length. The polygon view of the GGE biplot helped identify location specific adapted accessions. The discrimination vs representativeness view of GGE biplot showed that, Bengaluru followed by Athiyandal are most representative locations whereas Vizianagaram was the least representative centre for grain yield. The identified stable germplasm accessions for grain yield and other traits maybe directly evaluated further for release as cultivars or may act as potential trait donors for use in hybridization programmes.

**Keywords:** Finger millet, Germplasm characterization, GGE biplot, Multi-whorled, Multi-location evaluation

**134(P-134)**

### **Morpho-physiological phenotyping of fifteen different local rice cultivars and its partial grain quality assessment related to nutrition**

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Rice is accepted as main nutritious staple food among all cereals. Early vigor is important for crop establishment in rice. It depends on several physiological traits such as chlorophyll content, carotenoids, etc. As a C3 group of plants various cytosolic as well as mitochondrial metabolic enzymes (malate dehydrogenase and succinate dehydrogenase) play vital role in seedling establishment and further growth. For better adaptability, plant accumulate certain stress related compound like proline. Considering the grain quality along with protein rice grain contain certain essential micronutrients like vitamins. Considering the anti-oxidant capability, phenolic compounds are non-enzymatic anti-oxidant that are present in significant amount within rice plant. Alpha amylase is the main



NCPGRM

enzyme that hydrolyses the storage carbohydrates (in form of starch) during seed germination and seedling establishment. The present study was conducted following (1) UV-Vis spectrophotometric estimation of (a) chlorophyll & carotenoid (Arnon 1973), (b) protein content – BSA (Lowry et. al. 1951), (c) reducing sugar – (Miller et. al. 1972), (d) proline content – (Bates et. al. 1973), (e) total phenol content – (Malick1980); (2) enzyme activity determination following (a) succinate dehydrogenase- (Kun et. al. 1949), (b) Malate dehydrogenase- (Yue et. al. 1966); (3) alpha-amylase activity measurement (Xie et. al 2007); and (4) anti-oxidant – free radical scavenging capability using DPPH. Different cultivars responded differently to various metabolic enzymes. These enzymes are strongly linked to their better seedling establishment and plant vigor. By estimating the activity of enzyme alpha-amylase, can conclude the utilization capacity of storage carbohydrate starch by specific cultivar. Estimation of grain micronutrients shows the comparative nutritional quality of different local rice cultivars.

**Keywords:** Alpha-amylase, Morpho-physiological, Phenotyping, Landraces, Rice

### 135 (P-135)

#### **Assessment of genetic diversity in wild bean (*Vigna vexillata* (L.) A. Rich) germplasm accessions using SSR markers**

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*Vigna vexillata* (L.) A. Rich, a member of Fabaceae family is commonly known as wild bean, zombie pea or tuber cowpea. Tubers and seed of wild bean are mainly consumed due to its high protein and fibre contents. Wild bean is known to be tolerant for several abiotic stresses such as salinity, drought, waterlogged conditions as well as for biotic stress including viral diseases and insect pests. Being a wild relative of cowpea (*Vigna unguiculata*), it is potential source genes for biotic and abiotic stress tolerance for genetic enhancement of cowpea. National genebank (NGB) conserves diverse accessions of wild bean, however, the molecular genetic diversity and population structure is largely unknown. In present paper, cross species transferability of cowpea using SSRs was studied on wild bean accessions. All the 21 studied cowpea SSR showed amplification of expected size in wild bean accessions. These 21 SSRs were then used to study genetic diversity of 25 wild bean accessions. A total of 39 alleles were observed across 21 SSR loci. Cluster analysis based on SSR dissimilarity matrix showed 3 clusters with 9 accessions each in two clusters and 6 accessions in 3rd cluster, whereas two accessions were outliers. The genetic population structure of 25 wild bean accessions was studied based on SSR data of 21 loci using a model-based programme STRUCTURE. The number of distinct populations based on maximum Delta K value was 3(K = 3) which was in congruence with phylogenetic



analysis. Number of effective allele ( $N_e$ ) and the Shannon's information Index ( $I$ ) were in range of 1.187 to 1.313 and 0.186 to 0.256, respectively. The effective heterozygosity ( $H_e$ ) ranged from 0.120 to 0.157 in different populations. This study gave an insight into genetic diversity and structure for wild bean accessions in NGB.

**Keywords:** Wild bean, Tuber cowpea, SSR, Genetic diversity, National Genebank

### 136 (P-136)

#### **Genetic dissection of test seed weight (TSW) in linseed (*Linum usitatissimum* L.) using multi-locus genome wide association study**

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Linseed is an important oilseed crop having application in the food, nutraceutical and paint industry. India ranks seventh in terms of production and eleventh in terms of export and its seed productivity is far below the world average. Test seed weight (TSW) is one of the most crucial determinants of seed yield in linseed. Here, quantitative trait nucleotides (QTNs) associated with test seed weight (thousand seed weight) have been identified using multi-locus Genome Wide Association Study (ML-GWAS). Field evaluation was carried out in five environments in multi-year, multi-location trial at New Delhi (28°38'53.7"N 77°09'05.4"E) for three *rabi* seasons (2017-18: DL17-18; 2018-19: DL18-19 and 2019-20: DL19-20) and at Akola (20°42'03.2"N 77°01'53.6"E) for two *rabi* seasons (2018-19: AK18-19 and 2019-20: AK19-20). SNP genotyping information of the AM panel of 131 accessions with 68,925 SNPs were employed for ML-GWAS. Six ML-GWAS methods: FASTmrEMMA, FASTmrMLM, ISIS EM-BLASSO, mrMLM, and pLARmEB were employed for detection of QTNs. ML-GWAS identified total 84 unique significant QTNs for 1000-seed weight trait. QTNs identified in  $\geq 2$  methods/environments were considered as stable QTNs. Accordingly, 30 QTNs have been identified stable for TSW explaining up to 38.65% variation. Alleles with positive effect on trait were analyzed for 12 strong QTNs with  $r^2 \geq 10.00$  showing significant association of specific allele 3 or more environments. Putative candidate genes have been identified for TSW which included *SUMO-activating enzyme*, *Protein EMBRYO DEFECTIVE 2764*, *Protein SHOOT GRAVITROPISM 1* and *Peroxidase 6*. *In silico* gene expression analysis of putative candidate genes was performed to validate their possible role in different stages of seed development. The results from this study provide a new insight and elevate our understanding on genetic architecture of TSW trait in linseed.

**Keywords:** Multi-locus GWAS, Test seed weight, Linseed

### 137 (P-137)



## **Loquat (*Eriobotrya japonica*): dwindling fruit of northern and western plains of India**

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Loquat (*Eriobotrya japonica* Lindl.), a common minor fruit of north-west India was introduced as an ornamental tree from China and Japan. Loquat fruit is low in sodium and high in vitamin A, vitamin B6, dietary fiber, potassium, and manganese. About 6-8 wild species of *Eriobotrya* (now changed name of genus is *Rhaphiolepis*) namely *E. salwinensis*, *E. elliptica*, *E. longifolia*, *E. hookeriana* etc. distributed in eastern and north-eastern parts of India. Loquat generally grows in cooler region of China but is well adapted to warm climate of Indian, mainly in northern and western plains of Himachal Pradesh, Haryana, Jammu & Kashmir, Punjab, Uttar Pradesh and Tarai region of Uttarakhand. A survey in 12 districts of abovementioned states during April 2021 indicated present status of diversity of loquat. Besides farmer's orchards, Field Genebanks of State & Horticultural Departments, and Haryana & Punjab Agricultural University were also surveyed. Survey revealed that pure stands of loquat were used to maintain 20 years back but now it is planted in mixed orchard only. Presently, it has been observed that due to high return by annual crops, agricultural extension and urbanization, a lot of orchards are depleting at alarming rate. During survey, 53 loquat growing sites/orchards were visited and data recorded on availability of various varieties/cultivars being grown since last several decades. In this survey, 22 cultivars/varieties namely *Surkha yellow*, *Goal Surkha*, *Safeda*, *Pahadi*, *Talheta*, *Lamba Surkha*, *Chini gola red*, *Orange red*, *Saharanpur special*, *California*, *Tanaka*, *Golden yellow*, *Japani*, *Kathiya*, *Dum dum*, *Benzir*, *Californai advance*, *Japanigola*, and *Deshi* were recorded. Most of the orchards were dominated by *Surkha yellow* variety followed by *Goal Surkha*, *Safeda*, *Pahadi*, and *Talheta*. The substantial variability was observed in fruit colour, fruit shape, pulp colour, taste, fruit weight, fruit length and width. The new plantations were observed mostly in orchards located in Shamli, Saharanpur and Meerut (UP), but its area is depleting in Haryana, J&K, Punjab, Himachal Pradesh and Uttarakhand even existing orchards are being replaced by other crops. Therefore, there is an urgent need to collect and conserve the genetic diversity of this important minor fruit using complimentary conservation strategy in the Field genebanks and cryogenebanks.

**Keywords:** Loquat, Variability, Genetic diversity, Field genebanks

**138 (0-28)**

## **Local vegetables of Manipur: bioprospecting aspects and need for germplasm conservation**

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Manipur also known as the Jewel of India is situated in the North East region of India. It is situated in Indo-Burma region which is one amongst the four hotspots of the world located in India. The topography and climatic zones with diverse eco-systems and uneven rainfall pattern has endowed Manipur with a rich flora and fauna. There are many cultivated and wild vegetables used in this region which are not so familiar to the rest of the world. The local people have been using these bioresources for their survival and as healing herbs since ages. These vegetables are also cooked at home for local ailments and to improve immunity. The local Amaiba and Amaibis (the male and female local healers) use these plants for preparing various admixtures to cure different ailments and this traditional knowledge had been carried from generation to generation. Further, due to advent of modern medicine system people avoid to visit these local healers, therefore jeopardizing their livelihood opportunity, posing a threat to the existence of this traditional knowledge. Furthermore, rapid urbanization has taken its toll on biodiversity and therefore compromising the availability of wild vegetables for the local people. So, it is warranted to identify and develop inventory of the vegetables used by different ethnic communities of Manipur and conservation efforts of these germplasm should be promoted. As these plants have good bioprospecting aspects, it can be used for the upliftment of the local people and at the same time conservation of germplasm for future use.

**Keywords:** Biodiversity, Bioprospecting, Healing herbs, Wild vegetables, Ethnic communities, Traditional knowledge

**139 (0-06)**

### **Survey and collection of plant genetic resources from Andaman & Nicobar Islands representing Indo-Burma and Sundaland biodiversity hotspots**

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Andaman and Nicobar Islands form a part of two out of 36 world's mega biodiversity hotspots - the Indo-Burma and Sundaland, respectively, and assume greater significance for ex-situ agrobiodiversity conservation, as they hold unique flora of PGR importance which are largely unavailable in the genebanks elsewhere. Considering this, five well-planned explorations (2017-20) spanning over 70 field days were undertaken involving a multi-disciplinary team from ICAR-NBPGR, ICAR-CIARI, Port Blair and ICAR-IISR, Kozhikode. A total of 773 samples (wild-491; cultivated-282) consisting of 292 taxa (wild-216; cultivated-76) were collected primarily from diversity-rich areas like the Great Nicobar Biosphere Reserve and Nancowrie group of Islands in Nicobar, and Mt.



Manipur (Mt. Harriet), Rutland, Chidya Tapu, Little Andaman, Swaraj Dweep, Saddle Peak and Ross & Smith Islands in Andaman. Crop groups of vegetables (incl. tubers; 175 acc; 54 taxa), fruits (168; 55), spices (134; 40), medicinal and aromatic plants (114; 39) and other economically important plants (109; 72) predominated the collection. Eighty-three crop wild relatives (270 acc.) were assembled, which includes rich species diversity in *Vigna* (10 taxa), *Dioscorea* (9), *Curcuma* (8), *Piper* (8), *Solanum* (8), *Artocarpus* (7), *Citrus* (7), *Zingiber* (7), *Syzygium* (6), *Garcinia* (5) and *Musa* (5). Salient collections include semi-domesticates worth recruiting as future crops (e.g., *Alpinia nigra*, *Curcuma roscoeana*, *Garcinia speciosa*, *Gnetum gnemon*, *Macaranga nicobarica*, *Nypa fruticans*, *Pandanus leram*), progenitor/primitive form of sponge/ridge gourd, ash-gourd, and brinjal, variability in horticultural crops (citrus, taro, greater yam), *Oryza meyeriana* var. *indandamanica* (very rare and restricted to Andaman), and trait-specific germplasm (e.g., flowering betel leaf, rhizome weevil and fusarium wilt-resistant wild banana). Out of 292 taxa collected, 200 were collected for the first time from these islands, while 83 are distributed only in A&N Islands in the country, including 34 taxa strictly endemic to these islands. Further, potential areas for future explorations are identified.

**Keywords:** Agro-biodiversity, Crop wild relatives, Germplasm, Indo-Burma biodiversity hotspot, Sundaland biodiversity hotspot

## 140 (0-26)

### **G-DIRT: A germplasm duplicate identification tool based on identity-by-state analysis using SNP genotyping data**

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Identifying redundancies within and among germplasm collections has long been recognized as one of the key challenges of genebank management. The duplicate germplasms add to the cost of germplasm conservation by requiring huge financial and mechanical resources. Besides, genome-wide association studies with over-represented germplasms can be biased resulting in spurious marker-trait associations. The removal of duplicate germplasms using passport and phenotypic information is often associated with incomplete or missing passport information and data handling errors. However, this is less likely in the case of genotypic data. Therefore, G-DIRT has been developed to allow germplasm duplicate identification based on identity-by-state analysis using SNP genotyping data along with its pre-processing. We determined a homozygous genotypic difference threshold of 0.1% for germplasm duplicates for tetraploid wheat using SNP genotyping data with 94.97% of accuracy. Based on the genotypic difference, the tool constructs a dendrogram to visually depict the relationship between genotypes. The G-DIRT is believed to assist the genebank curators, breeders and other researchers across



the world in identifying germplasm duplicates from the global genebank collections by only using the easily sharable genotypic data instead of physical exchange of the seeds or propagating materials. The developed tool will complement the existing methods of germplasm duplicate identification based on passport or phenotypic information being freely available at <http://webtools.nbpgr.ernet.in/gdirt/>.

**Keywords:** GWAS, Identity-by-state, Duplicate identification, Genotype, Germplasm conservation, Genebank

#### 141 (P-141)

#### **Redundancy assessment for management of genebank collections- a case study in maize**

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The National genebank at ICAR-National Bureau of Plant Genetic Resources conserves one of the largest collections of maize germplasm, which comprises of indigenous maize diversity collected from throughout the country. A major collection is from the northeastern hill region, from where recent exploration missions have added large number of populations with unknown identity. The large collection size of such populations hamper their effective utilization since in maize, concerted efforts are required to address the genetic bottlenecks of trait introgression. Hence, the present study was undertaken to assess the extent of redundancy, through use of passport data, morphological data and molecular characterization data, in a selected set of 24 maize populations collected from four northern districts of Mizoram. The experiments involved 30 morphological descriptors and 93 microsatellite markers for an extensive analysis of multiple parameters. The analysis could identify redundant sets within genetic clusters, through integration of geographic, morphological and molecular data and from within 24 accessions, 16 accessions were marked for bulking, which would bring down the conservation size from 24 accessions to 14 accessions. The study also proposed an exploration strategy for mimban maize populations, which would enable their cost effective conservation and utilization i.e. within a district, samples collected from comparable altitude, having synchronized flowering behaviour and similar cob characteristics, should be pooled and submitted as single accession with recommended seed quantity. Further, application of this information in maize populations from other regions and also in other crop groups that are conserved in NGB, is envisaged.

**Keywords:** Maize germplasm, Accessions, Morphological and molecular data, Microsatellite markers

#### 142 (O-18)



## **Cryoconservation of shoot tips of *Swertia chirayita* (Roxb.) H. Karst., a critically endangered medicinal plant of India**

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*Swertia chirayita* (Roxb.) H. Karst. is a critically endangered medicinal plant species of India and is one among the 32 most highly prioritized medicinal plants of India as identified by The National Medicinal Plant Board, Government of India. It has high medicinal properties viz., antibacterial, antifungal, antiviral, anticancer, anti-inflammatory, antidiabetic and antioxidant. Two accessions of this valuable plant are conserved in the *In Vitro* Gene bank of Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi, India. Shoot tips (about 1 to 1.5 mm in length) were excised from 4-wk-old stock cultures pre-grown on Murashige and Skoog (MS) medium supplemented with 3 mg/l Kinetin, 2 mg/l Gibberellic acid, 0.3 M sucrose and shoot tips were precultured on MS + 0.3 M sucrose for 2 days. Thereafter, shoot tips were dehydrated with Plant Vitrification Solution 2 (PVS2) (10 to 40 min) and cryoconserved using vitrification and droplet-vitrification (DV) technique. Shoot tips subjected to PVS2 solution for 20 min reported high post-thaw regeneration using DV (44.44 %) in comparison to 21.67 % using V. Thus, standardized droplet-vitrification technique can be used for long-term conservation of *S. chirayita* germplasm.

**Keywords:** Cryoconservation, Endangered medicinal, PVS2

**143 (P-143)**

## ***In vitro* propagation and conservation of *Allium schoenoprasum* L. - an underutilized high value species at *in vitro* genebank, ICAR-NBPGR, New Delhi**

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*Allium schoenoprasum* L. is the smallest edible member of the *Allium* genus belongs to the family Amaryllidaceae and subfamily Allioideae. The name 'schoenoprasum' derived from the Greek words *skhonos* means grass and *prason* (fruit) means leek and the word Chive derived from the French word *cive* which is derived from the Latin word *cepa*, which signifies onion. It is used as substitute for onion and garlic and has insect repellent,



therapeutic and antioxidant properties. As this species mostly propagated through vegetatively and present in wild and grown in kitchen garden and, present in localized area of Himalayan region and still under sporadic cultivation. Hence, it is utmost important to conserve this species *in vitro*. Healthy bulbs (IC0645159) were treated with Tween-20, 70 % ethanol, 1.0% cetrinide + 0.1 % streptomycin + 0.5 % bavistin and 0.1 % HgCl<sub>2</sub> for different time interval for establishment of aseptic cultures. 0.1 % HgCl<sub>2</sub> for 15 minutes was found effective and > 90 % the culture were healthy, free from bacterial and fungal contamination and had normal growth. Experiments were conducted to induce multiple shoots on MS medium with different concentrations of NAA, BAP, 2iP and Kn (0 - 3.0 mg/l) alone or in combination. Among the tested 35 media combinations, highest number of shoots *i.e.* 5.5 shoots/explant were observed on MS medium supplemented with BAP (0.5 mg/l) + NAA (0.1 mg/l) with 30 g/l sucrose. Among the different media tested, subculture duration was 4 months on MS + BAP (0.5 mg/L) + NAA (0.1 mg/L) and 6 months on MS basal media. *In vitro* rooting was obtained on MS + NAA (0.1 mg/L) + 2iP (0.02 mg/L) and the rooted plantlets were successfully established *ex vitro* (50%).

**Keywords:** *Allium schoenoprasum*, *In vitro*, Genebank, Chive, Germplasm

#### 144 (P-144)

#### **Breeding durable root & stem rot (*MacrophominaPhaseolina*) resistant sesame genotypes**

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Developing and deploying of resistant varieties is an economic, eco-friendly and hassle free tool to keep diseases. However, resistance does not last long and frequently succumbs to the changes and shift in pathogen. The plant pathogens and pests are dynamic and keep on changing to counter the introgressed resistance. Host and pathogen evolve hand in hand and result in boom and bust cycle followed by susceptibility of a plant variety. Therefore, breeding for resistance has to be a continuous process. In this context we have identified resistant sesame genotypes against Root & Stem rot (*MacrophominaPhaseolina*). Sesame (*Sesamum indicum* L.) is one of the world's oldest oilseed crops and has been cultivated in Asia since ancient times and largely produced for its oil and is also used as a flavoring agent. The seeds of sesame contain 40 to 53 percent oil, which contains significant amount of oleic and linoleic acids. It plays an important role in the oil seed economy throughout the world. The fungal disease Root & Stem rot (*Macrophomina phaseolina* (Tassi) Goid is the most important disease and is widely, distributed in sesame growing region. The pathogen attacks plant at all growth stages. Due to soil borne nature practically no effective field control and no source of resistant is available. Twenty genotypes of different state of India were sown on *kharif* 2020 & 2021 along with local check VRI-1in Randomized block design in two row of 3 meter length and replicated thrice so as to screen for root and stem rot disease under sick



plot and same genotypes were sown in pot house under artificial inoculums. The Two years study *In vivo* & *In vitro* revealed that the genotypes PR21-02, PR10-39, VS16009, VS19023, RT-390, Sel-S-20-2001, Subhra, recorded the root and stem rot incidence less than 10% in both the studied.

**Keywords:** Resistant varieties, *Sesamum indicum*, *Macrophomina phaseolina*

## 145 (P-145)

### Characterization of linseed (*Linum usitatissimum*L.) genotypes for drought tolerance

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The fifty linseed genotypes were evaluated in randomized complete block design with three replications in two environments during *Rabi*, 2020-21. The first environment was normally irrigated but in second environment, the irrigation was withheld for 30 days in between 45 days (pre flowering) to 75 days after sowing to imposed water deficit or stressed or drought condition. The mean data of five randomly selected competitive plants of each genotype for ten quantitative traits under both normal ( $Y_{pi}$ ) and drought ( $Y_{si}$ ) condition were subjected two way analysis of variance while the mean yield data of each genotype under normal ( $Y_{pi}$ ) and drought ( $Y_{si}$ ) condition were used to estimate of five drought tolerant indices viz; Harmonic Mean (HM), Yield Stability Index (YSI), Yield Index (YI), Stress Susceptibility Index (SSI) and Stress Tolerance Index (STI) in order to identify drought tolerant genotypes. The genotypes, GP-1064, GP-955, GP-820, LMS-16-1-2, GP-807 and LMS-17-1-12 were recorded high value of HM, YI and STI and low value of SSI (<1), therefore these genotypes could be identified as tolerant to water stress condition. It is pertinent to reveal that the yield of each genotype equal or above the mean yield of respective normal and stress condition should be considered while ranking and classifying the genotypes on the basis of drought indices. The results also suggested that number of capsules per plant, number of seeds per capsule and biological yield per plant were characters with high consistency in both the tolerant and susceptible groups and environments. Therefore, selection of suitable genotypes considering these traits along with their yield performance may be useful when breeding for broad adaptation of linseed for cultivation under drought conditions.

**Keywords:** Linseed, Yield stability index, Yield index

## 146 (P-146)

### Studies on molecular characterization of kokum (*Garcinia indica* Choisy) genotypes under hill zone of Karnataka



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An experiment was carried out at the farmer's field, located near Sirsi taluk, Uttara Kannada district of Karnataka where about 10 years old 47 uniformly grown kokum trees were randomly selected for the experiment. Out of which, 36 nos. were red fruiting and 11 nos. were of yellow fruiting types. Data on different morphological, yield and quality were collected for three consecutive years from 2016-17 to 2018-19. Estimated genetic variability recorded maximum values of heritability for morphological characters. All the genotypes were grouped into five clusters through D<sup>2</sup> analysis. The inter-cluster values ranged from 1.23 (cluster III and IV) to 951.30 (II and IV) for morphological characters. Whereas, it was ranged from 7.42 (cluster I and III) to 30.13 (cluster III and cluster IV) for biochemical characters which indicated that crosses between the clusters would result in better recombinants. Based on the morphological characters 28 genotypes were selected for the molecular characterization. Amplified markers bands were ranging in size from 140 bp to 1000 bp. Dendrogram based on Euclidean distances obtained from the cluster analysis revealed one major cluster, cluster II with three genotypes and cluster I with two genotypes. Cluster II was sub-divided into two sub-clusters (cluster IIa and cluster IIb). Clusters I included two genotypes GI-01 and GI-03. The second cluster comprised of two sub clusters (cluster IIa and cluster IIb). Sub-cluster, cluster IIa consisted of genotype GI-07 (Y) and IIb consisted of genotypes GI-05 and GI-06 (Y). Cluster III was sub-divided into 17 sub-clusters which constituted of genotypes GI-09, GI-10, GI-14 (Y), GI-15 (Y), GI-23, GI-24, GI-25 (Y), GI-28, GI-31, GI-39, GI-47, GI-37, GI-38 (Y), GI-18 (Y), GI-32, GI-43, GI-44, GI-12, GI-13, GI-08 (Y), GI-11, GI-33 and GI-35. The present study distinguished the selected genotypes into different groups. Among the 28 genotypes polymorphism was observed for 18 of the SSR primers, whereas two were monomorphic.

**Keywords:** Garcinia, Morphological and molecular characterization, D<sup>2</sup> analysis

**147 (P-147)**

**Identification of novel soil salinity tolerance resources in an international barley panel based on field seed germination response**

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Soil salinity is one of the major abiotic stresses affecting crop production globally with an estimate of approximately 20% of the total arable land being affected to some degree. Barley (*Hordeum vulgare*) is considered as one among the most salt tolerant crops tolerating salinity levels of upto 25 dS/m. Therefore, the systematic breeding of the salinity tolerant improved varieties needs immediate attention as the area under salinity in the country is on constant rise. In the present study, the germination response of 320



diverse barley genotypes from ICARDA with different geographical origin, was evaluated to identify salt tolerant genetic resources. The experiment was conducted in a saline field with the 8.33 pH and 13.33 dS/mEC. The germination percentage ranged from 0 to 100%, indicating presence of high genetic diversity for salinity tolerance in the germplasm panel under investigation. The maximum number of genotypes (50) exhibited a germination percentage of 30 % followed by 49 genotypes exhibiting 20% germination. Thirty (30) genotypes failed to germinate, while 38 genotypes exhibited a germination percentage of 10 %. However, four genotypes achieved 100% germination percentage with another 32 genotypes ranging from 70 to 90%. The genotypes with  $\geq 70\%$  germination percentage can be considered as useful resources for inclusion in the soil salinity tolerant barley breeding programme of the country.

**Keywords:** Barley, Genotype, Germination percentage

### 148 (P-148)

#### **Plant Breeder's Rights in India and neighbouring countries: Status, challenges and opportunities**

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Mandated by TRIPS, India and many neighbouring countries such as Philippines, Thailand, Vietnam, Malaysia and Indonesia developed a sui generis system for protection of plant variety or adopted UPOV PBR regime and many countries are yet to implement PVP laws i.e. Pakistan, Nepal and Bangladesh. The paper also examines similarities and differences in the various PVP regimes by analysing relevant provisions i.e. material (hybrid Vs Parent) and species eligible for protection, registration process, rights, opposition, compulsory licensing etc existing in text of law. It also provides a results in form of comparison of various aspects and also registrations in various countries by private and other players in crops like rice and corn. This paper aims to examine the laws of India and neighbouring countries by highlighting challenges and suggesting some possible solutions to strengthen agriculture ecosystem.

**Keywords:** PPV & FRA 2001, Period of protection, Opposition, Compulsory license, UPOV, Sui-generis system

### 149 (P-149)

#### **Agro-morphological characterization of fifty local rice varieties (*Oryza sativa* L.) and analysis of caryopsis ultrastructure by using scanning electron microscope**

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The rice germplasm (50 cultivars) were collected from different regions of Sikkim and North Bengal, and were characterized based on qualitative and quantitative agromorphological descriptors. The fifty rice varieties were characterized by using the DUS (Distinctiveness, uniformity stability) protocol such as vegetative data (anthocyanin pigmentation, coleoptile colour), reproductive data (colour of stigma, attitude of flag leaf), along with grain quality traits: length of grain and kernel, width of grain and kernel, 1000 grain weight, grain number, panicle length etc, and analysis of caryopsis ultrastructure is done by using scanning electron microscope. Highest grain weight was found in cultivar Anandi (30.8 g/1000 seeds) and least grain weight was 7.02 g/1000 seeds) in Konijoha. Maturity time of cultivars Addey (98 days), was found to be very early (<100 days). Grains numbers per panicle were 152 in Kalo-nunia and 145 in Ekley. Grain length varies from 5 mm to 9.7 mm and width varies to 2.0 to 3.0 mm. Among the 50 rice varieties around 10 rice varieties are aromatic rice with mild to strong aroma. Five rice cultivars were with the awn whose length varies from 2 to 5 mm. Kernel colour varies from white to black. Scanning electron microscope, clearly reveal the pericarp layer, then seed coat (testa), aleurone layer and endosperm layer in centripetal manner in transverse cross section of rice grains. In most cultivars, the pericarp and testa were found to be fused whereas, aleurone layer and endosperm were very distinct. Aleurone layer of rice grains are found were four layer (kalonunia), three (Manipuri), two (Ekley) and one (kalodhan). More number of protein bodies were seen rice cultivars (Jallangga, Biringful and Rajmukut) ranging from 0.926  $\mu\text{m}$  to 1.233  $\mu\text{m}$ . These germplasm showed the useful traits that can be used by breeder for crop improvement programme.

**Keywords:** Rice germplasm, Agro-morphological, Characterization, DUS descriptors, SEM.

## 150 (P-150)

### Seedling mango germplasms: the vanishing treasure

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There are huge possibilities to exploit seedling origin mango trees for specific traits like polyembryony, attractive peel colour, suitability as rootstock, pest and disease resistance, tolerance to abiotic stresses, etc. On the other hand, seedling mango trees are vanishing at a faster rate than never before. Identification and conservation of seedling mango germplasm has been carried out at Agriculture Experimental Station, NAU, Paria, Gujarat as a part of research activities under AICRP on fruits. Elite germplasms having traits with horticultural importance have been identified and their conservation work has been carried out. There are some practical problems associated with the identification and conservation of elite seedling mango germplasms. One of the major reasons is, fruits of seedling mango trees get very less market price as compared with the commercial mango varieties. Many seedling mango trees bear fruits which have good eating qualities, but they hardly get a fair price in market. Another major reason is, there are few scientists



working on conservation of seedling mango germplasm because it needs many years to conserve and its utilization at a commercial scale which makes it unattractive in terms of academic benefits. Moreover, there is only a month of time for survey work during fruit maturation period. Limitations of travelling to the far distances from the work place makes the survey work even more difficult. Normally seedling mango trees are unique and only single tree is available. That makes them very vulnerable because many a times such trees get vanished due to pest-disease problem, cutting of trees for wood, conversion into commercial mango variety, to create a space for commercial plantation, etc. There are needs to find out different non-conventional ways to conserve seedling mango germplasms for better future.

**Keywords:** Mango germplasm, Vulnerable, Conservation.

**151 (P-151)**

### ***In-situ* conservation of seedling mango germplasm**

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Identification, collection and conservation of seedling mango germplasms in field gene bank is tedious, time consuming and long term process which also require dedication of the persons involved in the work. It requires large piece of land which again needs continuous maintenance and care. Moreover, field gene bank can accommodate only a limited number of germplasm due to large tree size, scarcity of land, higher cost of maintenance, etc. Alternatively, *in-situ* conservation of seedling mango germplasm on farmers' field should be encouraged as a farmer centric tool for solving the problems associated with germplasm conservation in field gene bank. The risk of loss of germplasm at farmers' field will be higher but one can conserve much higher number of germplasms at *in-situ* level as compared with the traditional field gene banks. Marking of selected elite trees with indication of name of owners and institute can create awareness for conservation of seedling origin mango germplasm. Technological tools like GPS chip can be utilized for tracking of such trees whenever required. There are possibilities to encourage farmers in germplasm conservation by giving credit to their efforts and provision of socio-economic benefits.

**Keywords:** Collection, Conservation, Mango germplasm, Traditional field genebanks

**152 (P-152)**

### **Digitization of ICAR-NBPGR Plant diversity using Mobile App with QR code**

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In modern digital era, “Urban forestry” is an upcoming thrust area taking up massive drive for tree plantation in cities and towns across the country to develop an urban jungle to plant trees. Multiple benefits of the trees to enhance quality of environment, adding beauty and conserving biodiversity are well known. In this direction, ICAR-NBPGR has taken initiative to create Mobile application ‘NBPGR Plant Diversity’ and QR codes that contain total of 102 species – trees, herbs and perennial herbs in all the premises of ICAR-NBPGR, Delhi. Some significant trees - *Morindacitrifolia*, *Feronia limonia* Swingle, *Phyllanthus emblica* L, *Terminalia arjuna* (Roxb. ex DC.), *Cycas revoluta*, *Thuja occidentalis* have been included; common ornamentals are also included. The diversity of perennials represented in the ICAR-NBPGR campus would facilitate enhanced knowledge by creating awareness on inventorying of plants in the form of check-list with the botanical name and detailed notes, besides sensitizing staff, students and visitors. Mobile application and each QR code contains plant details like Botanical name, family, common name, native place, their use and location. It is freely hand handled App which works offline and standalone manner with 9 M.B. size after installation. This application was developed on android platform which supports android version 4.1(API 16) to version 10.0(API 30) smartphones which covered around 98% android users with using offline inbuilt SQLite DB, Core Java program code in Android Studio Platform. ICAR-NBPGR-Plant Diversity application developed in Android studio also provides a unified environment where it is possible to build for Android phones, tablets, Android Wear, Android TV, and Android Auto. Presently found very useful and effective, not only saves time but reduce chances of error and is more reliable. Further modifications as suggested by the users have been included after validation. Creating awareness amongst the type of explorers are expected to yield dividends in the era of ‘Digital India’.

**Keywords:** Mobile application, Android platform, Checklist, Users

### 153 (P-153)

#### **Potential fruit resources of Indian arid and semi-arid regions: Augmentation, evaluation and conservation strategies**

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The arid zone of India covers about 12% of its geographical area. Major constraints of habitants are less and erratic rainfall ( $\leq 420$  mm/year), high temperature ( $46^{\circ}\text{C}$ ) poor soil fertility and high wind flow during summer season. Indian population is increasing rapidly (1.38 billion) and to provide people stable, safe and nutritious quality food with a meager 2.4% of the world surface area is the greatest challenge. Hence, it is essential to popularize and conserve the indigenous horticultural resources such as Ber (*Ziziphus mauritiana*), Aonla (*Emblica officinalis*), Bael (*Aegle marmelos*), Mulberry (*Morus alba*), Phalsa (*Grewia subinaequalis*), Karonda (*Carissa carandus*) Ker (*Caparis decidua*), and Pilu (*Salvadoraoleoides*), etc., for the prosperity and nutritional security of nation. These



fruits resources are rich in vitamins and mineral contents found mostly as wild or semi wild although some has been now domesticated. It is well known fact the horticultural genetic resources of arid areas are precious for human welfare. Therefore, their effective management is crucial for conservation of genetic diversity. Presently, ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), Regional Station Jodhpur, Rajasthan, India had conserved about 453 accessions of horticultural genetic resources of arid and semi-arid origin in its field gene bank. Total 233 accessions of various horticultural crops including Ber (26), Karonda (18), Aonla (41), Phalsa (19), Ker (15), Bael (19) and Jojoba (95) were characterized and evaluated for various quantitative and quality parameters. Some of the superior genotypes identified based on evaluation are in Ber IC625863 with high TSS content (24.2 oB), IC 625864 for high phenol content (256.2 mg/100gm) and IC625848 for higher shelf life while in Ker, IC 103393 found promising in terms of higher fruit weight (13.8gm) and aonla IC644659 promising in term of pink colour retention on shoulder of fruit .

**Keywords:** Arid, Germplasm, FGB, Fruit, Conservation

#### 154 (P-154)

#### **DUS characterization of advanced breeding lines of Linseed (*Linum usitatissimum* L.)**

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One hundred and twenty-one germplasm accessions, 170 accessions of core collection and 242 mutant stocks of linseed were characterized and evaluated at MULLaRP centre, UAS, Dharwad. Among these genotypes, 68 genotypes of linseed were studied for the establishment of the distinctness, for seventeen characters. Characterization for seventeen agro-morphological traits following Distinctness, Uniformity and Stability test (DUS) in the four *rabi* seasons from 2018 to 2021 was done at F block , Main Agricultural Research Station, University of Agricultural Sciences, Dharwad, Karnataka. Out of Sixty-eight accessions studied, fifty per cent of the genotypes showed medium sized corolla, 72 per cent had disc shaped flowers, 50 per cent exhibited medium sized flowers, 80.88 per cent possessed light violet blue coloured corolla. Considering the petal aestivation, 58.82 per cent of the accessions showed semi twisted aestivation followed by 35.29 per cent with valvate aestivation. This study will be useful for breeders, researchers and farmers to identify and choose the restoration and conservation of beneficial genes for crop improvement and also to seek protection under Protection of Plant Varieties and Farmer's Rights Act 2001.

**Keywords:** Germplasm, Linseed, Genetic variability, DUS test

#### 155 (P-155)



## **Exchange and utilization of faba bean (*Vicia faba*) germplasm for yield and yield related traits**

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ICAR-National Bureau of Plant Genetic Resources (NBPGR) being the nodal agency for import and export of seed/ planting material for research purposes has realized the importance of potential crops in general and faba bean (*Vicia faba*) in particular and made efforts for introduction of promising genetic resources from diverse climatic conditions. Over the last decade a total of 1150 accessions of faba bean have been introduced from ICARDA centers Lebanon and Cyprus. Faba bean (*Vicia faba*) also known as broad bean, is an annual crop used both for human consumption and as well as live stock feed. It is mainly grown in hills and northern plains for its protein rich pulse and green pods which are used as vegetable. Faba bean is grown in over 3 million hectares in the world with a total production is over 4.5 million tons. Efforts have been made to evaluate, characterize, conserve and catalogue the genetic resources of faba bean. Improvement for the seed and protein yields are receiving foremost attention in this crop. Hence there is a need to intensify efforts to search for appropriate donors for utilization in the locations specific breeding programmes. In the present paper an attempt has been made to evaluate the genetic resources of a faba bean augmented recently to assess their potential use in varietal development programme for faba bean. Thirty-five faba bean genotypes were assessed for nine agronomic traits against two elite varieties HFB-1 and Vikrant in Augmented Block Design during Rabi 2018-19 and 2019-20 under the multilocation programme of AICRN on potential crops. There was significant difference among the blocks for pod length and 100 seed weight but no difference was observed for days to flowering, days to maturity, plant height, number of pods per plant, number of seed per pod and yield per plant. Among germplasm line, ET218772 (33.81 g), ET218776 (30.78 g), ET218725 (28.69 g), ET218786 (28.29 g) showed highest seed yield per plant as compare to check variety Vikrant (27.62 g).

**Keywords:** Germplasm, Faba bean, Diversity, Potential Crop

**156 (0-15)**

## **Genome-Wide Association study reveals QTLs for plant height in a subset of 3K Rice Genome (RG) panel**

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Rice (*Oryza sativa* L.) is the major source of nutrition for over half of the global population. Growing demand coupled with increasing temperatures creates an urgent need to develop new, high yielding varieties. Plant height is an important agronomic trait related to rice yield and lodging. Several studies have deciphered that plant height in rice is governed by multiple genes and QTLs, however, their genetic mechanisms are not fully elucidated and remains to be explored. In this study, a genome-wide association study (GWAS) was conducted in 198 diverse rice accessions selected from the Rice Genome (RG) panel to identify loci governing plant height in rice. We discovered new seven QTLs designated as qPH1-1, qPH1-2, qPH1-3, qPH2-1, qPH3-1, qPH4-1 and qPH8-1 on chromosomes 1,2,3,4 and 8 and two marker-trait associations (MTAs), (MTA4-1 and MTA6) on chromosome 4 and 6, respectively. Among these QTLs, qPH1-1, qPH2-1, qPH3-1, qPH4-1 and qPH8-1 were potentially colocalized with already known genes such as IAA1, SD1, pH1, OVATE; OsGS1, OsGID2; OsDWARF4, OsTUD1, OsHTD2; OsDWARF4L1, OsTDD1 and OsDOG, respectively. Detailed annotation, association and haplotype analysis of each of the significant loci were also performed to identify the candidate genes and elite alleles affecting plant height. We found that the plant height in rice can be improved by combining the superior haplotypes of different genes. Altogether, our findings potentially have serious implications for functional analysis and genetic improvement of plant height in rice.

**Keywords:** Rice (*Oryza sativa* L.), GWAS, Marker-trait associations, Haplotype, SNP

157 (0-32)

### **Origin of black rice from wild rice (*Oryza rufipogon*) of India - A pre-breeding approach**

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Rice (*Oryza sativa* L.) is an important staple food grain because more than half of the world's population depends on it for their livelihood. Narrow genetic base in released rice varieties has made the improvement in plateaus. Wild rice species, *O. Rufipogon* Griff. is known as an immediate ancestral progenitor of cultivated rice and is a valuable gene pool for the improvement of rice genetic base to break the yield plateaus. There is no black grain colour in wild rice accessions, indicating that black rice pericarp phenotype is a newly acquired trait and incorporated during the time of domestication of the cultivated rice. Black pericarp is predicted mostly to be regulated by three genes- Kala1, Kala 3, and Kala 4. In the present study, we report for the first time in the history of rice breeding that aromatic black rice lines were developed through interspecific hybridization and introgression in the genetic background of *O. sativa* cv. Badshabhog, Chenga and Ranjit. Possible reason may be the rearrangement and insertional mutation at the promoter



region of Kala 4 allele leading to ectopic expression resulting in black rice formation. Gene specific PCR amplification was carried out to detect the presence of Kala 4 locus among the breeding lines. Three different primer pairs were used to amplify the Kala 4 locus which confirms the presence of genetic configuration necessary to develop black pericarp. This is a first report in the history of pre-breeding, that black rice has been developed through wide crossing and introgression of genes (black genes) from wild rice *O. rufipogon*. Based on experimental evidences we propose a new model of black rice origin. Black rice (mainly indica type) of Indian subcontinent originated independently through natural out crossing, gene-flow and artificial selection in the course of domestication from the wild rice of India.

**Keywords:** New model, Black rice, *O. rufipogon*, Prebreeding lines, Kala 4 gene, Acquired trait, Introgression, Domestication, Interspecific gene flow

## 158 (O-10)

### Characterization of linseed germplasm conserved at National Genebank of India and development of core set

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The National Genebank (NGB) at National Bureau of Plant Genetic Resources, New Delhi, conserves the base collection of linseed with around 2800 accessions. The whole collection was characterized for 9 qualitative and 26 quantitative traits during *Rabi* season for four consecutive years (2018-19 to 2021-22) at ICAR-NBPGR farm, ICAR- IARI, New Delhi and for two years (2020-21 and 2021-22) at Akola to assess prevailing diversity and to develop the core set. Wide range of variation was observed for all the recorded traits at both locations. The quantitative trait data from all the six environments were subjected to analysis of variance according to Augmented Randomised Complete Block Design to obtain the adjusted means which along with qualitative and passport data were used for extraction of core set. Initially, five different core sets were derived using Core Hunter 3 software by optimisation of average genetic distances between each accession and nearest entry in the core (A-NE) and the average distance between each entry and nearest neighboring entry (E-NE) employing Gower distance. The core set developed with weightage of E-NE and A-NE in the ratio of 0.7 to 0.3 captured maximum



genetic diversity of the whole collection as evident from the desirable genetic distance, variance difference percentage (VD; 80%), coincidence rate of range (CR; 91.72%) and variable rate of coefficient of variance (VR; 117.63%), which were more than threshold value of VD (80%), CR (80%), and VR (100%) required for good core collection. The coefficient of variation and Shannon–Weaver diversity indices were increased in the core set as compared with the whole collection. Correlogram revealed that trait associations and their magnitude were conserved for most of the traits after sampling of the core set. The development of linseed core set will pave the way for expedited access to genetically diverse and agronomically important germplasm for breeding.

**Keywords:** Characterization, Core set, Diversity, Genebank, Linseed germplasm

**0159 (P-159)**

**Characterization of rice landraces using high density rice 80K SNP array**

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Rice landraces are essential genetic resources which can play a prominent role in food security as they possess valuable biotic, abiotic and nutritional traits. Replacement of local varieties by modern varieties results in genetic erosion. The functionality of the Single Nucleotide Polymorphism (SNP) markers in demonstrating the genomic structure of rice landraces can provide an insight into conservation, management and utilization of rice germplasm. SNP array technology provides efficient method to analyze the genotypes of multiple loci in the whole genome scale. Among the rice SNP arrays, 80K chip is a pan-genome based, which can identify genetic variations from both core as well as dispensable genome. Here, we report the characterization of 186 rice landraces using 80K chip resulting in 64,873 quality filtered SNPs including 48,796 SNPs (~75%) from 12 Nipponbare chromosomes and 16,077 SNP (~25%) from 12 pseudo chromosomes of 3K rice pan-genome. Polymorphism Information Content and Minor Allele Frequency observed in a range from 0.09 to 0.38 and 0.05 to 0.5 with a scoring mean of 0.28 and 0.25 across genome respectively. Estimated Nei's genetic diversity index is 0.35 signifying high genetic variation within the population. Population structure and principal component analysis resulted in two subpopulations. Phylogenetic analysis showed clustering of landraces irrespective of their geographical origin. Understanding the genetic diversity level and genetic structure of rice landraces populations may help in its utilization in genome wide association studies and marker assisted selection in rice breeding programs.

**Keywords:** Single Nucleotide Polymorphism, Array technology, Phylogenetic analysis



## 160 (P-160)

### **Genomics to genes: Forward and reverse genetics in pulses for nutritional security**

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Since 2013, ICAR has been instrumental in augmenting the genomics enabled crop improvement research. The initial base line work included large scale evaluation of the germplasm resources conserved in National Gene Bank at ICAR- National Bureau of Plant Genetic Resources (NBPGR), New Delhi, to develop core, mini-core and trait specific panels for targeted traits of economic importance. These were genotyped using high throughput approaches such as GBS/resequencing/SNP Chip and Genome-wide Association Studies carried out to identify marker trait associations (MTAs) and gene in many major crops. We have mapped SSR and SNP markers in pigeonpea, vigna, apple and pineapple; genes and ncRNAs contributing to abiotic stress tolerance utilizing resistance germplasm sources for moisture-deficit stress in pigeonpea, soybean and horsegram, flooding stress in pigeonpea and arabidopsis and high nitrogen fixation in different pulse crops including medicago, maize and wheat. Assembled genomes and mapped genes contributing to abiotic stress and biotic stress tolerance in cereals and legumes. Our work also included identified genes and networks of genes to elucidate putative targets for genome editing in cereals and legumes. Enhanced mineral nutrient content, genes contributing to yield traits and declining yield loss were also identified. We have also demonstrated that validation of the identified gene by genome editing is a reality in rice. We have associated markers for the above listed traits, identified germplasm donors and more than 75 pre-breeding lines. The novel resistant donors thus developed can be used in breeding programmes for development of new crop varieties and that may have a positive impact in imparting nutritional security after reaching supply chain.

**Keywords:** Pulses, SNP Chip, Genome-wide association studies

## 161 (P-161)

### **Survey and exploration to document the local cucurbit vegetables in parts of southern Rajasthan**

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Vegetable crops belonging to the family Cucurbitaceae are known as cucurbits or gourds. This family contains 36 genera and 100 species of cucumbers in India. Out of which 37 species belonging to 14 genera are reported from Rajasthan. Southern part of Rajasthan is predominantly a tribal dominated area having harsh climate, hence, only indigenous vegetables which are hardy, drought resistant and have short duration are grown. These vegetables grow naturally during rainy season and generate good source of nutrition for the tribals. Collection and conservation of the germplasm is first and foremost activity in the crop improvement programme. A survey was carried out in 03 districts of Rajasthan (Chittorgarh, Banswara and Dungarpur) during October, 2022 and thirty accessions of local landraces of cucurbits were collected from farmer's fields. Majority of the farmers cultivated the crop in small areas of maize fallow land. The rich variability was collected for fruit colour (yellow, light yellow, orange, dark orange), fruit shape (round, pear shape oblong), pulp colour (whitish/ light yellow, yellow, orange/red), taste (sweet, less sweet and less sour ), fruit weight, fruit length, fruit width, storage life and other traits in crops namely *kachari* (*Cucumis melo* var. *agrestis*), snap melon (*Cucumis melo* var. *momordica*), cucumber (*Cucumis sativus*), bottle gourd (*Lagenaria siceraria*), Luffa sps., pumpkin (*Cucurbita pepo*) and other cucurbits. These vegetables possess very good nutritive and medicinal value with resistance to biotic and abiotic stresses. A very good variability was found in desi kheera eg. *mandachra* for long shelf life upto 3-4 months, *balankakdi* for carotene rich yellow flesh and *singad* for large fruit size and weight. In melo, landrace *dangra* for large fruit size and weight (3-4 kg) and landrace *dochra* for dual purpose salad and fruit was observed. Seeds of collected germplasm will be further evaluated for their growth and yield parameters.

**Keywords:** Southern Rajasthan, Survey, Diversity, Variability, Plant Genetic Resources

**162 (P-162)**

**Morphological variability in natural teak (*Tectona grandis*L.f.) from central India - a hot spot of teak diversity**

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Teak is one of the most celebrated and premier timber tree in the world. India harbors rich genetic resources of teak with two major centers of teak variability. Teak resources have considerably decreased in density, quality and quantity over the natural range due to high demand coupled with population pressure. Although, central India is recognized as one of the major centre of genetic diversity, studies are very limited from this region compared to southern/peninsular region. Therefore, present investigation was undertaken. For this, total thirteen natural teak populations were sampled from thirteen different agro-climatic zones of central India states. Analysis revealed that in the overall studied populations of *T. grandis*, tree height ranged from 7.62 m to 38 m with mean value



of 19.79 m. Among the sampled populations, highest average height was observed in Jagdalpur (25.1 m) followed by Seoni (22.90 m), Balaghat (22.15 m), Khandwa (21.47 m), Betul (21.45 m) and Chandrapur (21.30 m). Coefficient of variation for tree height was observed to be 24%. Clear bole height varied from 2.21 m to 32.0 m with mean value of 12.61 m. It has recorded highest CV value i.e., 41%. Girth at breast height ranged from 70.0 cm to 265.0 cm with an average of 121.0 cm. 27% coefficient of variation was recorded for this trait. Highest average girth at breast height was also observed in Jagdalpur (169.55 cm) population. In state-wise analysis, populations sampled from Chhattisgarh state recorded highest average height followed by Madhya Pradesh, and Maharashtra. Similar trend was recorded for clear bole height and girth at breast height. Analysis also revealed that wood density ranged from 401.51-792.96 Kg/m<sup>3</sup> with an average of 584.55 Kg/m<sup>3</sup>; fiber length ranged from 734.41– 1266.78  $\mu\text{m}$  with an average of 987.03  $\mu\text{m}$ ; and fiber width ranged from 17.88– 33.33  $\mu\text{m}$  with an average of 24.73  $\mu\text{m}$ . Sambalpur (668.27 Kg/m<sup>3</sup>) recorded highest wood density followed by Khariar (660.42 Kg/m<sup>3</sup>) and Jabalpur (621.48 Kg/m<sup>3</sup>) populations. Compared to morphological traits, wood traits have recorded considerably low coefficient of variation. In order to adopt conservation measures and undertake genetic improvement of teak, results obtained from the present investigation will be useful.

**Keywords:** Teak, Clear bole height, Girth at breast height, Wood density, Central India

## 163 (P-163)

### **Assessment of natural regeneration of a near threatened deciduous tree *Pterocarpus marsupium* Roxb. in Madhya Pradesh**

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*Pterocarpus marsupium* Roxb. is a large deciduous, medicinally important forest tree of subtropical region of the World. In traditional medicine, this species has been used for centuries in the management of diabetes and hyperlipidemia. Besides medicinal importance, it is also valued for excellent timber that ranks next to teak and rosewood. Over-exploitation for timber and medicinal purposes placed severe strain on natural populations of this species. Presently, it has been included in IUCN Red List of Threatened Species. In present study, we have monitored changes in population structure and regeneration over 4 years in the tropical dry deciduous forests of Madhya Pradesh. Focusing on the effects of biotic disturbance, the study examined seven potential sites, for future restoration measures and management. We examined 46 plots of 0.1 ha size laid in these seven sites from 2017 to 2021. Results compared in all sites revealed that there were hardly any individuals surviving or growing at 'Sapling' stage, which is counted as crucial for successful regeneration of a tree species. Among all the study sites, SARA recorded highest average density of seedlings per sample plot followed by BAHO and LAMT. Positive change in 'Seedlings' category was recorded only at BAHO (+17.8%) and SARA (+9.1%). Whereas, BIRS recorded highest decline in average density of



seedlings (-42.2%) followed by SEMA (-24.3%) and BARH (-17.2%). Correlation analysis of biotic pressure on the species, revealed that weed infestation (-0.59) has highest adverse effect on the seedling density followed by Lopping/cutting (-0.33) and livestock & human population (-0.12). Although there were few positive changes in the seedling stage (BAHO +17.8%; SARA +9.1%), but conditions of most sites did not meet the standards necessary for the survival and growth of a tree species. We suggest initiating conservation measures for BAHO, SARA, LAMT and CHAD populations. As infestation/invasion of weeds affecting the natural regeneration significantly, assisted natural regeneration (ANR) activities should be undertaken for this species in its natural ranges.

**Key words:** Vijayasar, Natural regeneration, Deciduous forests, Biotic pressure, Seedling density

## 164 (P-164)

### **Molecular diversity analysis in grain amaranth (*Amaranthus hypochondriacus*) using SSR markers**

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Amaranth has emerged as a pseudocereal and gained lot of attention over the past few years. *Amaranthus hypochondriacus* belongs to the family Amaranthaceae which comprise of a group of species categorized into grains, vegetables, and ornamental species. Considering the high nutritional value of grain amaranth, it is regarded as a promising crop for the future. SSRs (Simple sequence repeats) are marker of choice in genetic studies due to their high degree of polymorphism and their abundance throughout the genome. In the present study the SSR makers developed in our laboratory by *In-silico* study were used to assess the extent of genetic diversity of 94 Amaranth accessions using 14 SSR markers. The 14 SSR marker generated a total of 241 alleles. The mean major allele frequency (MAF), gene diversity (GD) and Polymorphic information content (PIC) of the 14 SSR loci were 0.72, 0.34 and 0.27 respectively. The N-J tree generated based on 14 SSRs grouped 94 amaranth accessions into 2 clades with one out-group. The population structure analysis grouped the amaranth accessions into 2 populations, which corresponds to the tree generated in this study. PCoA showed cumulative 32.10 % variation with first two principal component axis-1 and 2, this shows a considerable amount of genetic diversity among the set of studied accessions. This study concludes that, the developed SSRs were very informative for diversity study of the amaranth accessions. The results of the present study will lay a foundation for future breeding programs, genetic improvement, and germplasm core collection development.

**Keywords:** Simple Sequence Repeats, Genetic diversity, Polymorphic information content, *Amaranthus hypochondriacus*



**165 (P-165)**

**Molecular characterization of *Bacopa monnieri* (L) accessions using RAPD markers**

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*Bacopa monnieri* L. (common name brahmi) is a perennial creeping herb. It is found mainly in wet, damp, and marshy areas of India, Australia and Africa. This plant has been long used in ayurveda for its therapeutic properties. Major active constituents of this plant include various alkaloids like brahmine, herpestine, and nicotine which have been used in treatment of Alzheimer's and Schizophrenia. These alkaloids also have antistroke properties. Over exploitation of this herbal plant and the necessity of biodiversity conservation have attracted global attention. In this study, thirty accessions of *Bacopa monnieri* were characterized using twenty randomly amplified polymorphic DNA (RAPD) markers to test their genetic variability and population structure. There were 78 distinct alleles between the size range of 200-1500 bp. Average number of alleles per locus scored was found to be 3.9. Genetic distance ranged from 0.16 to 2.11 and the average gene diversity value was found to be 0.29. The number of polymorphic loci was 54 and the percentage of polymorphic loci was 69.23%. Phylogenetic analysis divided the accessions into three groups. Factorial analysis also grouped the accessions into three different clusters. Clustering pattern was concordant in both the analysis. Population structure analysis divided the *Bacopa monnieri* accessions into two populations. Analysis of molecular variance (AMOVA) showed 31% variance among the populations and 69% variance within the populations. This study showed low genetic diversity among the *Bacopa monnieri* accessions which calls for attention and preservation of this medicinal plant with potential economic values.

**Keywords:** RAPD markers, Genetic diversity, *Bacopa monnieri*

**166 (P-166)**

**Exploring wild introgression lines and mutants to identify novel genes for yield contributing traits**

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Yield is the most important as well as complex trait which has the prime significance in all the breeding programmes especially for 'Rice' - one of the most important staple food crops in the world and consumed by half of the human population. Widening the genetic base of crosses can improve the yield considerably when the yield potential of most of



the cultivated varieties reach a plateau. Wild species can be considered as the potential donors in the rice improvement programmes to broaden the genetic base as well as to improve the yield and related traits. High yielding BILs from crosses of Swarna x *Oryza nivara* (IRGC81848 (S)-94 lines and IRGC81832 (K))-90 lines and mutants from a set of 300 EMS induced mutants of Nagina22 (N22) were selected based on their yield contributing traits. The stable identified lines with significantly high yield levels were used for crossing for the development of mapping populations along with popular cultivars. Mapping populations generated from crossing wild introgression lines and mutants were raised in the field and screened for identifying significant and stable breeding lines for yield contributing traits. Three promising crosses viz., C1 (Swarna x 166S)-F6, C3 (166S x 148S)-F5 and C2 (166S x 14S)-F5 were advanced and QTL mapping was carried out for yield traits. QTL mapping was conducted for BIL x BIL populations in F2, F3 and F4 generations of C2 (166S x 14S) using ICIM v4.0 software. In all, 21, 30 and 17 QTLs were identified in F2, F2:3 and F2:4 respectively for yield traits. QTL for TGW was identified consistently with PV ranging from 6.1 to 9.8% on chromosome 8 between RM3480-RM3452 in all three generations of F2, F3 and F4. Traits productive tiller number, single plant yield, total dry matter showed QTLs qPTN4.1, qSPY4.1, qTDM4.1 mapped at RM16649- RM8213 marker interval. High yielding lines identified for tolerance to various biotic stresses are submitted for multi-location trials under AICRIP and also for breeding station trials for various ecologies.

**Keywords:** Wild species, Introgression lines, Mutants

## 167 (O-24)

### **Long term conservation of *Vanilla planifolia* 'Andrews' using droplet vitrification based cryopreservation technique**

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Vanilla, the only orchid with edible fruits, is the source of the world's most widely used flavouring substance, vanillin. It is the second most expensive spice in the world supporting a large number of industries, such as confectionaries, cosmetics, and perfumery, to name a few. Nearly 60% of the extracted vanillin is used up in food industry, 33% in cosmetics and the remaining in pharmaceutical industries. It is exclusively propagated asexually either through cuttings or by tissue culture techniques. Vanilla germplasm is majorly conserved in field genebanks, however, field maintenance is labour and cost intensive, and collections are exposed to pests and pathogens. Long term conservation of vanilla germplasm is not well reported and protocols for its conservation by cryopreservation are limited. Hence the present study was undertaken to develop a protocol for long term conservation of *V. planifolia* shoot tips using the droplet vitrification technique. Mother cultures were grown on Murashige and Skoog (MS) medium with 0.1 mg/l BAP and 3% sucrose. First, optimal duration of preculture was standardized by culturing shoot tips isolated from one month old cultures on MS



medium supplemented with 0.3M sucrose for different time intervals (1, 3, 5, 7 and 10 days) and preculture duration of 3 days was found to be optimal for further cryopreservation experiments. Further, the shoot tips were dehydrated in loading solution for 20 min and best responding cryoprotectant (PVS2) dehydration duration was optimized by treating the shoot tips with PVS2 for 10, 20, 30, 45 and 60 min. Shoot tips were then immersed in liquid nitrogen. After freezing, shoot tips were thawed in unloading solution and regrowth was recorded on MS medium containing 0.1 mg/l BAP. Data on post-thaw survival and shoot regeneration was recorded and 20 min PVS2 treatment was found to be the best with 20% post-thaw survival observed. Thus, *V. planifolia* can be cryopreserved using the DV technique, however the protocol can be further refined for its applicability for long term conservation of its germplasm.

**Keywords:** Vanilla, Droplet vitrification technique, PVS2

## 168 (P-168)

### **Community Seed Banks: Challenges and prospects to conserve agrobiodiversity, improve nutrition and livelihood security**

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From centuries, the informal seed system, while meeting the demand of seeds of the farmers, also embodied knowledge on how to conserve, grow, change and guide it to fruitful expression. Few decades back, researchers initiated an institution-Community Seed Bank (CSB) to boost seed availability of landraces, mostly in remote and diversity rich areas, wherein, improved varieties are either inaccessible or not suitable to local environment, and to facilitate on-farm conservation, adaptation and evolutionary process. The CSBs are small scale local institutions, owned and managed by farming communities, function like a bank that provide seed on loan and in return take back the seed upon harvest of crops. It caters seed demand of small area, group of villages.

Authors have analyzed the status of selected CSB's in India and discussed in this paper. Study revealed that CSBs managed by NGOs, FPOs and institutions are doing well. However, those CSBs do not have regular support of institutions, sufficient facilities for seed testing, grading, containers for storage and proper building, are facing difficulty to manage them. When desired varieties reach to all farmers, seed demand is diminished consequently, bank lose its relevance, hence introduction of diversity, new varieties and training on participatory breeding is essential. Since CSBs function on no profit - no loss basis, in absence of income their sustainability is compromised, rendering idle after exit of projects. Hence, regular income is essential, but legislation don't permit business of unlabeled and unbranded seed. Seed standard of landraces and underutilized crops for labelling and business are scanty. Since, CSBs cater the diverse seed need of small holder farmers, particularly locally adapted varieties and crops, in remote and rainfed areas, for



which and where, improved input responsive varieties generally do not perform well, there is need for co-financing, corpus fund, policy support and strengthen linkage with public institutions. Champion/custodian farmers should lead these banks and diversify their portfolio including seed production, FPO's etc.

**Keywords:** Conservation, Community seed banks, Landraces

## 169 (P-169)

### **Digital herbarium - A tool in smart management of PGR**

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Herbarium is the long-term preservation of dried plant specimens stored in an accepted classification system. Concept of digital herbarium has become popular across the world and efforts are made across the herbaria for extending wide accessibility to users through internet access. Herbarium at ICAR-NBPGR (called as NHCP) holds 25,590 herbarium specimens. Digital herbarium has well-organized collection of e-images of plants (over 10,000), along with detailed passport information available for consultation and use by various researchers. This platform namely 'Digital herbarium/e-herbarium/virtual herbarium' enhances the potential for research studies besides supporting others. Authenticated herbarium specimens are scanned with flatbed scanners by resolution of 300-600 dpi and stored in digital form (preferably JPEG or TIFF images) and classified in family folders for easy access. Digital images with good resolution (600 dpi for close-up of macro characters, and 1200 dpi for micro-characters) facilitates an accurate and efficient access of material for identification. The same process of digitization can be followed by smaller herbaria with the help of good quality camera. The virtual herbarium provides access to digital images in a virtual mode at any time from anywhere. It provides images of specimens with associated data, additional information such as passport data and notes on taxonomic identity with every specimen. The database of ICAR-NBPGR (<http://www.nbpgr.ernet.in:8080/nhcp/NHCP-Index.aspx>) is being facilitated through digital herbarium to the variable users.

**Keywords:** Herbarium, Digital herbarium, Virtual herbarium

## 170 (P-170)

### **Germplasm maintenance, evaluation and genetic improvement of local aromatic rice (*Oryza sativa* L.) using tissue culture**

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Genetic improvement of local aromatic rice is hindered due to their cross incompatibility with other rice groups and due to undesirable linkages in the resultant recombinants therefore, research programme involving both *in vitro* culture and conventional breeding methods for genetic enhancement of yield, while maintaining their aroma and taste is required. Out of the 110 aromatic rice genotypes maintained at the Regional Research and Technology Transfer Station, Bhawanipatna (OUAT) comprising of Basmati types, local landraces, traditional and released varieties; 36 local aromatic rice genotypes along with 4 released varieties were chosen. On the basis of genetic variability and divergence study, 10 genotypes were selected for tissue culture while four of these were subjected to *in vitro* mutagenesis using 0.2% EMS. Desirable mutants with increased yield were identified, data for nine quantitative traits studied in M<sub>4</sub> generation of the mutants adopting ANOVA for RBD was analysed. Genetic diversity and multivariate analysis for 9 quantitative characters grouped the forty genotypes into ten clusters and 10 genotypes, (Basumati, Kalikati, Parijat, Kanakchampa, Jeerakasal, Karpurajeera, Parbatjeera, Gangabali, Dhanaprasad and CR Dhan 907) promising and best performing genotype from each cluster, were selected for tissue culture. Four genotypes (Gangabali, Kalikati, Karpurajeera and Basumati) exhibiting >50% shoot regeneration efficiency (SRE) were selected for *in vitro* mutagenesis because SRE is the most important character for selecting a genotype for *in vitro* genetic transformation. As the contribution of individual plant yield sums to produce the final yield so high single plant yield was used as an important selection index for grain yield and on the basis of replicated yield trial values, out of 32 desirable mutants, eleven were identified in the M<sub>4</sub> generation to be advanced to M<sub>5</sub> generation and rest added to the germplasm.

**Keywords:** Aromatic rice, Genotypes, In-vitro mutagenesis

**171 (0-31)**

### **Mainstreaming of mountain native crops for Nutritional and Livelihood security in Himachal Pradesh**

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Mountain native crops diversity in era of increasing importance of cash crops has taken the back seat despite having high economic, nutritional and climate resilience values. Mainstreaming of six mountain crops namely Red Rice, Kidney Beans, Amaranth, Buckwheat, Barley and Rice Beans was carried out in villages of two Panchyats namely,



Kandhi Kamrunag and Jahal of Gohar Block in Mandi District of Himachal Pradesh (N31°30.409, E77°04.745, altitude between 1800-2500 meter). More than 500 farmers were oriented and involved in baby and crowd sourcing for generating production statistics. In all 109 varieties of six crops were used for baby and crowd sourcing trials. Each variety was tested for 10-15 parameters in these trials. Data was collected with farmer's responses and documented for uploading in ClimMob application for. On the basis of data analysis 17 landraces/varieties of selected six target crops with better performance were identified for further multiplication, value chain and product development. Community seed bank initiated at site was enriched with collection of cereals, non cereals, oil crops, vegetables of mountain areas and is serving as the feeding centre for the cultivation of target crops by the farmers in future. Farmer producer Company was incorporated for taking up the complete model from production to marketing of the farmers produce with new brand and packaging having nutritional profile as per FSSAI standards for the products of Red Rice, Kidney Beans, Buckwheat, Barley, Rice Beans and Amaranth. Infrastructure facility for de-husking of Red Rice, showcasing of products and Community Seed Bank were also developed for long term sustainability. It is anticipated that selling of product as brand in good packaging with nutritional profiling will increase farmers returns equivalent or more than commercial crops. This model is expected to empower mountain communities for nutritional and livelihood security with mitigation of women drudgery and climate change.

**Keywords:** Native crops, Landraces, Community seed bank

**172 (P-172)**

### **National Herbarium of Cultivated Plants (NHCP): Towards preservation of crop genetic resources**

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The National Herbarium of Cultivated Plants (NHCP) is one of the major 25 herbaria in India which is focussing on preservation of crop taxa and crop wild relatives (CWR). It is located in the ICAR-National Bureau of Plant Genetic Resources, New Delhi and holds more than 25,000 specimens belonging to the 4,378 taxa (including species, subspecies and varieties), 1,546 genera and 267 families. In addition to this, economic seed samples and carpological samples also preserved as supplementary collection to facilitate identification of taxa and served as repository for identification, taxonomic study and for teaching. The vouchers of cultigens, cultivars, as well as wild relatives of crops are represented in the repository. The NHCP differs in its mandate from the general herbaria across the country in representing wide range of variability in crop plants depicted as cultivars, primitive types/ landraces, wild/semi-domesticated forms and crop wild relatives (CWR)/ weedy types and also the minor economic species collected from different agro-ecological regions of India under various PGR programmes. Significant



collections include the taxa under genera namely *Abelmoschus*, *Allium*, *Amaranthus*, *Cajanus*, *Cucumis*, *Curcuma*, *Luffa*, *Medicago*, *Melilotus*, *Momordica*, *Ocimum*, *Oryza*, *Piper*, *Sesamum*, *Solanum*, *Sorghum*, *Trichosanthes*, *Trifolium*, *Triticum* and *Vigna*. The repository has its own database(<http://www.nbpg.ernet.in:8080/nhcp/NHCP-Index.aspx>) to facilitate digital herbarium. Authenticated certificates are provided to the users to conduct their research activity. NHCP provides the wide platform for consultation in authentication, identification, visit, validation and for herbarium procedures to wide range of researchers and students.

**Keywords:** Cultivated plants, Crop wild relatives (CWR), Repository

### 173 (P-173)

#### Access and utilization of cucurbit genetic resources for nutritional security

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Cucurbits are among the most important group of vegetables of the Indian subcontinent. These are used in diverse form such as salad, vegetables, dessert etc. An analysis of the status of cucurbit germplasm available in different countries and their utilization globally was carried out to determine the extent of interdependence. Genesys is a free online portal which allows access of germplasm through a single website and contains information for more than 4 million genebank accessions. The primary cucurbit holdings documented in GeneSys are cucumber 6,899 accessions, melons 8,152 accessions, water melon 5,791 and squashes 19,119 accessions. One of the important holding institutes for these collections is NPGS-USDA which distributes germplasm free of charge for research use. India has been exchanging germplasm since time immemorial but formal exchange was initiated in 1976 with the establishment of the Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources (ICAR-NBPGR). The National Genebank of ICAR-NBPGR holds 6,115 accessions of cucurbits which are freely available for research use in the country and also available to other countries under extant national regulation. Exchange of genetic resources for food and nutritional security is very important and some classical examples of this interdependence in cucumber are - CMV resistance derived from cultivar Chinese Long/China; gynocious sex expression gene from PI260860/Korea; deployment of the anthracnose resistance gene from PI 197087/India and downy mildew resistant genes from PI 197086, PI 197087 and PI 197088/India. More recently, PI 197087 from India has been identified as a source of resistance to ToLCNDV. Several carotenoid rich lines from NE India were identified and are available for use. Enhanced utilisation and smooth flow of germplasm around the world is necessary for conservation and sustainable utilisation of genetic resources for food and nutritional security, both in India and across the world.



**Keywords:** Genetic resources, Cucurbit germplasm, National Genebank

**174 (P-174)**

**High-Throughput screening of seedling growth in Indian mustard (*Brassica juncea*) under saline condition**

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Salinity is one of the major abiotic factors affecting crop productivity. In Indian mustard, the increase in mean salinity levels from 1.65 to 6.76 dS m<sup>-1</sup> results in a >70% reduction in overall seed yield. Root systems are key to improving crop salt tolerance as they can enhance access to water and nutrient uptake, thus limiting salt acquisition. The scope of study of root phenotype of plants grown under natural conditions is limited by the fact that it is difficult to monitor at regular intervals. To circumvent this, an alternative is to study the behavior of roots grown under hydroponic conditions. To assess the root system's resilience during saline conditions at seedling stages in Indian mustard germplasm, high-throughput screening was conducted. The seeds were allowed to germinate in a controlled using a hydroponic system (Water/saline). A customized high-throughput phenotyping platform was used to screen seedling behavior. The platform was designed in a comb shape so that it can hold germination papers containing seeds in a vertical position. In the present study, 2100 Indian mustard germplasm were initially screened at EC 9 ds m<sup>-1</sup> saline condition. Such primary screening identified 195 lines showing ~< 20% reduction in root length growth as compared to control (Water). To test the repeatability of root phenotype, 195 lines were further subjected to secondary screening under saline conditions (EC ~9-, 10-, and 11- ds m<sup>-1</sup>). A comparison of seedling growth of germplasm to that of saline-tolerant control lines identified 55 lines showing relatively similar root length growth. Further, to test the genetic stability of the root phenotype of germplasm, identified during secondary screening, were pursued. Seeds of 55 lines were sown in the farm field and selfed seeds were collected individually from four-five plants of each line. The harvested seeds were subsequently screened under three different saline conditions (EC ~9-, 10- and 11- ds m<sup>-1</sup>). The above screening revealed only 5 lines were able to show genetic stability in root length phenotype. Further, it is interesting to note that even in those five lines one or two sublines of each line didn't show stability in root phenotype.

**Keywords:** High-throughput screening, Seedlings, Salinity, Indian mustard

**175 (O-01)**



## **Are sorghum landraces of Telangana climate resilient?**

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Sorghum [*Sorghum bicolor* (L.) Moench] is the most important subsistence crop in Telangana State which is inhabited by the number of tribal communities' viz., *Andh, Gond, Kolam, Koya, Lambada, Manne, Naikpod* etc. Sorghum forms a staple food consumed in the form of leavened bread and porridge providing the much needed nutritional security and straw as a feed for livestock and also for thatching roofs of huts and erecting watch towers in farmers' field. The landraces of Telangana are *Aragidi Jonna, Badigi Jonna, Boda Jonna, Chikkati Jonna, Chinna Jonna, Chinnaboda Jonna, Dambral, Dhane jowar, Darawat Jonna, Erra Jonna, Gadda Jonna, Gundu Jonna, Gunjidi Jonna, Gunjidipedda Jonna, Guvvi Jonna, Kathani Jonna, Konkadala Jonna, Leha Jonna, Moddu Jonna, Pachchaboda Jonna, Pandari Jonna, Pandimutte Jonna, Parasa Jonna, Pasupu Jonna, Pedda Jonna, Pelala Jonna, Potiki Jonna, Purabodaka Jonna, Pyri Jonna, Rabi Jonna, Sanna Jonna, Sai Jonna, Sevata Jonna, Sivira Jonna, Tekedari Jonna, Tella Jonna, Tellaboda Jonna, Varagadi Jonna, Vayunowka Jonna, Vubiripatti Jonna and Vullipitta Jonna*. The inhabited tribal groups due to their long association in the cultivation of sorghum landraces named cultivars in their traditional dialects mostly based on the phenotypic characters. The characters used in naming include midrib colour (*Vubiripatti Jonna*), earhead shape (*Pandimutte Jonna*), panicle/grain size (*Chinna Jonna/Chinnaboda Jonna, Pedda Jonna*), glume colour (*Tekedari Jonna*), glume hairiness (*Leha Jonna*), grain shape (*Sevata Jonna*), grain colour (*Erra Jonna/Pachcha Jonna*), assured yield named after Sai Baba (*Sai Jonna*), special types (*Pelala Jonna*) and seasons (*Rabi Jonna*) etc. All these landraces were well adapted to local agro-climatic conditions. Maximum entropy method (Maxent) for modelling of sorghum landraces geographic distributions with presence-only data from Telangana state, India for future climate was attempted. Variability occurs among the models generated for specific landraces indicating that the sorghum landraces are climate resilient. Specific potential districts in Telangana state were identified for further cultivation and on-farm conservation of sorghum landraces in the light of climate change regime.

**Keywords:** *Sorghum*, Landraces, Telangana, MaxEnt, DIVA-GIS

**176 (0-20)**

## **Makhana (*Euryale ferox* Salisb.) genetic resources and utilization**

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Makhana (*Euryale ferox* Salisb.) also known as Foxnut is an important aquatic fruit crop and belong to family Nymphaeaceae. It is the most widely grown crop in Mithilanchal, Bihar. The crop is expanding to non-traditional growing areas mainly due to its unique natural life cycle completed in submerged condition (depth of water up to 10 feet), high nutritional and medicinal value, soil ameliorating properties, and global demand as super food. The calorific value of raw seeds (362 k cal/100g) and puffed seeds (328 k cal/100g) lie close to staple foods like wheat, rice, other cereals and some aquatic plants like *Nelumbo* and *Trapa*. The crop is suitable under cereal crop-based cropping systems in warm humid regions of Northern-East region (Kosi) of Bihar. Makhana cultivation covers over 35,000 ha of land in India with annual production of around 7.4 lakhs quintals of seed. Narrow genetic base, disease pest proneness, and photo-thermo-sensitivity are the major problems resulting in the poor yield of the crop. The utilization of very few parental genotypes in Makhana breeding programs has led to the narrowed genetic base of the Makhana varieties. This has posed a serious threat to the Makhana cultivation amid newly emerging pests and pathogens of the crop. Transboundary movement of germplasm has also helped in the development and release of varieties in several countries. Enhanced and efficient utilization of *ex-situ* conserved Makhana and related wild species germplasm in breeding programs with the help of modern genomic tools would help in the development of desired genotypes with higher yield potential. Keeping in view, the potential of this minor fruit crop in our country, an exploration trip was conducted and samples were collected from 10 to 45m msl particularly in the districts Cooch Behar, Uttar Dinajpur and Malda of West Bengal. The exploration tour was conducted by ICAR- NBPGR, New Delhi in collaboration with Bihar Agricultural University-BSP Agricultural College, Purnea during 2018-19. The present study showed that the makhana diversity is available in the explored regions, discussed in this paper.

**Keywords:** Makhana, Conservation, Utilization

**177 (0-29)**

### **Assessment of ethnobotanical uses, household and regional genetic diversity of edible Aroid species grown in Northeastern India**

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Aroids is an important indigenous group of tuber crops belong to family Araceae, grown widely for its leaves, petioles, stolon, corm and cormels. To assess the ethnobotanical uses and genetic diversity in aroid species, a total 53 accessions collected from the region were evaluated during 2016-18. At household level (Rombagre, Meghalaya), total 16 accessions of Aroids with different ethnobotanical uses were observed, and based on the population study in *Jhum*/Shifting farming accession Rengma was dominated with 47% of the total population followed by Tamachonkham (36%) and Tasakrek (12%). However, in backyards, Pugarkusu (33%) and Chigi (24%) were major accessions. The Simpson's diversity index of the backyards was higher 0.80 as compare to *Jhum* field (0.63). The wider variability was observed for growth and yield attributes like, plant



height ranged from 89.4 – 206.1 cm, number of side shoots (1.84 - 5.92), corm weight (38.0 – 683.3 g), cormel weight (14.0 – 348.3 g), yield (0.24 – 1.83 kg. plant<sup>-1</sup>). Similarly, quality traits total sugar ranges from 1.93 – 4.94 %; starch content 15.32 – 32.49 %, oxalic acid 0.10 – 0.63 % and dry matter 16.75 – 27.08 %. Except oxalic acid all the growth and yield attributes have shown high heritability and genetic advance. Molecular analysis (33 polymorphic SSR markers), detected a total of 136 alleles ranged 3 to 8 alleles per marker. The heterozygosity ranges from 0.00 – 0.84 and observed average heterozygosity (0.24) was less than the expected heterozygosity (0.69). The group wise maximum genetic divergence was observed between *Colocasia fallax* (cv. Chigi) to *Colocasia esculenta* var. *Aquatilis* (cv. Tharsing); *Colocasia fallax* (cv. Chigi) to *Colocasia gigantea* (cv. Ganima) and *Colocasia gigantea* (cv. Ganima) to *Xanthosoma* spp., while it was least between eddo (*Colocasia esculenta* var. *antiquorum*) and dasheen (*Colocasia esculenta* var. *esculenta*). The findings of the study indicated, the presence of wider diversity and distinct ethnobotanical uses of the landraces of Aroid species at house hold levels, that need to be conserved and popularized for ensuring nutritional security.

**Keywords:** Aroid, Taro, Genetic diversity, Starch, Oxalic acid, Molecular marker

## 178 (P-178)

### **Intrinsic and extrinsic factors in conservation of threatened plants in western Rajasthan**

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Conservation of plant genetic resources is a very challenging task in climatically extreme but floristically rich Indian hot arid zone which is under pressure of habitat destruction, high grazing/browsing pressure, increasing irrigation, changes in land-use pattern, mining, dilution of customary conservation practices, climate change and unsustainable exploitation of vegetation resources. Consequently, many of the plant species of traditional importance are adversely affected and marginalized to the extent of being threatened to varying degrees. Seven threatened hot arid species viz., *Ceropegia bulbosa*, *Calligonum polygonoides*, *Caralluma edulis*, *Glossonema varians*, *Dipcadi erythraeum*, *Ephedra ciliata* and *Anogeissus sericea* var. *nummularia* were studied for improving their conservation status in western Rajasthan. In order to assess their present population status with reference to previous reported status, published literature, check lists, herbarium and other historical data were studied for western Rajasthan. Based on analysis of different factors at the native sites of occurrence of these threatened species as well as observations during their regeneration studies including survival, the critical factors that can possibly limit species populations have been identified in the form of extrinsic and intrinsic factors along with their severity. The intrinsic factors are: poor growth of plant, extreme sensitivity to abrupt shifts in weather, prolonged dormancy of seeds, poor and short duration viability of seed in some species, failure to pollinate, failure to seed set, and premature dispersal. Extrinsic factors inhibiting regeneration and



population build-up are habitat degradation and fragmentation, removal of propagules, pest attack, and climatic harshness which would require management action for success in conservation program. Evidently the extrinsic factors play major role in limiting the populations of studied threatened plant species. These extrinsic and intrinsic factors can become guidelines for enhancing regeneration success.

**Keywords:** Threatened arid species, Conservation practices, Extrinsic factors

**179 (P-179)**

### **Towards developing DNA fingerprinting protocols in potential crops using simple sequence repeat (SSR) markers**

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Potential crops are crops of subsistence farming systems invariably grown by small and marginal farmers. These crops are widely accepted by local farmers for sub-optimal growing conditions and are rich in nutritional profile. Poor investment in research and genetic improvement have forced these crops to be neglected by the scientific community. A plausible reason for this is that these crops are not traded internationally at a rate comparable to other major food crops. Breeding new varieties is a resource-intensive activity in terms of costs, infrastructure, genetic resources, and the breeders' knowledge and experience. Hence, protection of ownership of new varieties is important to secure investment returns and infringement of breeders' rights. Unique identification is the key in order to protect the plant varieties. The conventional approach to varietal identification involves analysis and recording of their morphological characters which is highly influenced by environmental factors and is time consuming. Availability of molecular markers in large number in all the major crops has opened new avenue for their utilization in plant variety identification and protection. In the present study attempts were made to develop DNA fingerprinting protocol in chenopodium (*Chenopodium album*), buck wheat (*Fagopyrum esculentum*) and faba bean (*Vicia faba*) using SSR markers. Concentrations of PCR component such as 10x buffer, MgCl<sub>2</sub>, dNTP's, primer, Taq DNA polymerase and template DNA were varied to get optimum amplification of PCR products. Thirteen accessions of chenopodium were scanned using 18 SSR markers which produced 88 bands with size range of 100-190 base pairs. Using 24 SSR markers in 13 accessions of buckwheat, 83 bands were in the size range of 90-220 base pairs were observed. Using 24 SSR markers in 18 accessions of faba bean, 90 bands were recorded with size range of 110-510 base pairs. Further analysis with respect to various statistical parameters was carried out for developing the protocols in these orphan crops.

**Keywords:** Potential crops, DNA finger printing, SSR markers



## 180 (P-180)

### **Genetic integrity analysis of some stored accessions of cotton (*Gossypium hirsutum* L.) in the National Genebank**

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Maintaining genetic integrity is the foremost concern that genebank managers face during the regeneration of germplasm accessions. In this study, the genetic integrity of stored accessions of cotton in the National Genebank regenerated over the years was analysed using microsatellite markers. We selected seven accessions which had been regenerated during the years 2000, 2007 and 2015. The number of seeds of these accessions ranged from 33 to 70 across the three years of regeneration. The DNA from individual seeds of these seven accessions was extracted following CTAB method with some modifications. A set of minimum five SSR primers was used to observe any genetic changes in each accession across the three years. Further analysis for various parameters such as number of bands, polymorphic bands, allele frequency, observed and expected heterozygosity etc. was carried out using the softwares Powermarker and Genalex. In all the accessions, for major bands, no significant changes in the number of bands and band frequency were observed, but in some, a few minor bands were either missing or altogether new minor bands were observed. These observations could be attributed to admixtures or pollen contamination that might have happened inadvertently during the regeneration of cotton accessions, or else, these might be some PCR artefacts. Consequences of these results for conservation in the National Genebank would be discussed further.

**Keywords:** Cotton, National Genebank, Powermarker and Genalex softwares

## 181 (P-181)

### **Genotype x Environment interaction in Sesame (*Sesamum indicum*) for morphological traits in various environmental conditions**

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To achieve the objective of investigation, ten genetically diverse sesame parents, namely, RT-346, TKG-22, RT-372, TC-25, PRAGATI, RT-46, RT-125, RT-103, GT-10 and RT-351 were crossed in half diallel fashion excluding reciprocals in *kharif* 2019-20. These ten parents along with their 45 F<sub>1</sub> progenies were evaluated in a randomized block design



with three replications during *khari* 2020-21 at Agronomy Farm of SKN College of Agriculture, Jobner (Rajasthan). Genotype X environment interaction was significant for all the traits under study. On basis of stability analysis, parents TKG-22, GT-10 and RT-351 and crosses TKG-22 x GT-10, RT-372 x RT-103, TC-25 x RT-46, TC-25 x RT-46, RT-103 x GT-10 exhibited stable performance for seed yield per plant in different environmental conditions. On the other hand, crosses RT-346 x TKG-22, RT-346 x RT-351, TKG-22 x RT-372, TKG-22 x TC-25 and RT-372 x RT-351 indicated its suitability and stability under better environmental conditions. These crosses could be utilized as a promising breeding material for the development of new set of sesame varieties. It was concluded that an appreciable progress could be achieved through diallel selective mating or biparental mating in early segregating generations followed by selection.

**Keywords:** Sesame, Genotype x Environment, Genotypes, Stability, Physiological Traits

## 182 (P-182)

### **Chemical composition of novel *Callistemon citrinus* (Curtis) Skeels aerial part essential oil and its pharmacological applications, neurodegenerative inhibitory and genotoxic efficiencies**

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*Callistemon citrinus* aerial part essential oil (CCEO) was analyzed for chemical compositions using GC/MS. Pharmacological; neurodegenerative inhibitory activities such as antioxidant, anti-inflammatory, antimicrobial, acetylcholinesterase activities were evaluated using standard methodologies. Genotoxicity was investigated using *Allium cepa* assay. GC/MS analysis identified 27 compounds; eucalyptol (55.40%) was the major component. Radical scavenging activity showed IC<sub>50</sub> 16.71 µg/mL. Protein denaturation assay showed IC<sub>50</sub> value of 21.19µg/mL and 19.53µg/mL in protease inhibitor activity. MIC assay revealed strong antimicrobial potential of CCEO against microbial strains *B. cereus* (2.00), *S. typhimurium* (4.50), *S. mutans* (2.50), *C. albicans* (4.00), *S.cerevisiae*(4.50). Mitotic index value (MI) of CCEO showed negligible genotoxicity with MI 17.25% close to distilled water 18.22%. Acetylcholinesterase strong inhibitory activity of CCEO was observed from IC<sub>50</sub>= 6.335 µg/mL. CCEO could be a cheap and easy source for the extraction of the pure compound eucalyptol and possess various biological activities which increase its pharmacological value as well as its applicability in the field of flavor and fragrance industries.

**Keywords:** *Callistemon citrinus*, Neurodegenerative inhibitory activities, Genotoxicity

## 183 (O-11)



## **Assessment of molecular diversity of core collection of ginger germplasm from Northeast India**

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*Zingiber officinale* Rosc. commonly known as 'Ginger' of the Zingiberaceae family is an important cash crop used since ancient times. Being a biodiversity hotspot, the Northeast India is a rich hub of ginger diversity. The biodiversity of the ginger from the entire Northeast region has not been exploited so far which could lead to identification of promising lines. In view of this a total of 150 ginger germplasm was collected from seven states of Northeast India which were assessed for molecular diversity using 28 SSR markers. The statistical analyses were performed on POPGENE (1.32 version), GenAEx (6.5 version) and Darwin (version 6). The 28 SSR primers produced a total of 70 bands. The polymorphic information content ranged from 0.672-0.089 while the marker index ranged from 2.015-0.044 and resolving power ranged from 2.041-0.280. On the basis of the molecular analysis the primer RM125 was found to be the most efficient. The highest polymorphic was found to be Arunachal Pradesh and the least was found to be Mizoram population. The Meghalaya and Sikkim population were found to be least genetically distant and most similar while Nagaland and Meghalaya were found to be the most distant and least similar population. The results of the cluster analysis revealed three main clusters for the genotypes which have been further divided into sub-clusters. The principal coordinate analysis was also found to be in similar line with the results of cluster analysis. The present study is the first report on genetic diversity involving large number of germplasm from seven states of Northeast India.

**Keywords:** *Zingiber officinale*, North-east India, Genetic diversity

**184 (P-184)**

## **Chemical composition of *Syzygium cumini* (L.) Skeels (Jambolan) leaf essential oil with respect to its uses from North-east region of India**

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*Syzygium cumini* (L.) Skeels (Jambolan) is a widespread summer fruit plant, well-known for various therapeutic uses such as anti-diabetic, antimicrobial, antioxidant properties. The fruit helps to convert starch into energy which helps in regulating blood sugar levels

and possesses a low glycemic index. The present study is aimed to estimate the chemical composition of the essential oil of leaves of *Syzygium cumini* through GC/MS. The essential oil was extracted by hydrodistillation using a Clevenger apparatus which was further analyzed through GC/MS. The GC/MS analysis identified twenty-five components with a total area percentage of 95.66 %. The major identified components were  $\tau$ -cadinol (21.44 %) and tau-muurolol (12.01 %). The compounds of intermediate concentration were globulol (7.98 %), caryophyllene (6.69 %),  $\delta$ -cadinene (6.56%) and  $\alpha$ -pinene (6.32 %). While  $\beta$ -eudesmol (4.42 %),  $\beta$ -pinene (4.32 %),  $\gamma$ -cadinene (3.87 %), camphene (2.98 %),  $\alpha$ -terpinenol (2.72 %), camphor (2.23 %), humulene 6,7-epoxide (2.17 %), cubeban-11-ol (1.98 %),  $\alpha$ -muurolene (1.81 %), epicubenol (1.43 %),  $\alpha$ -copaene (1.26 %), viridiflorene (1.02 %),  $\beta$ -guanine (0.65 %),  $\beta$ -bourbonene (0.23 %), terpinen-4-ol (0.13 %), endo-borneol (0.12 %), levoverbeneone (0.12 %) and isobornyl acetate (0.12 %) were the compounds present in minor concentrations. Among the identified compounds there were monoterpene hydrocarbons(13.62 %), bicyclic-monoterpenoid (0.36 %), terpenoid ketones (2.23 %), monocyclic monoterpene alcohol (2.85 %), non-oxygenated sesquiterpenes (25.17 %) and oxygenated sesquiterpenes (51.43 %). The present investigation also discusses the applications of various components found in *S. cumini* leaf essential oil and a comparative view on the essential oil composition of the leaves of the plant was reported earlier.

**Keywords:** *Syzygium cumini*, Essential oils, Hydro distillation

## 185 (0-21)

### ***In vitro* approach for regeneration of *Homalomena aromatica* Schott an endangered medicinal plant of NE India**

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Northeast India is one of the largest biodiversity hotspots with rich and diverse vegetation. One of the most highly valuable aromatic crop *Homalomena aromatica* Schott (Araceae) commonly known as “Sugandhmantri” is a tropical perennial herb. The leaves and rhizomes are mainly used in traditional medicines. On steam distillation of rhizome yields a yellow colored volatile essential oil about 1.0 % on dry basis rich in linalool which is widely used by Aroma industries for blending most oriental attars and presently reported as highly priced market value. Tissue culture can play a major role in the conservation and *in vitro* multiplication of this endangered species. Experiments were conducted where the rhizomes shoot buds have been taken as an explants which was inoculated in half strength Murashige and Skoog (MS) medium with various concentrations of BAP (6-benzylaminopurine), NAA (Naphthaleneacetic acid), GA<sub>3</sub> (Gibberellic acid), KIN (kinetin) for the initiation stage, which was found to be prominent in BAP 0.5 mg/L and GA<sub>3</sub> 0.1 mg/L. In full strength MS medium the shoot establishment under different cytokinin and auxin concentrations were performed where BAP 2.0 mg/L and NAA 0.2 mg/L resulted in significant growth. In this study shoot initiation was observed between 15-20 days which was followed by shoot multiplication in 40-45 days.



Simultaneous multiplication of root and shoot was evident in 5.0 mg/l BAP + 0.2 mg/L NAA. The present study could be useful for commercial *in vitro* production of *H. aromatica*.

**Keywords:** *Homalomena aromatica*, Endangered, Linalool, Traditional medicine, *In vitro* multiplication

### 186 (P-186)

#### **Evaluation of wild species of banana from Andaman and Nicobar Islands with landraces of Kerala for resistance to pseudostem weevil, *Odoiporus longicollis***

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The banana pseudostem weevil (*Odoiporus longicollis* Oliver) is a principal production constraint in commercial cultivation of banana and plantain. Cultural and chemical control are feasible however, not sustainable. Whereas, host plant resistance is safe and has long term benefits. Field evaluation of four wild species of banana collected from Andaman and Nicobar Islands along with nine landraces of Kerala against pseudostem weevil has shown that two accessions (IC630992 and IC631126) of *Musa balbisiana* var. *andamanica* (wild species) were found free from the visible infestation of banana pseudostem weevil. Feeding marks and life stages of the weevil were not present in pseudostem of *M. balbisiana* var. *andamanica* accessions. Wild species namely, *M. kattuvazhana* and landrace *Beejakela* have shown resistant reaction and landrace, Njalipoovan has shown moderately resistant reaction to weevil infestation. Wild species namely, *M. acuminate* (IC631154), *M. inandamanensis* (IC631163) and landraces such as, Karpuravalli, Nendran and Mondan have shown susceptible reaction to infestation of pseudostem weevil. In-vivo screening of pseudostem pieces of wild and landraces against weevil has confirmed the same results. Tough fibrous and less water content (89%) in pseudostem of *Musa balbisiana* var. *andamanica* compared to 93-96% in other wild species and landraces may be possible reason for the resistance.

**Keywords:** Banana pseudostem weevil, Resistance, *In-vitro* screening

### 187 (P-187)

#### **Genetic diversity analysis by morpho-agronomic and genome wide SNP markers of *aus* rice diversity panel**

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Rice is the most important crop feeding around half of world's population. The productivity and yield stability of rice are increasingly challenged by abiotic stresses aggravated by climate change. *Aus* subpopulation of *Oryza sativa* is geographically confined to eastern and north-eastern parts of India, along with Bangladesh. Several important stress tolerance genes were identified from *aus* accessions, suggesting importance if *aus* rice for mining genes for adaptation to major abiotic stresses and developing climate resilient varieties. We used 181 *aus* accessions of 3000 Rice Genome Panel (3K-RGP) acquired from IRRI, Philippines. The geo-locations of the *aus* rice accessions indicated that most of these have been originated in Bangladesh and adjoining Indian states of Assam and West Bengal. The accessions were characterized in *Kharif* 2021 and *summer* 2022 for morpho-agronomic variability and drought at vegetative stage, respectively. Considerable variability was recorded in tiller number, flag leaf width, panicle weight, spikelets per panicle, harvest index, drought score and stomatal density. Multiple factor analysis using 42 traits revealed that a few agro-morphological traits such as Tiller number, spikelet number, panicle weight, colour of collar, basal leaf sheath, internode, apiculi and husk, culm strength and culm number are the major determinants of phenotypic diversity. Multivariate analyses indicated lack of phenotypic clusters within *aus* germplasm except lodging and non-lodging types. Population structure analysis using 399K SNPs revealed six clusters indicating that *aus* accessions from Bangladesh showed lower genetic diversity as compared to the accessions from India. Subsequently, we characterized these accessions under vegetative stage in drought and identified promising genotypes in terms of drought score and morpho-physiological traits such as stomatal density and stomatal conductance. The stress data has been used for identifying genes for drought tolerance through genome wide association studies.

**Keywords:** Rice Genome panel, SNPs, Genetic diversity

**188 (0-19)**

**Genetic resources of pigeon pea: conservation for utilization**

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Pigeonpea (*Cajanus cajan* L.), a diploid legume crop species ( $2n=2x=22$ ), is a member of the tribe Phaseoleae. Originated >3,500 years ago in India from its progenitor *Cajanus cajanifolius* (Haines) Maesen. pigeon pea has several unique features, by virtue of which it occupies a predominant place as a food and in several cropping systems all over the India. A total of 11940 accessions including 11576 indigenous and 364 exotics are being conserved as base collection in long-term storage facility at National Genebank (NGB) at ICAR-NBPGR, New Delhi. Wild species related to crops have proved useful to crop improvement as sources of a variety of valuable traits. In NGB, wild species of pigeon pea



viz., *Cajanus albicans* (Wight & Arn.) Maesen (6 accessions); *Cajanus cajanifolius* (2 accessions); *Cajanus mollis* (Benth.) Maesen (3 accessions); *Cajanus platycarpus* (Benth.) Maesen (2 accessions); *Cajanus scarabaeoides* (L.) Thouars (47 accessions); *Cajanus volubilis* (Blanco) Blanco (1 accession) are being conserved. Along with collected germplasm, trait specific germplasm registered (55 accessions) for different traits like, bold seed, short duration, determinate types, stable CGMS line, fertility restorer, disease (phytophthora stem blight disease, fusarium wilt, sterility mosaic) resistance, waterlogging tolerant are also maintained in NGB. To utilize the conserved germplasm, characterization of germplasm is utmost. Under Consortia Research Platform of Agrobiodiversity (CRP-AB), 9500 accessions were characterized by using 29 descriptors and descriptor states developed by Bioversity International. High variability was observed among the accessions viz., days to 50% flowering ranged from 57 days (IC245519) to 195 (IC398908). Similarly, 100 seed weight varied from 3.40 gm (IC348165) to 25.80 gm (IC634397), 27 accessions were found with >15 gm/100 seed weight, 10 accessions with >25 primary branches were identified. Thus, the conserved genetic resources of pigeon pea have shown a wide spectrum of variability for both qualitative and quantitative traits and has a great potential to be utilized in the future pigeon pea improvement programme.

**Keywords:** Legume crop species, National Genebank, Genetic resources

## 189 (S-01)

### Germplasm exchange for sustainable food security

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Food security depends on the continuous improvement of food and feed crops. For this purpose, global exchange of plant genetic resources and its efficient and sustainable utilization is critical to support agricultural production which is foundation to food security. Continued progress in crop improvement programmes is thus critical, which is highly dependent on unrestricted germplasm exchange. Implementation of Access and Benefit Sharing (ABS) Systems through Convention on Biological Diversity (CBD), Nagoya Protocol (NP) affected this exchange broadly resulting in reduced flow of germplasm, as genebank curators had to comply with national negotiations in augmenting and sharing germplasm. Germplasm Exchange today is affected by the policies and the ABS is complex being seen as having negative impact on research and development. The International Treaty for Plant Genetic Resources for Food and Agriculture (ITPGRFA) was negotiated to address the needs of food security and sustainable agriculture, in harmony with CBD. According to Article 10.2 of the Treaty Contracting Parties agreed to establish Multilateral System (MLS) which provides for facilitated access to PGRFA for the crops covered under Annex I of ITPGRFA and share in Fair and Equitable way the benefits arising from the utilization. The contracting parties were encouraged to include Material in the



Multilateral System. As of July 2022, total of 2,343,549 accessions are available for distribution under MLS. These accessions include 1,482,503 accessions by 85 contracting parties ; 8,05,124 accessions by CGIAR Centres and World Vegetable Centre; and 55,922 accessions by other genebanks and associations. The accessions available under MLS are available for supply under terms and conditions of Standard Material Transfer Agreement (SMTA). The benefit sharing under SMTA is as such that, if the recipient commercializes a product, and product is available without restriction to others, the recipient can make voluntary payments, however if the product is made available with restrictions the recipient needs to pay a fixed percentage of the sales of the commercialized product into the mechanism. At the 9<sup>th</sup> Governing body of the Treaty Ad Hoc Open-ended Working Group was re-established to enhance the Functioning of the MLS. As users of MLS, expansion of the list will ensure greater conservation of the biodiversity as well as enhanced exchange and sharing of PGRFA. There is need to enhance conservation and open exchange for potential use of diverse germplasm to address food security issues.

**Keywords:** Plant Genetic Resources, CGIAR Centres, STMA, PGRFA

## 190 (P-190)

### **A pilot study on monitoring genetically modified (GM) ingredients in bakery and confectionery food products in the marketplace**

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Bakery and confectionery products are rich in demand by the consumers, contributing to the rise in its market globally as well as in India. These products mostly comprise of wheat, rice and cornflour. Genetically modified (GM) corn, rice and wheat have been approved for use as food or for cultivation in many countries. However in India, the GM food products have not yet been approved. As per the Food Safety and Standards Authority of India (FSSAI) Order dated 21 August 2020, every consignment of 24 selected food crops including corn, rice and wheat, needs to be accompanied with the non-GMO certification. Hence, there is need to monitor the food products in the marketplace as well as in the supply chain for the GM status for regulatory compliance. In order to check the GM ingredients in the imported as well as in the domestic food products, a study has been conducted to check GM status of twenty-five bakery and confectionery food products including biscuits, cake, breads, cookies and chocolates collected from the retails shops and market. DNA extraction procedures have been optimized to obtain DNA extracts of acceptable quality and concentration, which could be employed for GM testing as well as other PCR-based testing in bakery and confectionery food products. DNA amplifiability was ensured using endogenous gene-specific PCR based assays. GM status of these samples was checked using PCR assays targeting the commonly employed screening elements: *CaMV 35S* promoter (*P-35S*), *nos* terminator (*T-nos*), and *Figwort Mosaic Virus*



promoter (*P-FMV*). Based on the tests conducted, none of the samples were found positive for the targets screened.

**Keywords:** GM detection, Bakery and Confectionery food products, PCR

**191 (O-22)**

***In vitro* mass multiplication and field acclimatization of spine gourd (*Momordica dioica* Roxb.)**

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Spine gourd (*Momordica dioica* Roxb.) commonly known as Kankoda, is a perennial dioecious climber of cucurbitaceous family distributed in India, China, Nepal, Bangladesh, Myanmar, Pakistan and Sri Lanka. It is one of those rarest plants where almost all parts of the plant are edible i.e. immature green fruits, young leaves, flowers and tubers are consumed in a variety of ways. Besides being rich in proteins, calcium, phosphorous and iron, the fruits contain highest amount of carotene amongst the cucurbitaceous vegetables. This species also possesses a range of therapeutic and medical benefits. Due to its dioecious nature and vegetative mode of reproduction, this vegetable has remained underutilized and underexploited despite having high market demand. Availability of the tubers and stem cuttings during growing season is a limiting factor due to low multiplication of tuberous roots and availability of stem cuttings late in fruiting season. Also, when propagated using stem-cuttings, very less sprouting and survival was recorded (less than 40%) in the field. Seeds are not preferred propagules as they show dormancy, unpredictable sex ratio and segregation in seedling progenies. Male plants dominate in the natural populations and sex determination is possible only when the plants start flowering. Since female plants are preferred for maximum fruit yield, only 5-10% of male plants are recommended for pollination in commercial fields for good fruit set. As the traditional methods of spine gourd propagation have several limitations; efficient clonal propagation to aid in the production of disease-free, high-quality planting material in genotype (RMDSG/2020-2) was developed using the tubers. The nodal segments and shoot-tip explants of the sprouted tubers were used as explants to establish aseptic cultures under *in vitro* system. Shoot induction was obtained on Murashige and Skoog's (MS) medium supplemented with 0.88  $\mu$ M 6-benzyladenine (BA) while maximum shoot proliferation of 6 $\pm$ 1.2 shoots per explants was recorded on MS medium supplemented with 2.22  $\mu$ M BA. Profuse rooting was observed on half-strength MS medium containing 4.9 $\mu$ M indole-3-butyric acid as well as on media containing half-strength MS salts with 5.71  $\mu$ M indole-3-acetic acid. The roots were thick and short on media supplemented with IBA while roots were long and slender in IAA supplemented media. Plantlets hardened successfully in potting mix containing soil, sand, and vermiculite (3:1:1). Using the developed protocol, long-term cryoconservation of vegetative propagules, will be attempted in the future to conserve true-to-type genotypes.

**Keywords:** Spine gourd, MS medium, Cryoconservation

## 192 (P-192)

### Utilization of exotic cowpea germplasm for revitalizing the Indian cowpea improvement programme

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Cowpea is a grain legume native to Africa and is a primary source of protein for millions of people in the developing world. It is mainly grown in subsistence farming systems in India. The crop species has evolved in a diverse range of agroclimatic conditions and therefore the germplasm has rich genetic diversity. The International Institute of Tropical Agriculture (IITA) maintains the world's largest collection of cowpea germplasm of over 15,000 accessions. However, this diversity has not been explored to assess their performance in Indian conditions. Utilization of exotic germplasm is one way to broaden genetic variation in breeding populations. Sharing and exchange of germplasm within and beyond national boundaries generate opportunities to enrich the plant wealth of a country. Therefore, a study was performed on global core sets developed by IITA, Nigeria (645 accessions) using 12 quantitative and 15 qualitative traits to understand the expression of the crop and identify trait-specific germplasm in the Indian environment. A wide range of variation was observed for days to flowering, days to maturity, pod length, the number of seeds/pod and 100-seed weight. Germplasm identified as early (<60 days maturity: EC723684; EC724530; EC723880), erect, bold seededness (>25 g: EC724449) and determinate may serve the need of the Indian breeding programme. Principal component analysis (PCA) revealed that the first five principal components (PCs) explained 71.87% of the total variation. The maximum variance was explained by PC1 (21.58%) followed by PC2 (16.99%). The agro-morphological variability and its genetic nature revealed from this study may prove very useful in ongoing and future breeding programmes

**Keywords:** Cowpea, Quantitative traits, Principal component analysis

## 193 (P-193)

### DUS characterization in Snap melon farmers' varieties of Vindhyan region of Eastern Uttar Pradesh

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Snap melon (*Cucumis melo* L. var. *momordica*) belongs to family Cucurbitaceae with chromosome number ( $2n=2x=24$ ) is a tropical old-world cucurbit species. A modest gene bank of snap melon has been established in the Department of Vegetable Crops, Punjab



Agricultural University, Ludhiana. The study was performed to determine the morphological characteristics of 17 references snap melon landraces (*Cucumis melo L. momocardica*) collected from various district of Allahabad region. DUS testing using the Botanical descriptors are based on PPV and FRA DUS guidelines of muskmelon. Of the 34 morphological characters studied, 19 were visually assessed and 15 were measured. Based on fruit length, snap melon landraces are divided into three categories. Short, (no varieties) medium (CAIV-40, CSAK-30), long (almost all varieties are naturally long). Most of the cultivars have a long shape, and the cross-sectional shape of the fruit has been confirmed to be ovate (ASKP-552, KSKP-553, ASTP-554, RSCP-556, KSNP-561, BSKP - 562, DSKP-567), elongated globe (ASNP-560, RSCP-564), round (CSAK-39) and oval (SSJP-551, ASKP-555, MSSP-557, BSKP-558, ASTP-563, CAIV-40). The fruit skin colour is yellow (BSKP-558, BSKP-562) and yellowish green (ASKP-552, ASKP-554, ASKP-555, MSSP-557, ASTP-559, ASNP-560, RSCP-564) and orange (KSKP-553, RSCP-556, KSNP-561). Sutures on the surface of the fruit have been found to be absent in all snap melon landraces. Regarding fruit surface netting, landraces were grouped as absent netting and moderate netting, while all 17 landraces showed absence of netting on surface. Skin colour is cream white (BSKP-558), white (SSJP-551), orange (ASKP-552, KSKP-553, ASTP-554, ASKP-555, RSCP-556, MSSP-557, ASTP-559, KSNP-561, BSRP-562, ASTP-563, RSCP-564, DSKP-567, CAIV-40, ASNP-560, CSAK-39). Seed colour was observed to be cream colour (SSJP-551, ASKP-552, KSKP-553, RSCP-556, MSSP-557, ASTP-559, ASNP-560, ASTP-563, CAIV-40 and CSAK-39) and yellowish (ASTP-554, BSKP-558, KSNP-561, BSKP-562, RSCP-564 and DSKP-567). The results showed no intra-breed variation was observed for any of the imaging characteristics examined. Furthermore, the expression of characters in different landraces remained the same for three consecutive years, confirming the homogeneity and stability of the landraces with respect to the visual characteristics. Landraces have been grouped into different categories for each trait based on 34 descriptors. The grouping was done for 6 traits as grouping traits, viz. sex [removed] at full bloom), shape of fruit in longitudinal section, color of rind, sutures in rind, surface of fruit and colour of flesh. The morphological characterization of the existing landraces has been completed to determine the distinctiveness of the tested landraces from other check varieties in order to use these landraces as a reference for the protection of other varieties, according to PPV & FR legislation.

**Keywords:** Characters, Snap melon, Farmers Varieties, DUS, Groups

**194 (P-194)**

**Genome-wide identification and characterization of trehalose-6-phosphate synthase gene family in linseed (*Linum usitatissimum* L.)**

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Linseed (*Linum usitatissimum* L.) is second most important *rabi* oil seed crop in India and is mainly grown for its fiber and seeds oil. Early flowering and maturity is considered an important trait as it helps crop to escape several biotic and abiotic stress. Role of trehalose-6-phosphate synthase 1 has been established in flowering time regulation in Arabidopsis. In present study, genome wide identification and characterization of trehalose-6-phosphate synthase (TPS) gene family have been carried out in linseed and a total of 18 TPS genes were identified *in-silico*. Orthologous nomenclature of linseed TPS genes was done having *Arabidopsis thaliana* TPS genes as reference. It was found that every Arabidopsis ortholog of TPS in linseed has a paralog, suggesting gene duplication event(s) in linseed. 18 TPS genes were grouped into two clusters having 4 and 14 genes in cluster I and II, respectively. In order to study allelic variation, linseed TPS gene family was PCR amplified from 2 early and 2 late flowering-maturing linseed germplasm accessions and sequenced. Sequence analysis revealed SNPs ranging from 1 to 6 in 9 out of 18 TPS genes. Interestingly, SNPs identified in *LuTPS6.1* and *LuTPS10.2* genes could distinguish early and late accessions. Further, 2.5Kb promoter sequence of *LuTPS6.1* and *LuTPS10.2* genes was also PCR amplified and sequenced. Sequence analysis revealed total 12 and 19 SNPs in promoter sequence of *LuTPS6.1* and *LuTPS10.2*, respectively. Identified SNPs in promoter sequence of *LuTPS6.1* and *LuTPS10.2* genes also resulted in change in predicted binding sites of a few important transcription factors. Present study gives an insight into TPS gene family in linseed in perspective of flowering and maturity time traits.

**Keywords:** Trehalose-6-phosphate synthase, Gene family, Flowering, Maturity, Linseed

**195 (P-195)**

### **Strategies for detection of stacked genetically modified events of cotton**

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The advances in recombinant DNA technology and plant genetic transformation have enabled the rapid development of genetically modified (GM) crops with single and multiple desirable traits to overcome various biotic and abiotic stresses. In India, *Bt* cotton event MON531 (Bollgard® I), expressing the Cry1Ac protein for insect resistance, was the first GM crop approved for commercial cultivation. Following that, a stacked GM event, namely, *Bt* cotton event MON15985(Bollgard® II)expressing Cry1Ac and Cry2Ab2 proteins for resistance to a broad range of insect pests, was approved. Other stacked GM cotton events such as Bollgard® III (MON15985xCot102), *Bt*Roundup Ready Flex (MON15985xMON88913), and Bollgard® III-Roundup Ready Flex (MON15985xMON88913xCot102) were imported for research purposes through ICAR-NBPGR, New Delhi after the technical clearance by the Review Committee on Genetic Manipulation. Looking into the global scenario of approved stacked GM events and their import for research purposes, a decision support matrix based appropriate molecular strategies to differentiate the single and/or stacked events of cotton have been



developed. The diagnostics for GM stacked events are being utilized for molecular detection of imported transgenics. This study would also play a key role in the authentication of seeds of stacked GM events, allowing stakeholders to reap the maximum benefits of gene stacking. In addition, regulatory and enforcement bodies, as well as GMO testing laboratories would benefit from this information when making decisions about stacked GMOs.

**Keywords:** Bt Cotton, Decision support matrix, Genetically modified, Molecular detection, Stacked event

## 196 (P-196)

### **Evaluation of specific gravity of Indigenous Potato (*Solanum tuberosum* L.) genotypes**

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Potato is the third most important growing crop worldwide after wheat and rice. In potato varietal improvement programme, many tubers traits are recorded like tuber shape, tuber skin colour, tuber eye depth and tuber flesh colour besides tuber yield and tuber numbers. Specific gravity and tuber dry matter % of potatoes is one of the most important trait, which determines the water content in potato at the time of harvest and genotypes with high tuber dry matter and low reducing sugars are considered suitable for processing. In the present study, sixty two indigenous potato genotypes were evaluated for specific gravity at ICAR-Central Potato Research Institute, Regional Station, Modipuram, during 2021-2022 from the crop grown in randomized complete block design with three replications. The results displayed high level of variability among the genotypes for the specific gravity and tuber dry matter content. The minimum specific gravity and tuber dry matter of 1.047 and 13.26% was recorded in genotype namely 1001, Bengal Jyoti and Champaran Lal. The highest specific gravity and tuber dry matter content was recorded in indigenous genotypes namely Jeevan Jyoti (1.084 and 21.07%) followed by KP/PC-292 (1.079 and 20.01%), DRR (1.077 and 19.65%), Lady Rosetta (1.076 and 19.42%), Deshla Lal (1.074 and 19.05), Lah Saw Smit (1.073 and 18.83%), DRR Blue, DRR Red, ON-1645, SisaPani (1.070 and 18.11%), Assamia Aloo, Bhura Aloo and Lal Mitti-2 (1.069 and 17.99%). The present study reflected enough genetic variability for specific gravity of tubers and tuber dry matter in indigenous genotypes and with high specific gravity can be used in breeding programme.

**Keywords:** Specific gravity and dry matter, *Solanum tuberosum*, Variability

## 197 (P-197)

### **Stability analysis of quality protein maize hybrids under heat stress across different environments of Prayagraj district in northern India**



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Maize is considered important because of its special characteristics that include its, wider adaptability, higher multiplication ratio, desirable architecture, superior transpiration efficiency and high versatile use etc. This study claims to determine whether such a statement is accurate and to examine stability in terms of gene action. The study was carried out in three research sites representative different places in CRF, SHUATS, Prayagraj City at an elevation of 98 meters above sea level at 25.87° N latitude and 81.54° E longitude. and all the locations has sub-tropical climate with extremes of summer and winter. During winter season especially in month of December and January, temperature drops down to as low as 1-2° C, while during summer the temperature reaches up to 45°C (NICMEIT 2022). This experiment was undertaken under Randomized Block Design with three replications for assessing their stability. The mean squares due to genotypes, parents, hybrids, and parent vs. hybrids were very significant for all eighteen quantitative and qualitative characters under study, according to the analysis of variance for diallel analysis (model I method II). A stability study was carried out to determine the grain yield of 45 maize hybrids under three environments (E1, E2 and E3), using Eberhart and Russel model. The analysis of variance for combining ability revealed the mean squares due to general combining ability (GCA) and specific combining ability (SCA) were highly significant for all characters studied. Inbred lines P4, P5 and P2 showed significant to highly significant positive GCA effects on grain yield per plant and its attributes, indicating that both parents were good general combiners for this trait. Four hybrids (P5 X P7, P5 X P6, P4 X P8 and P4 X P5) exhibited significant to highly significant SCA effects for grain yield per plant. The estimates of standard heterosis over the best check (HQPM-5) for grain yield per plant revealed five top cross combinations (P5 X P7, P5 X P6, P4 X P8, P5 X P9 and P4 X P5), exhibiting highly significant positive standard heterosis regarding their high and stable performance across environments. The single cross hybrids over all the environments P5 X P6, P5 X P7 and P4 X P5 were found promising for the majority of characters studied, with high mean performance across environments. Based on regression coefficient close to unity ( $\beta_i \approx 1$ ) and a non-significant deviation from regression ( $s^2_{di}$ ), indicating their adaptability across all environments investigated, best performing hybrids were identified according to three different environments in E1, E2 and E3 were P1X P6, P2X P4, P2X P6, P2X P8, P3X P5, P4X P5, P4X P7, P4X P10, P5X P6, P5X P7, P6X P8, P7X P8, P7 X P9, regression coefficient near to unity ( $\beta_i \approx 1$ ) and non-significant deviation from regression ( $s^2_{di}$ ) there by indicating its adaptability over all environments, thus indicating stable performance in different environments for most of the characters.

**Keywords:** Combining ability, Diallel crossing, G x E interaction, Heat tolerance, Heterosis effect

**198 (P-198)**

**RT-PCR detection and identification of monopartite *Bean common mosaic virus***



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Using ELISA positive sample, reverse transcription polymerase chain reaction (RT-PCR) was optimised for detection of *Bean common mosaic virus* targeting partial coat protein and polyprotein gene. Three pairs of specific primers that flank BCMV coat protein and polyprotein gene were designed to amplify fragments approximately ranging from 191 to 205 bp. Further, the specificity and sensitivity of primer pair BCMV 2 established. The BCMV2 primer pair specifically amplified the target amplicon (200bp) from the suspected leaf sample and no amplicon was observed when tested against other pathotypes of potyvirus such as BCMNV, BYMV, CABMV, SMV and PeMoV. The designed primer was sensitive enough to detect 0.05% (~100pg) of target cDNA. Further, the RT-PCR protocol was validated using field samples collected from Hyderabad, Telangana. ELISA in combination with the developed BCMV specific RT-PCR will ensure a foolproof, sensitive and rapid, procedure for diagnosis of BCMV in quarantine processing of imported germplasm and helps in conserving BCMV free seeds in gene bank for posterity which is important as it is a seed borne virus.

**Keywords:** *Bean common mosaic virus* (BCMV), RT-PCR, ELISA, Genebank

## 199\_(P-199)

**Physico-chemical characterization of bael [*Aegle marmelos*(L.) Correa] genotypes collected from Achanakmar-Amarkantak Biosphere Reserve, Chhattisgarh, India**

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Bael (family Rutaceae) is an important indigenous fruit tree found throughout India. It has the capability to grow in semi-arid regions, forests, hills, and plains. An exploration was conducted to collect the distinct diversity in bael germplasm during April-May, 2022 from different locations in Achanakmar-Amarkantak Biosphere Reserve in Chhattisgarh. A total of 32 accessions were collected from the surveyed areas and out of which 21 distinct forms of fruits were identified and evaluated for various physical and biochemical traits viz., fruit weight, percent shell/skull weight, number of seeds, percent edible portion, total soluble solids (TSS), ascorbic acid, carotenoids, phenolics, ferric



reducing antioxidant power assay (FRAP) antioxidant activity and flavonoids content. Among the physical parameters of collected fruits; average fruit weight ranged from 77.65-2542.5g, number of seeds per fruit 13-151, pulp/edible content 35.59-71.22 percent, skull portion 17.08-45.09 percent, while dry matter of pulp ranged from 19.49-50.53 percent in different genotypes. In biochemical parameters, TSS content ranged from 26.81 to 54.16 °B while total carotenoids ranged from 0.62- 6.21µg/g. The vitamin-C content varied from 0.308 to 0.691 and FRAP antioxidant activity was observed in the range of 0.09502-0.20199 percent QE. Phenolic content was found highest in accession IC0645480(2.27 percent GAE) followed by IC0645504(2.22 percent GAE) and the lowest was found in IC0645501 (1.22 percent GAE). The flavonoid content was ranged from 0.122-0.618 percent QE in different bael genotypes. These results shows rich diversity exists in shape size, skull thickness and availability of health-promoting bioactive compounds in explored area and great potential for further exploration in its improvement & breeding programs. The tree having high content of pulp, TSS, carotenoids, antioxidants etc. can be multiplied and used in cultivation.

**Keywords:** Exploration, Ascorbic acid, Carotenoids, Phenolics, Antioxidant activity and Flavonoid content

## 200 (S-06)

### **Genetic Resources of MAPs conserved at CSIR-NEIST, Jorhat for trait specific breeding with special reference to NE India**

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The exploration of medicinal and aromatic germplasm along with conservation is the most crucial for development of Medicinal and aromatic plants (MAPs) with elite traits lines. Therefore, CSIR-NEIST is trying to conserve a large number of germplasm (>2807) of different MAP species like Java citronella (72), Lemongrass (534), *Kaempferia galanga* (143), *Kaempferia parviflora* (42), *Kaempferia rotundus* (21), *Acorus calamus* (230), *Zingiber zerumbet* (124), *Clerodendron colebrookianum* (42), *Capsicum chinense* (>274), *Solanum khasianum* (286), Patchouli (83), *Curcuma caesia* (136), *Curcuma longa* (>350), *Curcuma zedoaria* (86), *Zingiber officinale* (>590), *Bixa orellana*(42), *Homalomena aromatica* (126) and *Cannabis sativa* (43) some of which are rare, endangered and all of them are medicinally important plant species. Most of the germplasm have been submitted to ICAR-NBPGR, New Delhi for allocation of the indigenous collection number (IC) and all of them have been conserved *ex-situ* at experimental farm of CSIR-NEIST, Jorhat, Assam. This repository can be considered as the largest *ex-situ* gene bank of medicinal and aromatic plants in the entire Northeast India which includes *Solanum khasianum*, *Kaempferia galanga*, lemon grass, Java citronella and Patchouli. So far, a total of 21 trait specific germplasm were identified/ developed from this repository using various breeding techniques like selection or mutation breeding. The developed



germplasm was checked for stability in different macro and micro environments which has performed well under varied environmental conditions. Some of the unique germplasm identified were elemicin rich, methyl eugenol rich, myrcene-methyl isoeugenol rich, geraniol rich lemon grass; red berries, white berries, high fruit yield and spineless lines of *S. khasianum*. These elite germplasms are high performing at commercial scale owing to which 43 technologies have been transferred so far generating high revenue as well.

**Keywords:** Medicinal and aromatic plants, Varietal development, Largest repository

## 201 (P-201)

### **Predicting chickpea flavonol content with NIR Spectroscopy and machine learning algorithms**

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Plants use flavonoids in many ways. Flavonoids are synthesised in specific sites in plants and provide colour, aroma, seed, spore, and seedling germination, growth, and development. Flavonols, a major class of flavonoids, have antioxidant, antimicrobial, hepatoprotective, anti-inflammatory, and vasodilation properties and may be anticancer agents. Chickpea is the third major pulse produced globally, with 11.6 million tonnes produced per annum. Near-Infrared (NIR) spectroscopy is a non-destructive, versatile and powerful analytical technique. This study uses NIR and machine learning prediction models to measure chickpea flavonol concentration. NIR spectroscopy data must be pre-processed to extract useful information for building models to predict physical or chemical components. Flavonol prediction models are developed using Linear Regression (LR), Artificial Neural Network (ANN), Random Forest (RF), Support Vector Regression (SVR), and Decision Tree Regression (DTR) algorithms. Performance of the models is evaluated using measures namely, Root Mean Square Error (RMSE), Residual Standard Error (RSE), coefficient of determination ( $R^2$ ) and adjusted coefficient of determination (adjusted  $R^2$ ). It was discovered that ANN and RF prediction models perform best in the wavelength range 400-1444 nm, to predict flavonol concentration of chickpea. The model created by the ANN algorithm was discovered to have the lowest RMSE value of 0.06 and RSE values of 0.07. The  $R^2$  and adjusted  $R^2$  values of 0.89 and 0.84, respectively, are the highest of the five models. The RMSE, RSE,  $R^2$ , and adjusted  $R^2$  values of the RF model are 0.05, 0.06, 0.85, and 0.84, respectively, with only minimal deviations from those of the ANN model in terms of accuracy. This research can be carried out quickly and cheaply for other crops to identify concentrations of other components.



**Keywords:** Chickpea, Flavonols, Germplasm, Machine learning, Near-Infrared spectroscopy

## 202 (S-03)

### Collection, conservation and multiplication of pearl millet landraces in Rajasthan

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Pearl Millet is globally known for its nutritional quality parameters and to promote millets, the year 2023 declared as the International Year of Millets by UN. Pearl millet landraces are adaptable to the local conditions to evade the risk of uncertainty in production thus, these play an important role in yield stability of farmers; hence an attempt was made to collect different pearl millet landraces across the Rajasthan State to evaluate them for further selection. The seeds of collected landraces were assigned codes and the coded packets were grown as crowd sourcing trials (mother trials and baby trials) at research stations as well as farmers' fields during *Kharif* season of 2019, 2020 and 2021. The data recorded on different parameters were fed in CLIMMOB app to draw conclusion. Out of 102, 7 landraces viz., *Moochwali Bajri*, *Pili Bajri*, *Sulkhaniya Bajri*, *Sundaram Verma Local*, *DR-1*, *DR-2* and *Chanana Bajri* were found promising in yield as well as nutritional parameters which were submitted to NBPGR for conservation and allocation of IC numbers. *Sulkhaniya Bajri* yielded maximum grain yield (12 q/ha) whereas *Moochwali Bajri* had maximum fat content (5.2%). The DUS testing of the promising landraces were also undertaken during *Kharif* 2020 and 2021. The nutritional profiling of these landraces were done at ICAR-NBPGR and it was found that *Sulkhaniya Bajri* had the maximum TSS (2.65%) whereas, maximum starch (62.45%) was recorded by *Pili Bajri*. The protein was found maximum (15.90%) in DR-2 whereas, DR-1 had maximum amylose content (26.25%). The maximum total dietary fibre (TDF) (13.23%) and Phytic acid (0.94%) was found in *Chanana Bajri*. The seeds of these landraces have been conserved at gene bank of ICAR-NBPGR, New Delhi and further multiplication for promotion at community level in selected sites of Rajasthan state.

**Keywords:** Collection, Conservation, Landraces, Pearl Millet, Rajasthan

## 203 (P-203)



## **Characterization and evaluation for agronomic traits of an orphan oilseed crop; Niger (*Guizotia abyssinica* L.F. Cass)**

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Niger is mainly cultivated as an oilseed crop in Ethiopia, India, Pakistan, and Nepal. The crop is mainly grown by tribal farmers as their traditional crop and it requires fewer inputs for cultivation. For the niger to be competitive with other crops, its seed yield must be significantly improved. Niger being a self-incompatible and cross-pollinated crop, it has a wide genetic base. However, the wealth of niger genetic diversity has so far remained largely unexploited. Hence, the present study was conducted to characterize and evaluate 1800 accessions. For characterization, 10 qualitative traits and 18 quantitative traits were included and evaluation was done for 8 major agronomic traits in Augmented Block Design with three checks *viz.*, JNS-9, JNS-28 and JNS-30 in two seasons. Pooled data of two year studies was used for the estimation of the variability parameters, association study and path analysis. Analysis of variance showed that the genotypes used in the study significantly differ from each other for all the characters under study revealing presence of high variability in the panel being evaluated. Variation for plant height ranged from 16.8 cm to 93.6 cm; Days to 50% flowering from 25 to 90 days; number of primary branches/plant 2 to 8; number of capitula/plant 18 to 170; Seed yield/plant 0.3 g to 14.8g; oil content 11.9% to 44.5%; and 1000 seed weight was 3.2 g to 7.4 g. In addition, novel phenotypes like two male sterile accessions (IC 856 and IC 0585545) and eight self-compatible accessions were identified. This is the first report of evaluation of 1800 accessions for two consecutive years. The novel and promising accessions will be further utilized in developing improved breeding populations in niger.

**Keywords:** Niger accessions, DUS traits, Self-compatibility, Male sterility

**204 (0-12)**

## **Introduction and morphological characterization of *Heeng* (*Ferula assa-foetida*) accessions in cold deserts of Indian Himalayas**

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*Heeng* (*Ferula assa-foetida*) is one of the important spice and medicinal plants in India. *Ferula assa-foetida*, a native of Iran, Afghanistan, and Uzbekistan, is an herbaceous perennial plant of the family Apiaceae. It is a plant of cold deserts, take five years from the germination to first flowering and also to produce the oleo-gum resin called as asafoetida or *Heeng*. Raw *Heeng* is extracted from the fleshy tap roots, about one-meter long. India alone consumes approximately 40% of the world's *Heeng* produce and is completely dependent on imports (valued about ₹1000 crores annually). Recognizing the importance of *Heeng*, CSIR-Institute of Himalayan Bioresource Technology (IHBT), Palampur introduced its seeds in the country through ICAR-NBPGR, New Delhi. DNA barcoding of the received seed samples was performed to confirm the authenticity of *Heeng*. After standardization of germination by overcoming the seed dormancy, seedlings were raised in controlled conditions at CSIR-IHBT, Palampur and initial trials were conducted at Centre for High Altitude Biology (CeHAB), Ribling, Lahaul & Spiti (a regional station of CSIR-IHBT) under the vigil of ICAR-NBPGR, New Delhi. Field trials have been laid out at farmer's fields in five districts (Lahaul & Spiti, Kinnaur, Mandi, Kullu and Chamba) of Himachal Pradesh to evaluate their performance. Country's first "*Heeng* Germplasm Resource Centre" has been established at CSIR-IHBT, Palampur for the conservation of its valuable germplasm. Plant type and leaf shape of *Heeng* introduced from Afghanistan was highly different from the one introduced from Iran. A significant variation was recorded for the morphological traits viz. plant height, leaf type, leaf shape, number of leaves per plant, leaf length, primary and secondary leaflets number, primary root diameter etc.

**Keywords:** Domestication, *Ferula assa-foetida*, *Heeng*, Indian Himalayas, Introduction.

## 205 (O-02)

### **Species distribution, exploration, collection and conservation of *Salacia* species (high value anti-diabetic plant) of Western Ghats**

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Genus *Salacia* (Family: Celastraceae/Hippocrateaceae) comprises of woody climbing shrubs which are effective as antidiabetic, antiobese, hepatoprotective, hypolipidemic and antioxidant agent. The genus is an important source of chemicals of immense medicinal and pharmaceutical value such as salacinol, mangiferin and kotanalol which are derived from their roots, root barks, stems etc. As per the literature, the genus *Salacia* consists of about 200 species in the world predominantly distributed in tropics whereas in India genus *Salacia* is represented by 21 species of which 15 species are known to occur in Peninsular India and it is distributed in Karnataka (rare in semi-evergreen forests of Western Ghats), Kerala (coastal forests of Kollam, Western Ghats of Pathanamthitta and Idukki districts) and Southern Orissa. However, the reports related to species distribution of this genus in Peninsular India are very naive and hence the herbarium survey and expert consultation was taken before starting the work. Survey of



herbariums like Calicut University Herbarium, Kerala Forest Research Institute Herbarium, Botanical Survey of India-Regional station, Coimbatore and Rapinhat herbarium, Tiruchirapalli gave information on distribution and phenology of different *Salacia* species thereby guiding the exploration and collection missions. Exploration and collections undertaken in Western Ghats resulted in the collection of 46 accessions of *Salacia* belonging to *S. chinensis*, *S. oblonga*, *S. fruticosa*, *S. macrosperma*, *S. beddomei*, *S. malabarica*, *S. gambleana* etc which included many endemic species as well. It was found that *S. chinensis* and *S. macrosperma* are the most widely distributed species in the Western Ghats and in higher elevation (1000–1700m). Taxonomic identities of all the collected species were established based on expert opinion and field identification characters as there is no identification keys reported in this species. Soil microbial load and soil analysis was done from the samples collected during the exploration to know the association of any microorganisms for *Salacia* growth in natural habitat to facilitate the successful establishment of collected accessions in the field gene bank of ICAR-IIHR, Bengaluru. Integrated conservation approaches encompassing *in situ* and *ex situ* needs to be implemented in this species as it belongs to the IUCN vulnerable category. Hence, *in vitro* conservation studies were attempted in an elite line of *S. chinensis* already maintained in the field gene bank of ICAR-IIHR using nodal segments as explants in MS-medium supplemented with BAP alone (2.0 mg/l) and combination of BAP (2.0 mg/l) + NAA (0.8 mg/l). The combination gave promising results which needs to be further expanded to other species as well. Hence, the study is a holistic approach aimed at exploration, collection and conservation of a vulnerable medicinal plant species for sustained availability and utilization.

**Keywords:** Anti-diabetic, Germplasm conservation, Germplasm exploration, Species distribution, *Salacia* species, Western Ghats

## 206 (P-206)

### **A new orange-yellow coloured pure line with high beta carotene content in tomato (*L. esculentum*) for supplementing Vitamin A deficiency naturally**

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According to FAO, tomato is a part of healthy and balanced diet with per capita consumption of 19 kg per year. Tomato provides vitamins C and B with minor quantities of E and A, minerals and carotenoids which acts as antioxidants. According to FAO, Vitamin A deficiency is a public health problem in more than 118 countries. Tomatoes have red colour pigment i.e. lycopene but this cannot be converted into Vitamin A biologically. Although lycopene is a carotenoid, it is not utilized as provitamin A as is beta carotene. Considering the importance of tomato in daily diet of both rich and poor, varieties with higher beta carotene content can help in mitigating the deficiency disorders vis-à-vis in reducing the risk of associated health problems related with growth and reproduction including mortality and morbidity from infectious diseases. For this reason, varieties with high beta-carotene in tomatoes may prove beneficial. Few efforts



have been made to develop beta carotene rich tomato variety globally. Defence Institute of Bio-Energy Research (DIBER) Haldwani, a premier institute of Defence Research & Development Organisation, has made efforts to breed tomato varieties and hybrids for higher yield and cold tolerance. Efforts were also made to develop orange-yellow coloured tomato line with high beta carotene so that supplementation of vitamin A can be enhanced naturally in diet. This effort was made by screening more than 50 germplasm lines and segregating lines of tomato. The results revealed that newly developed tomato line with orange-yellow coloured fruits have beta carotene of 121.42 µg/g whereas red coloured varieties/lines exhibited very less beta carotene content (2.04-37.54 µg/g). Lycopene content of beta carotene rich line was quite lower (75.58 µg/g) compared to red coloured varieties and lines. This line has been submitted to NBPGR and registration number has been allotted as IC0642490. The paper deals with the efforts made in development of beta carotene rich line of tomato and its nutritive value.

**Keywords:** Beta carotene, DIBER, IC0642490, Orange-yellow coloured tomato, Vitamin A

**207 (P-207)**

### **Interception of weed seeds in exotic rice germplasm**

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The exchange of rice seeds from one country to another and among research institutions is indispensable in rice improvement and production. However, rice seeds are potential carriers of weed seeds. Many noxious weeds in India are of foreign origin and have been introduced accidentally through the importation of planting materials, especially seeds. The most effective means of dealing with the weed seed contaminants in crop seeds for planting are prevention and decontamination. Application of stringent plant quarantine regulations have proven to be the most inexpensive solution to this problem. The incoming and outgoing rice seeds were examined as per provisions of the Plant Quarantine (Regulation of Import into India) Order, 2003. Weed seeds were separated from rice seed and segregated into different types on the basis of their shape, size, colour, texture and the presence of any attachment. All intercepted weed seeds were identified to species level based on their morphological characters. Seed-borne fungi of weed seeds were determined using the blotter method. Seed borne fungi were detected and identified after incubation using a stereoscopic microscope. Fifteen percent of the incoming rice seed shipments and 0.3% of the outgoing rice seed shipments were contaminated with weed seeds. Twenty weed species namely, *Aeschynomene indica*, *Aeschynomene* sp., *Stellaria media*, *Cyperus compactus*, *Cyperus difformis*, *Cyperus* sp., *Fimbristylis minacea*, *Fimbristylis* sp., *Scirpus juncooides*, *Scirpus supinus*, *Scirpus* Sp., *Digitaria*



sp. *Echinochloa* spp., *Isehaemum rugosum*, *Panicum* sp., *Paspalum conjugatum*, *Paspalum dilalatum*, *Paspalum distichum*, *Paspalum* sp. *Rottboellia cochinchinensis* were identified as rice seed contaminants. *Echinochloa* spp. were the most frequent, with as many as 36 seeds per seed-lot. *Echinochloa cru-pavonis*, which is a quarantine weed for India, was intercepted in five and seven shipments imported from IRRI, Philippines and China, respectively. Storage fungi *Penicillium* spp. *Aspergillus* sp. and *Rhizopus* sp. were detected in incoming *Echinochloa* spp. weed seeds. Pathogenic seed borne fungi such as *Bipolaris oryzae* and *Fusarium moniliforme* were detected on the *Echinochloa* spp. seeds intercepted in the rice seeds imported from IRRI, Philippines. More care in processing rice seeds for germplasm exchange is needed to prevent weed seed contamination and spread.

**Keywords:** Exotic germplasm, Quarantine, Rice, Weed

## 208 (P-208)

### **Introducing true cinnamon (*Cinnamomum verum*) in non-traditional areas of Himachal Pradesh**

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Cinnamon (*Dalchini*) is the peeled bark rolled in quills, has sweet spicy aroma, and is derived from an evergreen bushy tree *Cinnamomum verum*. However, the *Cinnamomum cassia* is yet another species whose bark is used in place of true cinnamon, but it has high coumarin content, which is not good for health. Realizing the large import (~ 45,000 tonnes annually) of cinnamon in the country and that the major one imported in India is deleterious *C. cassia*, it was envisioned to expend organized cultivation of *C. verum* in non-traditional areas. Therefore, to identify best-suited cinnamon genotypes for Himachal Pradesh, 153 diverse seedlings (obtained from ICAR-IISR, Kerala) are being evaluated in Palampur with three checks (Nithyasree, Konkan Tej and Local1) in an augmented design. The first year growth of all the test entries were measured as plant height (cm), number of branches, growth index and stem girth (mm). The analysis of variance showed a significant genetic variation in the tested set of entries. Stem girth is significantly and positively correlated with all the measured traits except number of branches. Entries CV33, CV77, CV89, CV107, and CV168 were the higher than overall mean for all the studied traits. Entries CV136, CV4 and CV 154 were recorded hieghest growth index with higher stem girth. The findings pointed out that cinnamon has the potential to be grown in Himachal Pradesh, and the identified superior genotypes (CV4, CV33, CV77, CV89, CV107, CV136, CV 154, and CV168,) should be focused on for future breeding programs and local adaptations in Himachal Pradesh.

**Keywords:** Evaluation, Germplasm, Variation, *Cinnamomum verum*



**209 (P-209)**

**Systematic detection of genetically modified ingredients in food derivatives**

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Genetically modified (GM) food crops have been developed for resistance to insect pests, tolerance to abiotic stress, and for improving different characteristics including color, flavor, texture, and shelf life along with nutritional enhancement. In India, genetically modified organisms (GMO) and GM-derived products are regulated under the Rules, 1989 notified under the Environment (Protection) Act, 1986. With respect to the Food Safety and Standards Authority of India (FSSAI) Order dated 21 August 2020, every consignment of 24 selected crops need to be accompanied with the non-GMO certification. Systematic GMO testing is essential for verification of non-GM status of food products. DNA-based methods are preferred for testing of raw or partially processed products or derivatives. Quality of DNA needs to be ensured as DNA amplifiability may be hampered by processing or presence of inhibitors due to complex constitution. In the present study, suitable DNA extraction procedures have been optimized and validated for range of food derivatives including babyfood and other products of corn and soybean. Amplifiability of DNA was ensured using endogenous gene-specific assays or/ and inhibition test. The developed/ validated PCR/ real-time PCR assays are being utilized to test the GM status of food derivatives collected from the retail shops and markets to track the unauthorized entry of GM products in supply chain as well as in the marketplace.

**Keywords:** GM detection, Food derivatives, PCR, Real-time PCR, Inhibition test

**210 (P-210)**

**Molecular diversity analysis reveals high amount of genetic variation and population differentiation in aromatic rice landraces of Indo-Gangetic Plain region of India**

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The presence of genetic diversity within a species is of paramount importance both for genetic improvement and conservation of diverse constellation of alleles found in the traditional landraces of cultivated crops. In view of identification of diverse alleles in the landraces of aromatic rices, we analysed molecular variation in 96 aromatic rice



landraces of Indo-Gangetic Plain region of India using 48 hypervariable microsatellite loci of a rice diversity panel with genome-wide coverage. High amount of allelic polymorphism was observed between landraces of aromatic rice. The mean number of alleles per locus was 11.06, which showed that a high level of DNA polymorphism exists among different landraces of aromatic rice analyzed. This was also supported by high value of polymorphism information content (0.87). The average frequency of unique alleles was 1.75, whereas the frequency of rare alleles was 2.75 in the total of 531 alleles scored using 48 SSR primer-pairs. The unique and rare alleles could be used for DNA fingerprinting and differentiation of genotypes. A high number of multiple alleles were observed in number of landrace accessions, which showed the presence of heterogeneity and heterozygotes in the landrace materials studied. The results of present study are useful for utilization of the landraces in genetic enhancement programmes specially designed for rice quality improvement and consumer's preference.

**Keywords:** Aromatic rice, Indo-Gangetic Plain, Landraces, Molecular diversity

## 211 (P-211)

### **Morphological and molecular characterization reveals high extent of genetic variation in accessions of wild rice species of AA genome**

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Crop genetic resources are invaluable germplasm for trait discovery and allelic diversity for genetic enhancement of cultivars of agricultural crops. Crop wild relatives (CWRs) of rice are vital genetic resources for identification of target traits and desirable allelic polymorphism for mainstreaming variability into cultivated gene pool. In this endeavour, we assessed phenotypic diversity in 93 accessions of CWRs of rice belonging to eight *Oryza* species of AA-genome. These accessions were phenotyped using 37 descriptors of IRRI-Bioversity International, which included 20 qualitative and 17 quantitative traits. A high amount of genetic variation observed for both qualitative and quantitative phenotypic traits. The qualitative traits namely basal leaf-sheath colour, culm angle, flag-leaf angle, ligule colour and shape, auricle colour, stigma colour, panicle type and exertion, awning and awn colour, pericarp and hull colour showed prominent variability. The quantitative traits viz., days to heading and flowering, plant height, flag-leaf length and width, culm length, awn length, panicle length, grains per panicle, 100-grain weight, grain length and breadth exhibited large extent of variation. Molecular characterization using 45 hypervariable microsatellites revealed the presence of high genetic variation in wild rice species accessions. A total of 678 alleles amplified, which ranged from 4 to 26 alleles with mean of 15.05 alleles per locus. The high value of



polymorphism information content (0.89) also revealed large extent of allelic polymorphism in the CWRs of rice analysed. The high frequency of unique alleles (1.95 alleles per accession) and rare alleles (3.68) showed that many CWRs possess private alleles, which could be used for genetic identity and differentiation of individual accessions. A high number of multiple alleles (two or three alleles per accession) observed in number of landrace accessions, which showed the presence of heterogeneity and heterozygotes in the accessions studied. The presence of diverse constellation of alleles for various traits in the CWRs of rice would be of immense utility for genetic improvement programmes

**Keywords:** Genetic variation, Morphology, Molecular characterization, Wild rice

## 212 (P-212)

### **Identification of diagnostic keys for selected wild genetic resources of grasses in southern India**

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Grasses are an important source of food for human beings (cereals, essential oils, flavouring agents, millets and sugar) and animals (seeds and fodder). They play a leading role in the food web being primary producers. Other than the food, they also have an economic, ecological and medicinal significance. India is one of the 17 mega biodiversity countries in the world and grasses play an important role. The grass family Poaceae with about 280 genera and 1525 taxa is the largest angiosperm family in India. Conservation of the gene pool of wild relatives of edible grasses is very important for breeding programmes and genetic engineering for increasing populations. India harbours many types of grasslands, which are the ideal habitats for various species of plants and animals. Therefore, correct taxonomic identification is a prerequisite to knowing our grass diversity and uses. Grass flora of any region is tedious work which includes botanical explorations and collections in all seasons, ecological studies in their habitat, collection of data like its uses and animal-plant interactions, if possible dissection of microscopic parts in fields, photography of habit, habitat and microscopic parts in fields, herbarium preparation and proper identification in the lab with the help of type specimens, other herbarium collections and relevant literature. Presently, taxonomic descriptions of grass taxa include a correct systematic position with the APG IV system of classification, bracketed keys to genera and species, citation of each taxon with updated nomenclature, type details, detailed descriptions, phenology, ecology, all types of uses and under notes other field observations along with associated plant communities.

**Keywords:** APG IV, Crop wild relatives, Grass diversity, Poaceae

## 213 (O-23)

### ***In vitro* regeneration protocol standardization of cultivated and wild species of okra**

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The present study was undertaken to evaluate the most suitable concentration of growth regulators for regeneration of okra (*Abelmoschus esculentus* L. Monech) via apical shoot culture and embryo culture. Cultivated okra genotypes like Pusa Sawani, DOV-92, Pusa Bhindi 5, Arka Anamika, Parbhani Kranti were used for both apical shoot culture and embryo culture while wild *sps.A.moschata*, *A. tetraphyllus* were taken for standardization of embryo culture. Epicotyl culture, shoot tip explants of 2 cm was used whereas for embryo culture, embryos were isolated from seeds. Both the explants i.e. epicotyl and embryo were cultured on regeneration medium, (Murashige and Skoog, 1962) supplemented with indole-3-butyric acid (IBA) (0.5, 1.0, 1.5, 2.0 mg/L) along with naphthalene acetic acid (NAA) (0.5, 1.0, 1.5 and 2.0 mg/L) for 2 weeks. After regeneration, cultures were inoculated on elongation medium containing MS medium supplemented with kinetin (0.5, 1.0, 1.5 and 2.0 mg/L). After 4 weeks, elongated shoots with roots were washed with distilled water, kept for primary hardening for 5 days, and later shifted to pots with autoclaved sterile coco-peat, vermiculite and perlite in the ratio of 3:1:1. In epicotyl culture, Pusa Bhindi 5 had shoot length of 3.23 cm followed by Pusa Sawani (3.13 cm), Arka Anamika (2.86 cm), Parbhani Kranti (2.73 cm) and DOV-92 (1.63 cm). In embryo culture, Pusa Sawani has attained more embryo height (5.3 cm) after regeneration followed by DOV-92 (3.6 cm), Pusa Bhindi 5 (3.2 cm) and Arka Anamika (2.8 cm) and no proper regeneration was observed in Parbhani Kranti. Among the two wild species, maximum embryo height was observed in *A.moschata* (4.3) cm followed by *A.tetraphyllus* (3.8) cm. to the best of our knowledge This is the first report on regeneration via epicotyl and embryo culture for these varieties in okra.

**Keywords:** *Abelmoschus*, Embryo culture, Epicotyl culture, NAA, IBA, Kinetin

## 214 (P-214)

### **Morpho-metric evaluation of Indian cashew (*Anacardium occidentale* L.)**

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The cashew tree (*Anacardium occidentale* L.) has been described as 'dollar generating crop' of India. Morphological characters have been proved to be a powerful tool in selecting cultivars. The evaluation of cashew hybrids was done with respect to qualitative and quantitative morphological descriptors associated with yield contributing traits using measuring tapes, direct observations and comparison with descriptor schemes, electronic balance and 12.5 cm vernier caliper as suggested by AICRP Cashew, ICAR. Cashew hybrids were developed from five crosses (Local parent X 2/9 Dicherla; H-2/15 X Red Hazari, WBDC-V X JGM-1, BLA-39-4 X H-2/15 and H-2/15 X Yellow Hazari) involving 8 parents of Indian cashew. Most of the cashew hybrids were characterized as spreading type with oblong leaf and extensive branching pattern. Inflorescence branching were two sided with creamy coloured flowers with mostly conical-obovate apple yellow apple with round nut and angular nut apex. Mean performance of genotypes H-39, H-113, H-129 and H-49 showed maximum nut yield/tree in both the years. Different genotype groups (parents & their hybrids) showed significant variation with respect to quantitative characters in both years. From the study, the characterization of cashew hybrids developed using different parental crosses will help in the future breeding programme for the improvement of cashew.

**Keywords:** Cashew, Descriptors, Evaluation, Morphology

## 215 (P-215)

### **Mapping and mining of major genomic regions conferring resistance to Bruchine (*Callosobruchus maculatus*) in blackgram (*Vigna mungo* (L.) Hepper)**

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Storage pest bruchine, *Callosobruchus maculatus* (F) is a major production limiting factor in Blackgram (*Vigna mungo* (L.) Hepper). The present study was employed in a biparental mapping population derived from a cross between susceptible (MDU 1) and resistant (TU68) genotypes. Phenotyping was carried out under an artificial bruchine screening procedure. QTL studies revealed three major QTLs responsible for the total number of adult emergence (AE), percentage of seed damage (SD) and developmental time (DT). The QTL for AE and SD shared the same linkage group 5 named as *qbr\_AE@50DAI* and *qbr\_SD@50DAI* respectively. It explained for about 17.01% of phenotypic variation ( $R^2$ ) with a LOD score of 3.339. The QTL for the DT was mapped on linkage group 8 and named as *qbr\_Dev.T*. It explained 17.01 % of  $R^2$  with a LOD score of 3.488. The validation of identified QTLs was carried out on other mapping populations viz., VBN 6 x TU 68 and VBN 8 x TU 68 through single marker analysis. It revealed that markers CEDG020 and CEDG302 can be used in the future bruchine resistance breeding program. Genome mining on the QTL regions harbours several possible candidate genes



related to defense response against herbivory insects viz., serine/ threonine protein kinase proteins, zinc finger family proteins, F-box proteins, leucine – rich repeats regions and some transcription factors and enzymes etc. The outcome of this study will be useful for bruchine resistance breeding program.

**Keywords:** Blackgram, Bruchid, Genomic regions, QTL

## 216 (P-216)

### Development of tomato hybrids and parental lines through MABC and their evaluation for processing traits

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Keeping in view the growing demand for processed tomato products India, there is need for tomato processing varieties/hybrids. Along with superior processing traits, tolerance to biotic abiotic stresses, adaptability to local growing conditions high yield are also important traits should be the characteristics of these varieties/hybrids. Advanced marker assisted backcross (MABC) tomato breeding lines (BC<sub>2</sub>F<sub>7:8</sub>) were developed for tolerance to tomato leaf curl disease (ToLCD), fusarium wilt. The parental lines included Pusa Rohini, Pusa 120, Pusa Ruby and Pusa Gaurav. The donors were selected from F<sub>7:8</sub> breeding lines carrying various combinations of *Ty* genes for ToLCD including, *Ty-2+Ty-3*, *Ty-2*, *ty-5+Ty-2*; *ty-5+Ty-6*; for fusarium wilt (*I-2* gene). Among various *Ty* genes, *Ty-3* was found to be most effective for imparting tolerance to ToLCD in homozygous condition under epiphytotic conditions at ICAR-Indian Agricultural Research Institute, New Delhi, a naturally hot spot for ToLCD. All these breeding lines (BC<sub>2</sub>F<sub>7:8</sub>) were highly tolerant (<5 % disease severity index) to ToLCD compared to their recurrent parental lines, Pusa Rohini, Pusa 120, Pusa Ruby, Pusa Gaurav, which were highly susceptible (>95 % DSI). These lines were also highly tolerant (<5 % DSI) to fusarium wilt disease. A total of 65 advanced lines found promising for high yield (>60 t/ha), high resistance to ToLCD (<5 % DSI). More than 700 F<sub>1</sub>s were developed using these MABC lines and were evaluated under station and multilocation trials for ToLCD resistance, yield and quality parameters. Additionally, through genetic enhancement, advanced interspecific breeding using *Solanum habrochaites* accession (LA1777) were developed. Among these, one line, DTH-11 (F<sub>5:6</sub>) was found promising for high yield (62.5 t/ha), high TSS (5.3 °B), determinate growth habit and uniform ripening of fruits. Using these breeding lines, F<sub>1</sub>s with superior processing traits have been developed. A total of 60 F<sub>1</sub>s along with their parental lines were evaluated for processing traits as well as ToLCD under station trials. Among the various processing traits analyzed included average color (a/b ratio), average fruit weight (g), pericarp thickness (cm), locule number, juice (%), total soluble solids TSS (°B), acidity (%), lycopene (mg/100 g FW), ascorbic acid (mg/100 g FW), yield (t/ha), brix yield (q/ha), ToLCD resistance (PDI %). Among the promising hybrids and parental lines



found promising for processing traits included H-162, H-410 and H-4-3 and parental lines-H-17-34-3-1(2), H-38-3(1), H-38-3-4, selection-904113 and selection-904115. Further, they will be compared with commercial varieties to confirm their competitiveness for processability.

**Keywords:** DTH-11, MABC, Tomato, ToLCD resistance

## 217 (P-217)

### **Genotypic variation for drought stress tolerance in diverse set of sesame accessions**

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Sesame (*Sesamum indicum*) is an important oilseed crop due to its high oil content with a significant amount of unsaturated fatty acids and the presence of antioxidants such as sesamin, sesamol, and tocopherol. Sesame is generally considered to be a drought-tolerant crop, but it is sensitive to drought at vegetative and reproductive stages, leading to reduced growth and yield. To understand the physiological basis of tolerance to drought stress in sesame, a diverse set of 80 sesame accessions were evaluated under full and deficit irrigation regimes in the rainout shelter. Drought stress was induced in one set of plants at flowering till the plants showed wilting symptoms. Results showed that the chlorophyll content was not influenced by drought stress, however a significant reduction was recorded in seed yield (41%) and test-weight (17%) compared to control. Root traits like primary root length (PRL), total root length (TRL), root volume (RV), average root diameter (ARD), root surface area (RSA), and root biomass (RB) were significantly influenced by drought stress. TRL, RSA, and RB showed a significant correlation with the soil moisture content at different depths, but this relationship was not significant with other root traits. Relative water content and membrane stability index decreased by 35% and 20%, respectively under drought as compared to irrigated plants. The principal component analysis and hierarchical clustering based on Ward's methods using relative values of traits grouped accessions into four clusters. The efficient cluster (EC350648, IC129772, and KRJ5) showed less reduction in seed yield and test-weight and improved root growth with significant canopy temperature depression than the inefficient cluster, thus keeping the plants cooler. Accessions with considerable tolerance to drought stress can be either used as 'donors' in sesame breeding programme or can be cultivated in arid areas with limited water availability.

**Keywords:** Diversity, Drought, Evaluation, Root traits, Sesame



## 218 (P-218)

### **Genetic variability, heritability and correlations for fruit cracking in pomegranate**

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In the present study, initially sixty-eight pomegranate germplasm accessions screened for fruit cracking (%) at ICAR-NRCP, Solapur in a randomized block design with three replications. Analysis of Variance (ANOVA) showed significant differences between the genotypes both at 1% and 5% level of significance (Pvalue: 1.61\*\*). Fruit cracking (%) among the germplasm ranged from 0-53.90%. Based on the fruit cracking (%) data accessions were categorized. Further from different categories nine diverse pomegranate accessions were selected for genetic analysis during 2021-22. The genetic variability, heritability and correlation coefficients for nine morphological traits was estimated. The experiment was conducted in a randomized block design with three replications. Fruit cracking(%) among the accessions ranged from 0(IC-318718)-27.23% (Yercaud-I) with coefficient of variation(%). ANOVA showed significant differences between the genotypes both at 1% and 5% level of significance for fruit cracking (P value:  $1.27 \times 10^{-05}$ \*\*\*); fruit weight (0.0056\*\*) and rind moisture content (0.013\*) traits. The  $R^2$  value for these traits is 0.87; 0.69 and 0.67. Trait showed the genotypic coefficient of variation (60.32%), phenotypic coefficient of variation (67.57%), broad sense heritability (79.69) and mean genetic advance (110.92) is found to be high means this trait would respond to selection with high probability. Phenotypic correlation between the fruit cracking (%) and other morphological traits found that fruit cracking (%) is positively correlated with the fruit weight (0.50\*\*), rind moisture (0.398\*) and pedicel diameter (0.4885\*\*) characters. These identified traits associated with fruit cracking (%) will act as a selective marker in identifying promising genotypes in pomegranate breeding programmes.

**Keywords:** Analysis of variance, Fruit cracking, Genetic variability, Heritability, Morphological traits, Pomegranate

## 219 (P-219)

### **Evaluation of cross species transferability of SSR markers in wild relatives of Safflower**

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The species is closely associated with cultivate safflower are *C. lanatus*, *C. oxyacanthus* and *C. palestinus*. Among the three two of them were distributed in higher reach of western Himalayan region and western part of India. The collected accession along with imported accession are conserved in National seed gene bank at ICAR-NBPGR were used for this study. These wild relatives known to possess important traits such aphid resistance and moisture stress which can be used in varietal development program of safflower. In order to study the genetic diversity of these wild species available in the gene bank, genomic SSR markers developed in *C. tinctorius*an cultivated species was used. These SSR markers were evaluated for their cross-species transferability and estimation genetic diversity existed in the wild species. Total 71 accessions belong to two species viz. *C. lanatus* (23 accessions) and *C. oxyacanthus* (48 accessions) available in the gene bank were used study the genetic diversity in the species. Total 50 genomic SSR markers from *C. tinctorius* were used to evaluate transferability of these markers in both the species. Out of these markers 10 (20%) markers in *C. lanatus* and 14 (28%) in *C. oxyacanthus* displayed clear and reliable amplicon. The remaining markers were either not amplified or multiband amplification. These resultsshowed high level of transferability of SSR markers and genetic diversity in *C. oxyacanthus* than *C. lanatus*. Among the *C. lanatus* accessions, principal co-ordinate analysis grouped them based on their geographical distribution and the Indigenous accessions are formed separate group compared to exotic collections. In *C. oxyacanthus* grouping of accession based on the geographical distribution and temporal variation in collections.

**Keywords:** Cross species transferability, Evaluation, Safflower, SSR markers, Wild relatives

## 220 (P-220)

### Comparative studies on sequence based genotyping methods for molecular characterization of Safflower (*Carthamus tinctorius* L.) germplasm

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Safflower (*Carthamus tinctorius* L.) is an oilseed crop, rich in polyunsaturated fatty acids (linoleic acid) and monounsaturated fatty acids (oleic acid), which are used as edible oil. There are about 7000 accessions are conserved in the National Gene Bank at ICAR-NBPGR. In order to utilize this germplasm, the molecular characterization through genotyping is importance. This will help in systematically reduce number of accessions through molecular core development and identifying traits through GWAS. For genotyping two main approaches are available either PCR based markers or sequence-based approach. PCR based markers generate data with relatively small numbers of loci and oligonucleotide libraries significantly add more to overall costs as compared to



genome-wide sequencing approaches that deliver large number of loci and reducing the overall cost in a single run. Lack of prior studies in Safflower on genotyping by sequencing, leads to optimization of method and finding the suitable set of Restriction enzymes (REs) for the RAD seq (Restriction Site-Associated DNA Sequencing) experiment. In present study total diverse 48 accessions from safflower germplasm were used for single (ApeK1) double-digest RAD seq (NlaIII-MseI and EcoR1-MseI), for library preparation and sequencing. The single RE (ApeKI) enzyme generated in 1387415 average raw reads per sample, whereas among the double digest the NlaIII+MseI pair generated more reads than (10146613) EcoR1+MseI (5499049). Average mapping percentage for reads from selected restriction enzymes were 25.05%, 92.21%, 92.89% for ApeKI, NlaIII+MseI and EcoR1+MseI respectively. However, the representation of variants ( $\geq 0.05$  minor allele frequency) among the genotypes (90%) were drastically different between the two combinations. Hence, genotyping of safflower germplasm for molecular characterisation was carried out with, the ddRAD with enzyme combination EcoR1+MseI.

**Keywords:** Genotyping, Germplasm, Restriction enzymes, Safflower

## 221 (P-221)

### **X-ray Radiography for Biosecuring PGR from Bruchid Infestation during Quarantine**

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Insects like pulses beetles/weevils/ borers (Coleoptera: Bruchidae/ Curculionidae/ Scolytidae), seed wasps (Hymenoptera: Chalcidoidea) infest seeds without showing any external symptoms of their presence within. Quarantine risk becomes much higher with the exchange of seeds with such hidden infestation because cannot be detected through routine visual inspection. X-ray radiography is a tool used in quarantine processing of over 340 plant genera for detection of such hidden infestation. X-ray of 22,146 samples belonging to 55 plant genera from a total of 9,48,751 imported samples of various crops during 2009- 2018 revealed presence of hidden infestation caused by bruchids in 1971 samples. Seven exotic bruchid species viz., *Acanthoscelides desmanthi* in *Desmanthus* spp. from Colombia, *A. obtectus* in *Phaseolus vulgaris* from South Africa and USA and in *Lathyrus sativus* from Lebanon; *Bruchus atomarius* in *Lens culinaris* from Lebanon; *B. dentipes* in *Vicia* spp. from ICARDA (Syria) and Lebanon; *B. ervi* in *Pisum sativum* and *L. sativus* from Lebanon and *Lens culinaris* from ICARDA (Syria), Lebanon, Morocco and Syria; *B. tristis* in *L. culinaris* and *Lathyrus sativus* from Lebanon and ICARDA (Syria), respectively; and *Callosobruchus subinnotatus* in *V. subterranea* from Ghana were intercepted. Many of these were intercepted repeatedly from the same/ different source(s) year after year. All the infested samples were salvaged either through X-ray



radiography or by using suitable disinfestation treatments. Many of the intercepted pests are not yet reported from India, and are therefore, of high quarantine significance.

**Keywords:** Bruchids, Hidden infestation, Quarantine, X-ray radiography

**222 (P-222)**

**The Economic Cost of Conserving Rice Germplasm at National Genebank, ICAR-NBPGR, New Delhi**

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Farmers are inclined towards modern high yielding varieties and hybrids for higher yields and income which constitute a narrow genetic base. The genetic diversity, an important component of plant breeding is being ignored and going out of cultivation. This threat was felt after the advent of green revolution. *Ex-situ* conservation strategy adopted remains the most efficient and reliable method for making genetic resources accessible to the breeders and researchers engaged in rice improvement programmes. The National Genebank of ICAR- National Bureau of Plant Genetic Resources, New Delhi holds the second largest collections in the world with 116335 accessions after IRRI, Philippines (127916 accessions). The current study was conducted to estimate variable cost for conserving rice germplasm in Long-Term Storage (LTS at -20°C) in the National Genebank situated at New Delhi (India). The study excludes the expenses on machinery like modules, seed dryer, seed germinator and vacuum sealing machine etc. Whereas the variable costs considered being expenses to run this facility and other expenditure incurred for consumables like three layered aluminium foil pouch, perforated plastic tray and paper bags etc. As per the current expenditure, the running cost of conservation of a single paddy accession is approximately INR 117.70 per annum for long term conservation.

**Keywords:** Economic cost, Long term conservation, NBPGR genebank, Rice germplasm

223 (0-13)

**Characterization of wild and cultivated *Musa* species of India based on flow cytometric analysis of ploidy and nuclear dna content**

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*Musa* L. is regarded as one of the taxonomically complicated genera within the order Zingiberales due to its similarities in habit, large size, and difficulty in identifying taxa from herbarium specimens as it is difficult to collect specimens from tropical forests. This genus is mainly distributed in North-eastern states, Western Ghats and Andaman & Nicobar Islands of Indian subcontinent, and consists of wild seeded species to seedless cultivars with various ploidy. The In Vitro Gene Bank at ICAR-NBPGR has conserved most of the wild species and cultivated *Musa* distributed in India as in vitro cultures, whole seeds and/or excised embryos, depending on the species. The knowledge of total nuclear DNA content in terms of genome size is absolutely important in evolutionary and genomic studies especially in *Musa* where variation in ploidy is well-known. A total of 29 *Musa* accessions consisting of 19 species and 3 cultivars were used for estimating DNA content and ploidy level using flow cytometry method with *Raphanus sativus* as internal standard. For the first time the DNA content of 3 triploid cultivars and 8 wild species were estimated and reported. In section *Eumusa*, lowest nuclear DNA content was observed in the diploid species *Musa balbisiana* (1C= 459 Mb), while highest was recorded for the triploid cultivar *Meitei-hei*(1C=886Mb). Under the section *Rhodochlamys* with all diploid species the lowest nuclear DNA content was recorded in species *Musa rosae* (1C= 584Mb) and the highest in *Musa velutina*(1C=702Mb). The ploidy of plants with large chromosomes can easily be determined by chromosome counting but bananas present a challenge due to its small chromosomes which are always hard to spread out during squash preparations. Hence, the difference in genome sizes between species of *Musa* containing diploid, triploid, and tetraploid edible banana cultivars permit the use of flow cytometric analysis for rapid identification of ploidy level. Based on the DNA content the ploidy level of 26 accessions of diploid *Musa* under section *Eumusa* and *Rhodochlamys* and three accession triploids in the section *Eumusa* (2n=33) were confirmed from In Vitro Gene Bank.

**Keywords:** Characterization, Flow Cytometric Analysis, India, *Musa* species

## 224 (P-224)

### Genetic variability and inter-relationship in pumpkin (*Cucurbita moschata* L.) germplasm of Assam

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Thirty diverse germplasm of pumpkin were collected from eight districts of Assam particularly, four from each district of Sivasager, Dibrugarh, Karbi Anglong, Haflong, Jorhat and Majuli and three from each of Lakhimpur and Kokrajhar districts. The germplasm were grown in an experiment conducted during *rabi* season of 2019-20 at the Instruction cum Research (ICR) Farm of Assam Agricultural University, Jorhat. The statistical design followed was Randomized Block Design with three replications. The recorded data were subjected to analyses of variance for estimation of genetic variability parameters and correlation coefficients for 19 characters. The analysis of variance indicated significant genetic variation among the entries for all the characters studied. Genotypic and phenotypic coefficients of variation were recorded to be the highest for single fruit weight indicating presence of greater variability for the trait. The heritability in broad sense was recorded to be the highest for petiole length. The Genetic advance calculated as per cent of mean was recorded to be the highest for single fruit weight (99.44%), followed by yield per plant (74.91%). In association studies out of 18 traits, five traits viz., single fruit weight, flesh thickness, fruit diameter, fruit length and petiole length were positively correlated with fruit yield per plant. Hence, desirable yield improvement could be made by simple selection for these characters.

**Keywords:** Correlation coefficient, Genetic variability, Germplasm, Rabi season

## 225 (P-225)

### Evaluation for yield and quantitative characters in pumpkin (*Cucurbita moschata* L.) landraces of Assam

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Thirty diverse landraces of pumpkin were collected from eight districts of Assam particularly, four from each district of Sivasager, Dibrugarh, Karbi Anglong, Haflong, Jorhat and Majuli and three from each of Lakhimpur and Kokrajhar districts. The landraces were grown in an experiment conducted during *rabi* season of 2019-20 at the



Instruction cum Research (ICR) Farm of Assam Agricultural University, Jorhat. The statistical design followed was Randomized Block Design with three replications. The data were recorded for fruit yield and 11 other quantitative characters. The data were subjected to analyses of variance for estimation of genetic variation for all the characters. The analysis of variance indicated significant genetic differences among the entries for all the characters studied. The genotype showing the highest mean performance for fruit yield was Majuli - 4 (7.0 kg/plant) followed by N.Lakhimpur -1(5.3 kg/plant). Majuli - 4 showed 4.0 fruits per plant whereas fruit number in N.Lakhimpur -1 was 5.0 per plant. Single fruit weight in Majuli-4 was 1.86 kg whereas in N. Lakhimpur it was 1.13 kg only. The duration to first female flower opening and fruit maturity in Majuli 4 was 46 and 97 days respectively whereas in N. Lakhimpur-1, the duration to first female flower opening and maturity was 48 and 97 days respectively. These two landraces showed comparatively better performance for most of the characters studied as compared to all other genotypes. Hence, these two genotypes may be promoted for future study or utilized in the breeding programme for further improvement.

**Keywords:** Evaluation, Fruit yield, Landraces, Pumpkin, Quantitative.

## 226 (S-03)

### **Regulatory framework and quarantine for safe transboundary movement of transgenic germplasm**

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Import of GMOs/ LMOs in India is governed by the provisions of Environment Protection Act, 1986 and Rules 1989. Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi is the nodal organization for import and quarantine of transgenic planting material meant for contained use and is governed by the provisions of Plant Quarantine (Regulation of Import into India) Order 2003 and its amendments (herein after referred to as PQ Order 2003). Import permit (IP) is issued subject to import Clearance issued by the Review Committee on Genetic Manipulation (RCGM), Ministry of Science and Technology, Govt. of India. The documents, which should essentially accompany the consignment meant for contained use are: IP issued by Director, ICAR-NBPGR and Phytosanitary Certificate (PC) issued by the NPPO of the country of origin. Keeping in view the biosafety requirements, National Containment/Quarantine Facility has been established at ICAR-NBPGR, New Delhi to ensure that no viable biological material/ pollen/ pathogen enters or leaves the facility during quarantine processing of transgenics. Quarantine processing involves detection of pests in imported germplasm using conventional. Serological and molecular techniques and salvaging of infested/ infected material by using suitable detection and disinfestation procedures/ techniques. In addition, post-entry quarantine growing/inspection of the transgenics is also undertaken by ICAR-NBPGR. During 1997-2022, >16,000 samples of different transgenic crops, comprising *Arabidopsis thaliana*, *Brassica* spp., *Cicer arietinum*, *Eucalyptus camaldulensis*, *Glycine max*, *Gossypiumhirsutum*, *Manihot esculenta*, *Nicotiana tabacum*, *Oryza sativa*, *Solanumlycopersicum*, *S. tuberosum*, *Triticum aestivum* and *Zea mays* with different traits imported into India for research purposes were processed at ICAR-



NBPGR for quarantine clearance. As per the Plant Quarantine (Regulation of Import into India) Order 2003, 1,261 pests are regulated pests, which are of quarantine significance for India. A number of economically important pests (insects, mites, nematodes, fungi, bacteria and viruses) were intercepted including the ones not reported from India such as fungus: *Peronospora manshurica* on soybean and nine viruses viz., *Barley stripe mosaic virus*, *Bean mild mosaic virus*, *Cherry leaf roll virus*, *Cowpea severe mosaic virus*, High plains virus, *Maize chlorotic mottle virus*, *Raspberry ringspot virus*, *Tomatoringspot virus* and *Wheat streak mosaic virus*. Besides, *Arabidopsis mosaic virus* and *Maize dwarf mosaic virus* are not known to occur in India on soybean and wheat, respectively, were intercepted. Other important interceptions were, insects- *Cryptolestes ferrugineus*, *Rhizopertha dominica* and *Sitophilus oryzae*; nematode- *Aphelenchoides besseyi*; fungi- *Alternaria brassicae*, *A. brassicicola*, *Phoma lingam*; bacterium- *Xanthomonas campestris* pv. *Campestris*. The infected plants were uprooted and incinerated. If not intercepted, some of these pests could have been introduced into the country and caused economic yield losses. Adopting the reliable techniques with an appropriate strategy for pest detection would go a long way in ensuring biosecured agriculture against transboundary pests through quarantine.

**Keywords:** Biosecurity, Import permit, NBPGR, Plant Quarantine, Transboundary Pest,

## 227 (P-227)

### **Analysing indigenous sugar beet germplasm for genotypic variations in metric traits under water limiting conditions**

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The formation of sugar beet yield is impacted by drought stress. The development of sugar beet varieties with a higher tolerance for drought stress is becoming more important as a result of climate changes with longer drought episodes. Investigating genotypic variations in the response to drought stress was the study's main goal. Thirty-six samples were tested under drought conditions to find possible drought-resistant and sensitive genotypes. Morpho-physiological and biochemical traits were studied for the screening of germplasm. Sugar beet plants exposed to drought stress exhibited a significant decline in growth and development as evidenced by root and shoot growth characteristics. Single root weight, root length, root diameter, leaf weight, and root yield were seen under irrigated and drought conditions. Leaf weight was reduced in most of the germplasm but LKC 2020 and LKC 2006 had shown marginal differences under drought conditions. Drought-specific traits like relative water content and malondialdehyde had also shown LKC 2006, LKC 2007, LKC HB, LKC LB, and LKC 2010 performed better under drought conditions. Juice quality (sucrose %, purity %, Brix, and ethanol recovery %) were also observed under drought condition. LKC 2006, LKC 2007, LKC HB, LKC LB, and LKC 2010 had shown promising results in sucrose % ranging between 18-20% with high root weights (of >0.6 Kg) under drought stress conditions. LKC 2006, LKC 2007, LKC HB, LKC LB, and LKC 2010 were tested as drought-tolerant on the basis of morphological, agronomical, and qualitative features, whereas the remaining thirty-one germplasm were screened as drought-susceptible. The findings demonstrated that sugar beet germplasm varies in its resistance to drought; some exhibit better tolerance than commercial types. Growing drought-resistant sugar beet germplasm could be a sustainable method to boost sugar beet yield in such situations.



**Keywords:** Drought, Germplasm, Screening, Sucrose, Sugarbeet

## 228 (P-228)

### Identification of trait specific germplasm by biochemical phenotyping of representative set of kodo millet (*Paspalum scrobiculatum* L.) for protein content

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Kodo millet [*Paspalum scrobiculatum* L.; (2n = 4x = 40)] is a minor millet with an ability to grow on marginal soils and was domesticated in India ~3000 years ago. It is rich in protein, dietary fibre, minerals and phytochemicals. It is also an important source of vitamin B and lecithin. A large number of small millet genetic resource are available in Genebanks that need to be exploited by phenotyping (for agro-morphological and biochemical traits) and genotyping to harness their full potential for food and nutritional security. Around 2,397 accessions of kodo millet are conserved in National Genebank (NGB), ICAR-NBPGR, New Delhi and need to be characterized to know the level of diversity, identify trait specific germplasm and associated QTLs/genes/alleles. In the present study, a representative subset of 102 accessions belonging to 11 states (Madhya Pradesh, Maharashtra, Karnataka, Tamil Nadu, Uttar Pradesh, Gujarat, Chhattisgarh, Bihar, Odisha, West Bengal, Kerala) of India was procured from NGB. This set comprises of released varieties, landraces, elite lines, primitive cultivars, breeding line and was used to estimate protein content by Dumas method. A wide range (7.34 to 16.72%) of variability was observed in this subset and 20 potential lines having more than 13% protein content were identified and will be evaluated at multi-locations to find the promising lines stable across locations/environments. This study further emphasizes the necessity to characterize the whole set of kodo millet germplasm available at NGB to identify sufficient number of promising accessions for protein content as well as for other traits.

**Keywords:** Biochemical profiling, Kodo millet, Protein Content, Trait specific germplasm

## 229 (P-229)

### Induced mutagenesis in sorghum to sustain food and forage security

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Sorghum is an important cereal crop, cultivated for food, fodder and biofuel. Mutation breeding techniques are used to create genetic variability for qualitative and quantitative traits in crop plants. Aim of this study was to induce variability followed by stability analysis of confirmed promising mutants in multi-location trials. Physical mutagen, gamma rays(100gy,200gy,300gy400gy, Co<sup>60</sup> source, Bhabha Atomic Research Center, Mumbai, India), chemical mutagen,ethyl methane sulphonate(0.1,0.2,0.3, 0.4%,Sigma-Aldrich, Bangalore, India)and their combinations(100 Gy+ 0.1% EMS,100 Gy+0.2% EMS,200Gy+0.1% EMS,200Gy+0.2% EMS) were used to treat Parbhani Moti in 2016-17 at Department of Agricultural Botany, College ofAgriculture, VNMKV, Parbhani-431402 (M.S.) in collaboration withBARC, Trombay. The populations were advanced up to M<sub>6</sub>(2021-22). Mutagenic and genetic parameters were studied in early generations. Whereas, stability of promising mutants were studied in advanced generations in multi-location trials in MaharashtraStatefortwoyears. Based on the mutagenic sensitivity, lethal dose at 50% survivability(LD<sub>50</sub>) was found to be 269-281 Gy in case of gamma rays and 0.32-0.33% for EMS. Based on reduced germination and survivability, mutagenic sensitivity was dose-dependent. Among the favourable mutants, dwarf and brown midrib were isolated. A combined treatment, 100 Gy +0.1% EMS showed high mutagenic effectiveness and efficiency in M<sub>1</sub> generation. Enhanced genetic variation for quantitative traits as measured by wide range values and coefficient of variation was attributed to the effect ofphysicalandchemicalmutagensinM<sub>2</sub>andM<sub>3</sub>population. Stability analysis revealed that high yielding mutants viz., PME-5-21, PME-5-32,PME-5-36 were on par with control, Parbhani Moti and registered 25-30% superiority for grain yield coupled with near unity bi values and non-significant deviation from mean (S<sup>2</sup>di). BMRmutants viz., P-M-M (BMR)-14-16-8, P-M-M (BMR)-14-25-9 expressed uniformly as detected from brown pigmentation on mid-rib across locations. Stable mutants for plant height (91 to 110cm) were P-M-M(Dw)-15-8-10,P-M-M(Dw)-15-14-7. High-yielding mutants would be evaluated in co-ordinated trials for the identification of improved variety, whereas, BMR and dwarf mutants will be utilized for genetic improvement of forage and the development of genotypes suitable for mechanical harvesting after registration with NBPGR.

**Keywords:** Mutation, Sorghum, Stability, Variability

## 230 (P-230)

**Early stage-based identification of the climate-resilient genotypes utilizing a diverse panel of Brassica wild relatives, inbred lines, landraces, and the U-triangle species**

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Climate change has prompted the global temperature to rise in recent times. Due to the air temperature rising above the ideal level and causing irreparable damage or injury, this temperature rise results in heat stress. Besides that, heat stress affects almost every stage of plants, viz., seed germination, seedling growth, development, cellular metabolism, gene expression, and the anatomical, structural, and functional characteristics of leaves, flowers, siliqua, and seeds. It also changes the branching patterns, leaf surface and orientation, and the surface and orientation of leaves and ultimately impacting the seed yield and oil content. Therefore, identifying the heat-tolerant genotypes will be helpful for the breeding program. It is possible to find superior heat-tolerant genotypes by evaluating many germplasms in heat-stressed conditions. In this work, a panel of 84 different Brassica genotypes (wild relatives, landraces, inbred lines, and varieties) were screened under in vitro conditions at early germination and the seedling stages for heat tolerance. In contrast to the tolerant genotypes, which displayed improved growth characteristics, our results showed a significant decline in germination percentage, root length, and shoot length for the heat-sensitive genotypes after exposure to 42 °C for 4 hours per day for 5 days. Analysis of variance (ANOVA) revealed a significant differential effect of heat treatment on biochemical variables such as MDA, SOD, and electrochemical conductivity, demonstrating huge genetic variability among all genotypes for heat tolerance. Principal component analysis (PCA) was also used to assess the genotypes to identify the main features contributing to stress tolerance. Based on these results, P. agrani, RBJ 5, Kola sorioh, and MBT-121 were selected for further molecular analysis. The overall results of this work could be employed further for candidate gene mining using "omics" tools to create brassica crop plant's resilience to heat stress.

**Keywords:** Brassica, Climate resilience, Diverse panel, Germplasm

## 231(P-231)

**Study the effects of synthetic cytokinin on micro-propagation of endangered medicinal plant: *Vitex negundo*(L.)**

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An efficient and improved shoot regeneration technique for the micro-propagation of *Vitex negundo*, an aromatic and medicinal shrub through in vitro culture of nodal segments with axillary buds is described. The influences of plant growth regulators on shoot regeneration culture on MS medium with 1.0, 1.5, 2.0mg/l benzylaminopurine (BAP), Diphenyl urea (DPU ) and thidizuron (TDZ) were resulted to be the greatest percentage of shoot development was hundred percent at 2.0 mg/l BAP in MS medium. The genus *Vitex* is also known as a chaste tree, in which it is a large shrub of native to the tropical and subtropical regions of the world. A diverse range of species is distributed throughout Southern Europe, the Mediterranean and Central Asia. The *Vitex* tree,



including its leaves and fruits has been used for herbal remedies in the form of pastes and decoctions and dried fruits since ancient times. Benzylaminopurine( BAP) used at 2.0mg/l was the most effective in inducing bud break and growth and also in initiating multiple shoot proliferation from nodal explant as compare to other two synthetic cytokinins DPU and TDZ. By repeated subculturing of nodal explants, a high-frequency multiplication rate was established. Optimum shoot multiplication and elongation was achieved when BAP exposed explants were subculture on Murashige and Skoog( MS) media containing a BAP at 2.0mg/l concentration. The greatest average number of shoot multiplication at 2.0mg/l BAP in MS medium compare to other synthetic cytokinins DPU and TDZ in MS medium after seven weeks of culture. The result of MS medium at 2.0mg/l of BAP found the highest multiplication rate of nodes.

**Keywords:** *Vitex negundo*, subculturing,benzylaminopurine,diphenylurea,thidizuron, cytokinin

### 232 (P-232)

#### Identification of heat tolerant genotypes in chickpea

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Total 1000 desi chickpea accessions collected, characterized and evaluated to identify heat tolerant genotypes. The crop was grown during rabi 2021 and 2022 in the late sown condition in Augmented design. Observations were recorded for qualitative and quantitative traits and climate data. Promising genotypes [ICC 6462 (132), ICC 6471 (150), ICC 4409(135), ICC 4410 (210) and EC 267221 (137)] identified for filled and unfilled pods and high yielding ability was note in ICC 6462 (21.66 g), ICC 6471 (25.70 g), ICC 4409 (23.28 g), ICC 4410 (33.10g), EC 267221 (31.70 g). However, for 100-seed weight [ICC 5982 (28.8 g), ICC 6471 (21.2 g), ICC 0236 (15.3 g), IC 486922 (13.3 g) & ICC 2217 (13.3 g)], for maturity [ICC 6462 (107 d), ICC 6471 (109 d), ICC 4409 (104 d), ICC 4410 (103 d), EC 267221 (104 d), ICC - 2267 (107 d)] and days to 50 % flowering in EC 267221 (77d), IC 486922 (76d), ICC 2345 (76 d), ICC 2267 (81 d) and ICC 2217 (86d).These promising genotypes were selected for further evaluation and identification as a donor for chickpea improvement programme for heat tolerance.

**Keywords:** ABD, Desi chickpea, Donor, Germplasm, Heat tolerance

### 233 (P-233)

#### Distribution, collection and genetic resources study of wild *Allium* from Uttarakhand, India

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Genus *Allium* with more than 1,100 species globally distributed in the Northern hemisphere, about 40-45 species occur as cultivated and wild taxa in India. Many of the wild species from Indian region are of potential source of genes for widening the crop genetic base. Collection, identification and conservation of important primary, secondary and tertiary gene pools of *Allium* genetic resources (AGR) are an integral part of plant genetic resources (PGR) management programme at ICAR-National Bureau of Plant Genetic Resources. During explorations (2018-22) for germplasm collection of *Allium*, regional diversity of some potential species was collected and studied in field and under experimental conditions at NBPGR, New Delhi and Regional Station, Bhowali. In seven explorations from high hills of Uttarakhand, a total of 56 germplasm accessions representing 15 species mainly *Allium ampeloprasum*, *A. carolinianum*, *A. cepa* var *aggregatum*, *A. cepa* var *proliferum*, *A. humile*, *A. negianum*, *A. perzwalskianum*, *A. sativum*, *A. stracheyi*, *A. tuberosum* and *A. wallichii*, were collected and studied for diversity distribution, trends of domestication and the genetic resources value. Study was undertaken using live material available in fields (wild and under cultivation) and market samples, herbarium specimens, and feed-back from informants for use in the area of collection. Traditional knowledge on edible use and their availability in regional markets indicated their preference under cultivation for monetary gain of the farmers. The information generated through this study would help in identification of gaps for further collection and build-up of knowledge base for use in the genetic resource programme besides added germplasm collections in field genebank, tissue culture repository and as herbarium specimens.

**Keywords:** *Allium*, Domestication, Genebank, Germplasm, Plant Genetic Resources

234 (P-234)

### Uniform frequency NIRS modeling for malting quality traits in barley–A novel approach

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Barley is primarily exploited for baking, malting/brewing purposes worldwide. Malt for food supplements needs to be high in protein and  $\beta$ -glucan, whereas for brewing purposes should have a low content of protein,  $\beta$ -glucan, phenols, and a high amount of fermentable sugars. Quality breeding material and varieties with desirable traits are required to be bred, which also involves the introduction of related germplasm into the breeding cycles. NIRS provides a reliable, robust, and rapid screening method. The main



objective of this study was to develop robust NIRS calibration models for screening the germplasm collection at ICAR-NBPGR, New Delhi. NIRS spectra of 5500 hulled barley samples, including indigenous and exotic collection, was acquired. One hundred fifty highly diverse accessions were selected using stratified purposive sampling based on NIR spectral data. Of these, 100 accessions were used to train the model for starch,  $\beta$ -glucan, protein, and phenol content, and 50 samples were used to validate model performance.  $R^2$  values of 0.935, 0.930, 0.896, and 0.252 were obtained for starch,  $\beta$ -glucan, protein, and phenol. It was observed model for phenol could not be trained successfully, whereas, for other traits, models tend to fail on boundaries due to mean centering. This limitation was resolved by adopting a novel approach of keeping uniform frequency distribution in selecting the calibration set. It resulted in the development of a successful model for phenol with an  $R^{2(\text{Val})}$  value of 0.720. The resulting models also predicted each trait more accurately for very low and high values. The developed models can be used for screening germplasm collections, breeding lines, and industry for checking grain quality.

**Keywords:** Protein, Starch,  $\beta$ -glucan, Phenols, Prediction accuracy, Mean centering

235 (0-17)

**Wheat genetic resource mining for trait discovery towards achieving the sustainable development goal of food and nutritional security**

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Wheat production is facing critical challenges from various biotic and abiotic stresses due to climate change. It is becoming increasingly difficult to fulfil global food demand from limited land by cultivating existing modern cultivars as these become susceptible to new pathogenic races. Further nutritional global demand is also rising to alleviate malnutrition among poor people. Genetic resources, specifically landraces are in general rich source of genetic variability due to thousands of years of their cultivation under low input farming systems and extreme environmental conditions. Landraces serve as a potential reservoir of desirable allelic forms of valuable traits and therefore, could help in stabilization of crop production under rapidly changing climatic conditions. Therefore, characterization and evaluation of untapped and unexplored landrace genetic resources will be beneficial for harnessing genetic variability for economically important traits, biotic and abiotic stress tolerance and other desirable traits including quality, into



modern high-yielding cultivars. A large collection of wheat genetic resources including core set (~4000) in national genebank has been characterized and evaluated for disease resistance, drought and salinity tolerance alongwith grain quality parameters under consortium research on agrobiodiversity programme. These genetic resources revealed enormous variability for different traits and promising germplasm for various biotic and abiotic stresses and grain quality traits were identified within genebank collections. Further, with the advancement of modern technologies, untapped variation of genetic resources can be easily made accessible through extensive phenotyping and trait discovery by using high throughput genomics approaches.

**Keywords:** Core set, Genetic resource, SDG, Trait discovery, Wheat

### 236 (P-236)

#### **Agro-morphological and molecular characterization of cucumber gynoeocious lines revealed their usefulness in hybrid breeding**

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Cucumber (*Cucumis sativus* L.) is an important vegetable crop grown throughout the world. The cucumber is 4<sup>th</sup> most important vegetable crop globally and is cultivated in more than 150 countries. The F1 hybrids are highly popular for cultivation of cucumber under open field and protected condition and gynoeocious and gynoeocious parthenocarpic lines are preferred as parents of F1 hybrids because of their higher yield potential. A set of 27 gynoeocious and gynoeocious parthenocarpic inbreds of cucumber were characterised using a set of 72 SSRs uniformly distributed throughout the cucumber genome. Besides, these inbreds were also characterized for 9 economically important agronomic traits. Based on the molecular characterization the inbreds were divided into 4 distinct groups and all the gynoeocious parthenocarpic lines were placed together in one cluster. Similarly based on the agronomic traits the genotypes were divided into 5 groups and clustering patten did not match with the molecular data. The GCV and PCV of the genotypes indicated significant role of the environment in expression of most of traits and broad sense heritability of the traits were recorded more than 80%. There was no correlation between the GD based on the molecular analysis and PD based on the agronomic traits which indicated the need for extensive analysis using more number of markers and significant role of environment. The combined data generated through agronomic and molecular analysis can be used in selection of suitable parents and development of heterotic groups in cucumber.

**Keywords:** Characterization, Cucumber, Genotyping, Hybrid, Phenotyping

### 237 (P-237)

#### **Molecular and cytological characterization of Phytoplasma-associated infestation in *Linum usitatissimum***



NCPGRM

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*Linum usitatissimum*, commonly known as flax or linseed, is a member of the family *Linaceae*. It is grown globally as a dual purpose crop in temperate as well as tropical regions as a source of fibre and oil owing to immense domestic as well as industrial implications. Presently, China occupies the paramount position in terms of flax consumption and is the largest importer valuing 31,108 M US\$ in the past decade which accounts for 26.8% of total global flax import in the year 2020. Canada is the leading producer and exporter of flax worldwide over the past decade, while India ranks seventh in terms of production and eleventh in terms of export. However, over the past decade linseed productivity has witnessed a stagnant growth owing to varied biotic and abiotic factors. Phytoplasma-associated diseases represent one of the major biotic constraints in several parts of the world causing significant yield losses. The symptoms such as fasciated inflorescence, stunted and flattened stem with reduced leaves, phyllody and floral malformation were noticed for the first time on linseed at ICAR-NBPGR experimental farm, New Delhi for consecutive three years during *Rabi* season 2019-20 to 2021-22. Although the incidence was observed in less than 1.5 % plants yet its occurrence in new geographical area poses a serious threat as frequency of phytoplasma infections are growing worldwide. The present study aims to elucidate the molecular and cytological mechanism of the phytoplasma host environment for understanding their adaptation and genome condensation. Total DNA was isolated from six infected and two healthy plants. The 16S rDNA region was amplified using universal P1/P7 followed by R16F2n/R16R2 primer pair which showed the amplification of expected amplicon size (1250bp) from all the infected samples. The PCR amplified products were subjected for Sanger sequencing from both directions and the consensus sequences were obtained. The nBLAST search analysis revealed that the 16Sr RNA sequences shared maximum similarity (98%) with the reference sequence of *Candidatus* Phytoplasma. Further Transmission Electron Microscopy (TEM) revealed colonization of the bacterium primarily occurred in the phloem region of the infected plants, which were absent in the uninfected plants. Further studies will give more insight on the host-pathogen interaction.

**Keywords:** Flax, phytoplasma, stem fasciation, linseed, phyllody

**238 (P-238)**

**Nutritional profiling of zero cooking soft rice landraces – a unique specialty of Assam**

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Rice is a staple crop for more than half of the Indian population where North-East Indian states are primarily dependent on rice for their diets. Processing of brown rice including



parboiling, soaking, steaming can affect GI and bioactive compounds. 31 soft rice landraces of Assam, which are processed in way, that only requires soaking of rice grain in water at room temperature for cooking were analyzed for total amylose (AC), oil (OC), protein (PC), total dietary fibre (TDF) and starch (SC) contents using AOAC and standard methods. The mean AC, OC and PC were 9%, 4% and 7.4%, 4.4% and 75.8%, respectively. Amongst soft rice Komal Ronga (IC464351) exhibited least AC (6.4%) and highest OC (5.25%). Bhaja Roasted rice (IC14559) contained the highest PC (12.1%). PCA identified two principle components i.e. PC1 (69.4%) and PC2 (20.7%), with eigenvalue >1 as amylose (0.996) followed by protein (0.979) and starch (-0.948), which contributed in maximum variability. Correlational study indicated highly negative correlation between starch and protein ( $r=-0.91$ ;  $p<0.001$ ), starch and oil ( $r=-0.778$ ;  $p<0.001$ ), starch and TDF ( $r=-0.87$ ;  $p<0.001$ ). Significant positive correlation was observed between TDF and PC ( $r=0.81$ ;  $p<0.001$ ), TDF and OC ( $r=0.64$ ;  $p<0.001$ ). Information obtained through the nutritional profiling of the landraces also enabled identification of other land races which could be utilized for processing to make zero cooking soft rice.

**Keywords:** Processed rice, Nutritional profiling, PCA, Correlation

## 239 (P-239)

### Exploration and genetic diversity analysis of melon landraces 'vellari' (*Cucumis melo* var. *momordica* L.) in Tamilnadu, India

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A local traditionally important melon, "Vellari" (snap melon, *Cucumis melo* var. *momordica* L.) is a less-known crop of southern India least represented in the global studies and gene bank holdings due to meager germplasm collections and data available on morphological characterization and identification of significant quality traits. This cultivar is appreciated for its high demand in the local market for fresh fruits used as salad, vegetable and dessert of commercial value. Seventeen germplasm accessions from four districts representing diverse climatic zones of southern Indian districts of India, Tamilnadu were explored and distinct accessions of "Vellari" were studied for morphological traits of fruits and phenotypic variability. The organoleptic assessment study was conducted based on the consumers' preference. To estimate the phenotypic diversity, 29 quantitative and 27 qualitative descriptors were used. To ascertain the variability between the collections, Principal Component Analysis (PCA) was performed. The analysis revealed that the variations in leaf pubescence type, earliness of male and female flower, days to first flowering, days to 50% of flowering, peduncle length, flower bud shape, ovary pubescence, ovary shape, fruit shape, fruit size, fruit length-width ratio, time of maturity and days to first fruit were the defining characteristics which differentiate the snap melon accessions examined in this study. The cumulative percentage of variation explained by first five components was 84.29%.



Additionally, a wild taxon, “Sukkangai” (*Cucumis melo* ssp *agrestis* var *agrestis*) was reported for local use in the area of survey.

**Keywords:** *Cucumis melo*, Exploration, Genetic diversity, Tamilnadu, Vellari

## 240 (P-240)

**A study on genetic variability in tulsi *Ocimum* spp.**

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The 27 genotypes of Tulsi (*Ocimum* spp.) from ICAR, DMAPR Pusa, DMPAR, Anand, RSVKVV, Mandasaur, Faizabad, Rahuri and local germplasm were used to know the variability, interrelationship among yield and its components, their direct and indirect effects on dry leaves weight and genetic divergence of various *Ocimum* spp. genotypes. Green leaves weight per plant exhibited highest range of variability followed by plant height, dry leaves weight per plant, number of secondary branches, number of inflorescences per plant, number of flowers per inflorescence, days to 50 percent flowering. The variability was lowest for 1000 seed weight, length of inflorescence, number of primary branches. The character dry leaves weight, days to 50 per cent flowering and 1000 seed weight exhibited highest estimates of genotypic and Phenotypic coefficient of variation indicating goodscope for their improvement through selection. All the characters exhibited high heritability. High heritability coupled with high genetic advance as percent of mean was observed. Indicating that these traits could be prominently governed by additive gene action and selection of these traits could be more effective for desired genetic improvement. Dry leaves weight showed strong significant and positive correlation with green leaves weight, plant spread, number of secondary branches, number of primary branches, plant height, number of inflorescences per plant and number of flowers per inflorescence. Dry leaves weight showed significant negative correlation with days to 50 percent flowering at both genotypic and phenotypic level. Path coefficient analysis revealed that green leaves weight had highest direct effect on dry leaves weight followed by number of primary branches, number of secondary branches, plant height and plant spread. These direct effects are mainly responsible for positive association of these character with dry leaves weight. number of inflorescences, length of inflorescence, and 1000 seed weight had negative direct effect on dry leaves weight. Based on inter cluster distance and cluster means the genotypes viz., lavang tulsi, ran tulsi, AB-10, sabjatulsi, OS-8, OS-5, Krishna tulsi were identified for their use in future crop improvement programme.

**Keywords:** Cluster analysis, Genetic variability, Germplasm, Tulsi

## 241 (P-241)



## **Neglected wetland converted into goldmine through Makhana (*Euryale ferox* Salisb.)**

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The total area of wetlands in India has been estimated to be 15.26 m ha approximately covering 5% of national geographic area. The survival of human civilization is inextricably linked with wetlands, which sustain the economic stability of hundreds of millions of people. And this swampy environment of the carboniferous period produced and preserved many of the fossil fuels on which we greatly depend now. Thus James (1995) has rightly termed these areas as Nature's Kidney." Makhana is an aquatic fruit plant requires a rich soil, preferably growing in waterlogged area. It mostly prefers tropical and sub-tropical climate. Generally, aquatic plants take up large quantities of nutrients and metals from environment, releasing them when they decay. They also differ both in their capacity to take up nutrient elements in root tissues and in the proportion of nutrient transferred to above ground parts. With this view, nutrient elements concentrations in different parts of the Makhana and their contribution to the soil system were studied. The study showed that Makhana tended to have highest tissue concentrations of N and P in the leaf parts while the less soluble Fe, Mn and intermediately soluble Zn exhibited greater concentrations in roots than in shoots. Thus, Makhana can also be proved to be a better option as an alternative crop to include it in cropping system mode under field condition to replenish the exhausted nutrients such as N, P and Zn by the cultivation of other cereal crops. So, it may be concluded that for better utilization of under-utilized wetland/lowland through Makhana cultivation, core germplasm collection of Makhana is required for development of improved varieties with high yield, quality pop recovery and net return.

**Keywords:** Germplasm, Makhana, Wetland

**242 (P-242)**

## **Variability of major nutrients in moth bean [*Vigna aconitifolia* (Jacq.) Marechal] germplasm**

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Moth bean [*Vigna aconitifolia* (Jacq.) Marechal] belonging to family *Fabaceae*, a minor legume crop, has been acknowledged as a heat and drought resistant legume. Despite being an underutilized food legume, it has been identified as a potential future crop for food and nutritional security. Seeds of moth bean are rich source of proteins, carbohydrates, fatty acids, minerals and vitamins, with substantial antioxidant and dietary fibre content. With an objective to effectively utilize the available germplasm in the genebanks, the diverse accessions of moth bean have been identified for selected nutritional content. A set of 525 accessions of moth bean were evaluated for nutritional content of proteins, amylose, starch and phenol using validated AOAC official methods of analysis and other standard methods. The accessions showed high variability for protein content ranging (from 20.2% to 32.6 %), starch content (from 23.6 % to 28.2%), phenol content (from 0.271 % to 0.439 %) and amylose content (from 12.0% to 23.2 %). Few accessions were identified from the above-mentioned set, viz. IC-36089 with high protein (>30%), IC-113705, IC-52152 with high starch (>35%) and IC-35938 with high phenolic content (.439%). The wide range of variability observed for key nutrients in the selected accessions may provide a platform to potentially address the food security by diversifying the food basket in developing countries. These accessions may further be utilized for crop improvement programmes.

**Keywords:** Legume, Potential crop, Nutritional profiling, Variability, Food security

**243 (0-14)**

### **Characterization of entire rice bean collections of Indian National Genebank and development of core set for enhanced utilization**

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Ricebean (*Vigna umbellata* (Thunb.) Ohwi & H. Ohashi) is an underutilized legume crop, widely distributed throughout the South, Southeast Asia and several other parts of the world. The species being a Leguminosae member is recognized to have a great potential in enhancing nutritional and food security, primarily in its traditional farming systems. The crop is known to possess resistance for various biotic and abiotic stresses; therefore, it can be a crop of future, amid climate change, and also can be the source of important



genes for other crops to be improved upon. Despite the crop having excellent qualities, the competition from other similar legume crops and prevalence of wild characteristics in almost entire ricebean germplasm has led to gradual decrease in its cultivated area. Therefore, with the objective of enhancing the utilization of ricebean germplasm for accelerating the ricebean crop improvement, we have characterised entire (1760) ricebean germplasm collections conserved in Indian National Genebank using 12 important agro-morphological traits and five seed morphometric traits during 2019 and 2020 at New Delhi and Almora locations. A good range of variability was observed for seed weight, stem diameter, flowering time, branches/plant, terminal leaflet size, seed and hypocotyl colour. Based on the characterization data, geographical origin, principal component score (PCS) and Core Hunter 3 statistical program, a core set of 252 accessions was developed. The quality check of the core set using coefficient of variation, Shannon's Diversity Index, Shannon' Equitability Index, PCS, hierarchical clustering, and trait correlation indicated excellent representation of entire ricebean diversity in the derived set of ricebean core. We hope that this ricebean core set will play a significant role in accelerating the utilization of ricebean germplasm by breeders and researchers to develop ricebean as a mainstream legume crop.

**Keywords:** Characterization, Core set, Genebank, Germplasm, India, Ricebean

#### 244 (P-244)

#### **Genetic variation and association analysis for fruit yield and its contributing traits in Farmers Varieties of Snap melon (*Cucumis melo var. momordica*)**

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The research work was investigated to estimate the genetic variability parameters, correlation and pathanalysis in 18 Snap melon genotypes for 17 quantitative traits grown in kharif 2021. Indicating considerable amount of genetic variation in different genotypes of Eastern Uttar Pradesh. The close proximity between PCV and GCV values for most of characters indicated less influence of environment on the expression of the traits under study. High heritability coupled with high genetic advance as percent mean was recorded for average fruit weight, followed by fruit length, fruit fresh thickness, fruit diameter, number of seeds per fruit, number of fruits per plant, indicating a predominance of additive gene effects and the possibilities of effective selection based on these traits for Snap melon improvement. Correlation and path analysis revealed that number of fruits per plant followed by days to first harvest, days to first male flower opening, node at first male flower appearance, seed cavity breadth, fruit diameter, average fruit weight show positive significant correlation and direct effect on yield. Therefore, these traits may be used as selection indices for genetic improvement of Snap melon genotypes.

**Keywords:** Variability parameters, Association analysis and Snap melon



**245 (P-245)**

**Diversity analysis in sesame germplasm based on seed morphology**

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Sesame (*Sesamum indicum*) is one of the most ancient and essential oilseed crop cultivated in many parts of the world. Seed size, shape and colour are among the most significant agronomic traits controlling the yield and oil quality in sesame. Grain size represents one of the important components of yield and contributes to seedling vigour. Whereas, seed colour affects the quality and quantity of sesame oil and is prerequisite for demand in confectionary. Therefore, plant research fields such as genetics, functional analysis, and genomics-assisted crop improvement, in addition to breeding programs, could benefit from quantitative evaluation of seed characteristics. The study was undertaken to determine diversity in the sesame seeds morphology and seed coat color. Sesame seeds were procured from National gene bank, ICAR-NBPGR, New Delhi, India. For measurement and analysis, 4000 sesame accessions were scanned using Epson V39 scanner. Various seeds parameters viz. area (mm<sup>2</sup>), length (mm), breadth (mm), perimeter (mm), eccentricity, diameter (mm) and roundness were analyzed using Grain analysis V1.3 software. Seed coat color was analyzed using color code given as per Royal Horticultural Society. High genetic variability was observed in different seed morphological parameters. Seed length ranged from 2.7-4.2 mm, breadth 1.8-2.3 mm, area 3.6-6.5 mm<sup>2</sup>, eccentricity 0.7-0.8, perimeter 7.1-10.5 mm, diameter 2.0-3.0 mm, roundness 0.5-0.7. The natural color of mature sesame seeds varied from black to white through different intermediates such as gray, dark brown, brown, pale brown, cream and yellow. This study will be beneficial for plant researchers to choose appropriate sesame seed for genetic enhancement and wide hybridization. A database would be developed further based on inimitability of sesame seed to identify/classify novel seeds for yield and quality related traits.

**Keywords:** Diversity analysis, Grain analysis, Seed morphology, Sesame

**246 (P-246)**

**Multivariate analysis of quantitative traits in sesame (*Sesamum indicum* L.)**

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Sesame is belongs to the family Pedaliaceae, also called as the “Queen of oil seeds” due to its excellent qualities of seed oil and meal. It is an important source of edible oil and is



widely used in food products especially in bakery foods and animal feed. The present study was carried out to know genetic divergence among sesame accessions and to select better accessions for sesame improvement program. A field study was conducted on sesame to evaluate agro-morphological traits in sesame (2020-21). An augmented block design (ABD) was used in the experiment to screen 3,928 sesame accessions at NBPGR (National Bureau of Plant Genetic Resources) fields, IARI (Indian Agricultural Research Institute), Pusa Campus, New Delhi, India (Latitude-28°38'52.15"N, Longitude- 77° 9'4.81"E) during *kharif* 2020. Different parameters such as plant height, days to flower initiation, days to 50% flower, number of days to maturity, no. of primary and secondary branches, no. of nodes to first flower, capsule length & width, no. of capsules per plant, test weight were measured. ANOVA (Analysis of variance) and further data analysis was carried out different software tools such as SPSS, Minitab etc. Large genetic variation exists in sesame traits considered under this study. Positive correlation was observed in no. of secondary and primary branches (0.60), days to flower initiation and no. of nodes to first flower; day to flower initiation and no. of days to 50% flowering (0.86); plant height and no. of capsules per plant (0.44); no. of primary branches and no. of capsules per plant (0.40); no. of secondary branches and no. of capsules per plant (0.50). Four principal components were identified which accounted for maximum variation in the sesame germplasm. All the accessions grouped into 8 clusters while accessions included in cluster 4 mainly comprised with days to flower initiation, no. of nodes to first flower and 50% flowering. Earlier studies indicated that large genetic variation exists in sesame germplasm due to prevailing environmental conditions. Our results have an important suggestion for morphological categorization and accessions recognized amongst sesame germplasm would be utilized further by sesame breeders/researchers for the improvement of landraces, genotypes and cultivars.

**Keywords:** Germplasm, Multivariate analysis, Quantitative traits, Sesame

247 (P-247)

### **Makhana (*Euryale ferox* Salisb.) genetic resources and utilization**

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Makhana (*Euryale ferox* Salisb.) also known as Foxnut is an important aquatic fruit crop belongs to the family Nymphaeaceae. It is the most widely grown crop in Mithilanchal, Bihar. The crop is expanding to non-traditional growing areas mainly due to its unique natural life cycle completed in submerged condition (depth of water up to 10 feet), high nutritional and medicinal value, soil ameliorating properties, and global demand as super food. The calorific value of raw seeds (362 k cal/100g) and puffed seeds (328 k cal/100g) lie close to staple foods like wheat, rice, other cereals and some aquatic plants like *Nelumbo* and *Trapa*. The crop is suitable under cereal crop-based cropping systems in warm humid regions of



Northern-East region (Kosi) of Bihar. Makhana cultivation covers over 35,000 ha of land in India with annual production of around 7.4 lakhs quintals of seed. Narrow genetic base, disease pest proneness, and photo-thermo-sensitivity are the major problems resulting in the poor yield of the crop. The utilization of very few parental genotypes in Makhana breeding programs has led to the narrowed genetic base of the Makhana varieties. This has posed a serious threat to the Makhana cultivation amid newly emerging pests and pathogens of the crop. Transboundary movement of germplasm has also helped in the development and release of varieties in several countries. Enhanced and efficient utilization of *ex-situ* conserved Makhana and related wild species germplasm in breeding programs with the help of modern genomic tools would help in the development of desired genotypes with higher yield potential. Keeping in view, the potential of this minor fruit crop in our country, an exploration trip was conducted and samples were collected from 10 to 45m msl particularly in the districts Cooch Behar, Uttar Dinajpur and Malda of West Bengal. The exploration tour was conducted by ICAR- NBPGR, New Delhi in collaboration with Bihar Agricultural University-BSP Agricultural College, Purnea during 2018-19. The present study showed that the makhana diversity is available in the explored regions, discussed in this paper.

**Keywords:** Bihar, Diversity, Germplasm Exploration, Makhana

**248 (P-248)**

### **Study of seed dormancy and its breaking methods in Paddy (*Oryza sativa* L.) cultivars**

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Rice is an important crop in Indian agriculture. For more than 70% of Indians, it is a staple diet and a source of income for 120-150 million rural households. The existence of seed dormancy in rice is indeed troublesome and advantageous. It is troublesome for post-harvest seed testing, crop production of two or three harvests annually and plant breeding where off-season crops are taken a couple of times. It is however, favorable in avoiding viviparous germination as in tropical cultivars grown during the monsoon season. The experiment was laid out in Factorial Completely Randomized Design (FCRD) with four replications in laboratory. The fresh seeds of twelve paddy cultivars were used to examine the variations in dormancy. The dormancy duration was observed by germination test conducted every day till all the cultivars recorded germination above minimum seed certification standard (80%). On the 14<sup>th</sup> day, the seeds were assessed (final count) for germination. Among twelve paddy cultivars three cultivars namely, Pawana, Raibhog and Ratnagiri Purple were reported the highest dormancy period of 28 days and categories as extremely strong dormant, whereas the cultivar Karjat-184 was reported the lowest dormancy duration of 20 days and categories as strongly dormant. The twelve paddy cultivars were used for image examination (with husk). The various parameters studied were, seed length and seed breadth. The seed length to breadth ratio and seed coat thickness was also worked out. Similarly, the efficiency of various dormancy breaking methods was studied. The laboratory testing involved of nine dormancy breaking treatments. Among the different physicochemical dormancy



breaking treatments, oven drying at 50 °C for 24 hours and soaking with GA<sub>3</sub> 100 ppm for 24 hours, followed by soaking with GA<sub>3</sub> 100 ppm for 24 hours were effective and could be recommended for breaking the dormancy in dormant paddy cultivars. The cultivar Karjat-184 recorded superior results with respect to seed quality, seed vigour, seedling parameters etc.

**Keywords:** Karjat-184, Paddy, Seed dormancy

## 249 (P-249)

### **Pre-Breeding and Inheritance studies for resistance to leaf curl virus disease in interspecific cross of chilli**

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Chilli (*Capsicum annuum* L.) is an important vegetable and spice crop in India. Chilli leaf curl virus disease (ChiLCVD) is the most destructive disease of chilli causing up to 100% loss of marketable fruit yield. A number of strategies have been used to manage and control the vector population without much success. However, development of resistant varieties is one of the effective ways to control viral diseases in chilli crop. Chilli leaf curl virus disease is transmitted by whitefly (*Bemisia tabaci*). Two Begomoviruses species viz., Tomato leaf curl New Delhi virus (ToLCNDV), and Chilli leaf curl virus (ChiLCV) are prevalent in Delhi. Upward and downward curling of leaves, rolling and puckering; blistering of interveinous areas, swelling of the veins, shortening of internodes and petioles, are important symptoms of Chilli leaf curl virus disease which cause stunted growth of whole plant. In order to develop pre-breeding genetic materials and to know the inheritance of resistance, a susceptible but high yielding line 'Tripura Sel-1' of *Capsicum chinense* was crossed with the resistant accession EC771555 of *Capsicum annuum*. All the plants of F<sub>1</sub> were found resistant against ChiLCVD in the field as well as under challenge inoculation indicating that the resistance to ChiLCVD is controlled by dominant gene. F<sub>2</sub> population comprising 189 plants was screened under field conditions at Delhi. The results revealed that the resistant and susceptible plants were segregated into 3:1 ratio (135 resistant and 54 susceptible plants). The results of Chi-square analysis indicated a good fit of ratio in the hypothesis. It suggests that the resistance carried by accession is controlled by a single dominant gene. Therefore, the identified accession EC771555 of *Capsicum annuum* may be used as a potential resistant donor for developing genotypes/ cultivars possessing desirable horticultural traits along with resistance to curl virus disease.

**Keywords:** Chilli, ChiLCVD, EC771555, Germplasm, Whitefly

## 250 (P-250)



## **Vegetable genetic resources: conservation and use**

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India is very rich in diversity of landraces, primitive cultivars and crop wild relatives (CWR) of many important vegetables, which are being cultivated from pre-historic times. Brinjal and some cucurbits are of Indian origin, whereas for okra and chilli, India is considered as secondary centre of origin. There are about 100 species of cucurbitaceae family reported to occur in India and more than 30 species are endemic viz., *Cucumis hardwickii*, *C. trigonus*, *C. prophetarum*, *C. setosus*, *C. hystrix*, *Luffa graveolens*, *L. acutangula* var. *amara*, *L. tuberosa*, *L. echinata*, *L. umbellata*, *Trichosanthes dioica*, *T. dicaeleosperma*, *T. khasiana*, *T. ovata*, *T. truncata*, *T. multiloba*, *T. anamalaiensis*, *T. bracteata*, *T. cuspidata*, *T. nervifolia*, *T. himalensis*, *Momordica cochinchinensis*, *M. macrophylla*, *M. subangulata*, *M. cymbalaria*, *M. dioica*, *M. cymbalaria*, *M. denticulata*, *M. balsamina*, *Neoluffa sikkimensis* and *Citrullus colocynthis*. The vegetable germplasm diversity has been further enriched with introduction of more vegetable crops from different parts of Asia. *Phaseolus vulgaris* (common bean), *Vigna angularis* (adzuki bean) from China and *Allium cepa* (onion), *Brassica rapa* (turnip), *Brassica oleracea* var. *capitata* (cabbage), *Coriandrum sativum* (coriander), *Cucumis melo* (muskmelon), *Dacus carota* (carrot) and *Pisum sativum* (pea) have been introduced from West and Central Asia. Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources (ICAR-NBPGR) has made headway in collection and conservation of trait specific germplasm, released varieties, landraces and crop wild relatives in almost all vegetable crops. The base collection in National Genebank (NGB) at ICAR-NBPGR, New Delhi, holds 28,633 accessions of different vegetable crop groups viz., Solaneceous (12,838), Cucurbitaceous (6,115), Malvaceous (4,074), Leguminous (2,061), Bulb&Root crops (1,702), Leafy and other minor vegetables (1,843), having resistance/tolerance to biotic and abiotic stresses, and also possess various agronomic, nutritional and other desirable traits of commercial importance. The details of promising accessions as sources of specific traits in major vegetable crops conserved in National Genebank (NGB), can be of great use in development of improved and climate resilient cultivars in crop improvement programmes. In addition, promising germplasm identified through characterization of more than 9,000 accessions under CRP-AB will serve as potential donors in vegetable breeding programmes.

**Keywords:** Conservation, Crop wild relatives, Genetic Resource, Vegetable

**251(P-251)**

## **Influence of artificial ageing on biochemical parameters and seed quality of wheat**

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Degradation and inactivation of enzymes due to changes in their macromolecular structures is one of the most important hypotheses proposed regarding the causes of ageing in wheat seeds. Controlled atmosphere during storage offers a pesticide residue free alternative to conventional storage and protection techniques. A model for accelerated ageing at 30-60°C at high relative humidity levels was developed which indicated that the condition of the seeds was crucial in determining seed life period and the accelerated ageing model can be used to accurate prediction of seed life. An experiment was conducted to determine the influence of artificial ageing on seed viability and longevity with factorial CRD design with three repetitions. Seeds of two varieties viz., V<sub>1</sub>: GW 496 and V<sub>2</sub>: Lok 1 were subjected to accelerated ageing for D<sub>1</sub>: 0 day (fresh seed), D<sub>2</sub>:1 day, D<sub>3</sub>:2 days, D<sub>4</sub>: 3 days, D<sub>5</sub>: 4 days and D<sub>6</sub>: 5 days. The seed quality parameters as well as biochemical changes viz., protein (%), carbohydrate (%) and α-amylase assay (micromoles/mg/min) were recorded for evaluation of biochemical parameters of seed and seed quality of wheat for two years. Seed quality parameters significantly differed in the wheat varieties during both the years. Lok 1 variety recorded significantly higher average pooled germination (81.97 %), seedling length (15.05 cm), seedling vigour index I (1471), seedling vigour index II (14.33), protein content (11.68 %), carbohydrate content (68.27 %), α amylase assay (8.73 micromoles/mg/min) and lowest electrical conductivity (21.64 μS cm<sup>-1</sup> g<sup>-1</sup>). Whereas, the other variety, GW 496, recorded higher deterioration and loosed seed quality at faster rate and showed lower values for all the quality parameters at the end of five days of accelerated ageing. Ageing duration showed significant effect on all the observed seed quality parameters. The fresh seeds (without ageing) recorded the highest average pooled germination (96.83 %), seedling vigour index I (2017), seedling vigour index II (14.33) at the end of five days of accelerated ageing. Progressive ageing duration showed negative effect on biochemical parameters of the seeds and recorded the lowest protein content (9.78 %), carbohydrate content (61.93 %), α amylase assay (6.42 micromoles/mg/min) and higher electrical conductivity (24.74 μS cm<sup>-1</sup> g<sup>-1</sup>) at the end of five days ageing. The combined effect of varieties and accelerated ageing duration showed significant effect on most of the seed quality parameters and also differed significantly during both the years. The fresh seeds of the variety Lok 1 recorded significantly higher seed quality which was found significantly lower in the five days aged seeds of wheat variety GW 496.

**Keywords:** Seedling vigour, α amylase assay, accelerated ageing

## 252(P-252)

### **Study of resilient agriculture in changing climate scenario of agro-biodiversity in tribal areas of Northern Hilly Region, Chhattisgarh, India**

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Chhattisgarh has an amazing variety of food production systems. It is one of the places on the earth to have a remembered history of enormous diversity of food resources. These food resources are included many varieties of germplasm, a wide range of millets and other dry land crops, pulses, oilseeds, fruits, edible flowers, tubers, mushrooms and other forest gathered foods. Many of these are dependent upon access to close proximity of the forests and tribal areas. Biodiversity portfolio approach acts to buffer against unpredictable environmental change in the Northern hills of Chhattisgarh state. Hot spot of the Surguja of Batauli block holds rich diversity in landraces of mandate crops under the GEF project. Using agricultural biodiversity in the fight against climate change is about building climate smart system, responding variety with climate resilient variety. Diversity can help farmers mitigate, adapt and ensure food and nutrition security by providing them with more options to manage climate risks and strengthen the resilience of their farms and surrounding landscapes. A study has been conducted at target sites of Chhattisgarh state during 2019-2021 under UN implemented GEF project entitled “Mainstreaming agricultural biodiversity conservation and utilization in agriculture sector to ensure ecosystem service and reduce vulnerability” executed by Alliance of Bioversity and CIAT. The triadic comparison of technologies (tricot) approach has been successfully utilized by demand-led breeding programmes to identify varieties for dissemination suited to specific geographic and climatic regions. Crowd sourced citizen science is an emerging approach in plant sciences. 380 varieties were tested in PVS trial and crowdsourcing trial among 560 farmers of the target sites using ClimMob and ODK application developed by Alliance of Bioversity International and CIAT. We have found few promising indigenous landraces along with improved varieties in rice crop viz. Jeeraphool, Vikram-TCR, TCDM-1, Chindmauri, Lalo Dhan, Indira Barani Dhan-1 RRF-105, Luchai Mutant, Kala Jeerashankar, Karhani and Sanchuria. Our results show that few native varieties are Climate resilient as Karhani (Drought Tolerant), Sanchuriya (Cold Tolerant) and improved variety as Indira Barani Dhan-1, RRF-105, VIKRAM-TCR (Drought Tolerant) suitable for rain fed condition. Teliya Urd, Indira Urd Pratham, Nar Urd and Motichoor in Black gram crop. Makadi Arhar, CG Arhar-1, Deshi Lal arhar, Beej Arhar in Pigeonpea crop, Bada Kodo, CG Kutaki-2, Bedo Kutaki, BL-4 in minor millets, RVG 203, Majhola Chana, RVG 205 in Chickpea crop and CG Rajgira 1, RMA-62 in Grain Amaranth crop. Many farmers demanding and preferring these varieties than improved variety due to climate resilient with higher nutritional value as well as yield. Jeeraphool rice variety was found highest rank among the all criteria due to its high market value and premium quality characters. This premium rice variety have been granted Geographical Indication for Surguja District of Chhattisgarh. The cultivation and use of indigenous climate resilient varieties will help the addressing the challenge of climate change.

**Keywords:** Climate change, ClimMob, Indigenous variety, PGR, Socio-economics, Tricot

253 (P-253)

**Responses to seed dormancy breaking treatments in wild *Luffa* species**

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Wild *Luffa* species have great problem of germination under normal condition and require long time to germinate. They have dormancy, because of the variation in the seed size, degree of hard seediness and variation in lignin content in seed coat among the species. Therefore, a systematic study was conducted to determine the most suitable pre sowing treatment for seed germination and seedling growth in two wild species of *Luffa graveolence* and *Luffa echinate* (Four accessions). Seeds were exposed to various pre-treatments such as scarification and different chemical treatment with gibberellic acid and potassium nitrate. Treated seeds were evaluated for their viability to assess the impact of given treatments. Among the various treatment tried scarification + GA<sub>3</sub> @ 200 ppm was found most effective in *Luffa echinate* and scarification + KNO<sub>3</sub> @ 0.2% for *Luffa graveolence* for germination percentage. The seedling vigour in terms of shoot length, root length, total fresh and dry weight were recorded highest with scarification + GA<sub>3</sub> @200 ppm for *Luffa echinata* and scarification + KNO<sub>3</sub>@ 0.2% for *Luffa graveolence*. The result of present investigation revealed that wild species required an additional pre sowing treatment to enhance seed germination, vigour and uniform plant stand in *Luffa*.

**Keywords:** Seed dormancy, Seedling vigour, Treatments, Wild *Luffa*

## 254 (P-254)

### Developing NIRS prediction model for oil, protein, amino acids and fatty acids in Amaranth and Buckwheat

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Pseudo-cereals are potential crops for adverse climatic conditions being tolerant to biotic and abiotic stresses. Amaranth and Buckwheat are two pseudo-cereals having superior nutritive values. Analysing biochemical traits in conventional methods require high cost, labour work and time. NIRS is a technique used to rapidly determine biochemical parameters of large germplasm in a non-destructive way. NIRS prediction models have been developed using MPLS regression technique in oil, palmitic acid, oleic acid, linoleic acid and linolenic acid in amaranth and buckwheat. Good RSQ<sub>external</sub> values were obtained for the above traits i.e, 0.854; 0.866, 0.788; 0.775, 0.817; 0.851, 0.835; 0.870 and 0.746; 0.819 in amaranth; buckwheat respectively. Good RSQ<sub>external</sub> for amino acids like arginine+threonine, leucine, methionine, phenylalanine, valine, cysteine, histidine, isoleucine and lysine were obtained for combined amaranth and buckwheat germplasm. RSQ<sub>external</sub> for above amino acids obtained were 0.793, 0.839, 0.929, 0.897, 0.842, 0.785, 0.792, 0.804 and 0.782 respectively. RPD values between 1.88-3.55 were obtained for



above mentioned traits indicating good prediction quality of the models. These predicted models will facilitate the screening of huge germplasm in a non-destructive way. Detailed nutrition profile can be obtained for these two crops rapidly in a non-destructive way which can also promote commercialisation of these crops.

**Keywords:** Pseudocereals, Potential Crops, Nutritional Profiling, RSQ<sub>external</sub>, RPD

255 (0-33)

### **Intellectual property protection and conservation of unique goods from crop genetic resources in Kerala**

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Kerala is a treasure trove of unique agricultural products produced in diverse agro-ecological conditions. Intellectual Property (IP) protection over unique crop genetic resources, biodiversity, unique products from crops and traditional knowledge is of high concern in the current scenario of globalization and trade liberalization. WTO members, including India, are enacting specific laws to protect the sovereignty over crop genetic resources and biodiversity. The IP rights over farmers' varieties, traditional varieties, extant varieties and new varieties are being protected under the Protection of Plant Varieties & Farmers' Rights Act, 2001. Under the Biodiversity Act, 2002 germplasm within the country is protected by regularizing its access, sustainable use, conservation and benefit sharing arising out of its use. IP rights of communities over unique products are protected and managed by the Geographical Indications (Registration and Protection) Act, 1999. An overview of the provisions, prospects and problems of protection and management of IP rights over unique goods from crop genetic resources in Kerala is highlighted in the paper. The unique medicinal rice '*Navara*' was the first to be registered as GI under the agricultural product in Kerala. The red kernelled rice varieties known as, *Palakkadan Matta* with high nutrient content also got GI tags. *Pokkali* rice varieties are internationally accepted salt tolerant gene donors. *Wayanad Gandhakasala* and *Wayanad Jeerakasala* are the popular unique traditional scented rice cultivars of Kerala having characteristic fragrance and aroma. There are 19 unique goods registered as GI under agricultural products from Kerala. The medicinal Tirur betel leaf, unique hand-made ball jaggery *Marayoor Sharkara*, malty and chocolaty flavoured Wayanad Robusta Coffee, golden brown sweeter crystalline Central Travancore Jaggery and golden yellow crispy *Vazhakulampineapple* are some among them. *Kuttiattoor* mango and *Edayur chilli* have recently been registered as GIs. It is imperative that the other unique goods from crop genetic resources need to be registered and to enhance marketability.

**Keywords:** Ball jaggery, Medicinal rice, Genetic resources, Intellectual Property



## 256 (P-256)

### Identification of heat tolerant genotypes in chickpea

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Total 1000 desi chickpea accessions were collected, characterized and evaluated to identify heat tolerant genotypes. The crop was grown during rabi 2021 and 2022 in the late sown condition in Augmented design. Observations were recorded for qualitative and quantitative traits along with climate data. Promising genotypes [ICC 6462 (132), ICC 6471 (150), ICC 4409(135), ICC 4410 (210) and EC 267221 (137)] were identified for filled and unfilled pods and high yielding ability was noted in ICC 6462 (21.66 g), ICC 6471 (25.70 g), ICC 4409 (23.28 g), ICC 4410 (33.10g), EC 267221 (31.70 g). However, for 100-seed weight [ICC 5982 (28.8 g), ICC 6471 (21.2 g), ICC 0236 (15.3 g), IC 486922 (13.3 g) & ICC 2217 (13.3 g)], for maturity [ICC 6462 (107 d), ICC 6471 (109 d), ICC 4409 (104 d), ICC 4410 (103 d), EC 267221 (104 d), ICC - 2267 (107 d)] and days to 50 % flowering in EC 267221 (77d), IC 486922 (76d), ICC 2345 (76 d), ICC 2267 (81 d) and ICC 2217 (86d). These promising genotypes were selected for further evaluation and identification as a donor for chickpea improvement programme for heat tolerance.

**Keywords:** Chickpea, Donor, Evaluation, Genotypes, Heat tolerant

## 257 (P-257)

### Creation of mutant population in grasspea using gama radiations and electron beam

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To create the genetic variability, total 8000 seeds (1600 in each category of dose) of grasspea, variety Mahateora, was treated with five doses viz., 200, 300, 400, 500 and 600 kGy of gamma rays as well as electron beam at BARC, Trombay, Mumbai and grown in the field alongwith non treated seeds (1600 in each category of doses) during rabi 2021-22. Observations were recorded for germination, growth and survival, flowering and seed set. LD 50 was recorded 300 kGy for gamma and 200 kGy for electron beam. Seedling germination data shows that only 34.75 % plants emerged in the highest dose 600 kGy of gamma rays followed by 41.18 % plants in 500 kGy. Similarly, 33.93 % (600 kGy) plants produced flower followed by 40.18 % (500 kGy) plants. 33.75 % plants (600 kGy) produced seed followed by 39.87 % (500 kGy) and 41.31 (400 kGy) whereas maximum plants (64.0 %) produced seed in 200 kGy as compared to control where all the plants



germinated and produced healthy seed. Similar trend was also noted in electron beam treated grasspea seeds where only 0.38 % plants emerged in 600 kGy dose followed by 0.75 % plants in 500 kGy and 22.62 % plants in 400 kGy dose of electron beam. Only one plant could flower in highest dose (600 kGy) category followed by two plants in 500 kGy dose. No seedset was observed in highest dose of electron beam (600 kGy) followed by 0.063 %, 0.25 % and 1.81 % seeds in 500,400 and 300 kGy doses of electron beam. Results clearly indicated that electron beam treatment was more lethal as compared to gamma rays. Seeds were collected separately to grow M2 populations.

**Keywords:** Electron beam, Grasspea, Gama radiations, Mutant population

## 258 (P-258)

### Identification of trait specific genotypes in pigeonpea

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Total 411 pigeonpea accessions characterized for agro-morphological traits in Augmented design at the IIPR Regional Station, Phanda, Bhopal during kharif 2021. Wide range of variations were observed for the seven quantitative traits (50% flowering, no. of primary branches, plant height, days to 75% maturity, seeds/pods, 100 seed weight, yield/plant). Wide range of variability was observed for 50% flowering (70-177 days), no. of primary branches (3.2-19.2), plant height (79-267.6 cm), days to 75% maturity (132-250 days), seeds/pods (2.3-6), 100 seed weight (4.5-21.5 g) and yield/plant (4-153.6 g). Promising genotypes identified for 50% Flowering [IC 525385 (70 days), IC 245484 (70 days) and IC 551744 (78 days)], Days to 75% Maturity [IC 245484 (132 days), IC 407467 (139 days), IC 523467 (149 days), IC 523465 (153 days) and IC 523466 (155 days)], 100 Seed Weight [IC 525757 (23.5 g), IC 525760 (21.1 g), IC 525881 (19.6 g), IC 527806 (15.4 g) and IC 527781 (14.9 g)], Yield/Plant [IC 527832 (153.6 g), IC 523461 (112.64 g), IC 527906 (110.8 g), IC 527752 (101.48 g). Further, other important traits such as pod dimensions [IC 525760 (9.3 X 0.8 cm), IC 525757 (8.1 X 1.1 cm) IC 527806 (7.9 X 0.9 cm), IC 525847 (7.0 X 1.0 cm)], no. of pods per pod [IC 523476 (882.8)], No. of Pods/cluster [IC 527763 (8.0), IC 525385 (7.0), IC 553036 (7.0), IC 548263 (7.0)], No. of Seeds/pod [IC 525760 (6.0)] and plant height [IC 525385(91.4 cm), EC 109901 (95.4 cm)]. The germplasm collections contain a significant amount of genetic diversity that could be utilized in pigeonpea enhancement programmes.

**Keywords:** Characterization, Genotypes, Pigeonpea, Trait specific



**259 (P-259)**

**Screening of Makhana genotypes against insect pests**

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Makhana (*Euryale ferox* Salisb) is an important aquatic fruit crop and about 85 per cent of the Makhana crop in the country is cultivated in Bihar. The area, production and productivity of this crop are 35000 ha., 7.4 lakhs quintals of seed and 21.25 q/ha, respectively. This crop is cultivated over 50 per cent area in field condition. Changing cropping pattern and crop ecology, the insect pests are now emerging as major constraints in getting maximum production and productivity from existing traditional land races of the makhana crops. Collection, conservation, multiplication, characterization and evaluation of 41 germplasm were started at Bihar Agricultural University, B.P.S. Agricultural College, Purnea from 2013 crop season to identify promising genotypes of makhana against insect and gastropod pest as well as for maximum yield. After two years of evaluation highest yield and moderately field resistance against important insect pest was found in BR-Makh-07 which was released as Sabour Makhana-1 (IC 620551).

**Keywords:** Makhana, Insect pest, Field resistance, Yield

**260 (P-260)**

**Development, generation advancement and preliminary characterization of *Abelmoschus* amphidiploids**

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Okra (*Abelmoschus esculentus* (L.) Moench), also known as bhendi or lady's finger, is a popular vegetable crop with high dietary fibre and protein, balanced in both lysine and tryptophan amino acids. However, the cultivation of okra is challenged by the incidence of Yellow Vein Mosaic Virus and Enation Leaf Curl Virus diseases. The field screening of various wild *Abelmoschus* species led to the identification of tolerant species, which were further used in intensive wide-crossing programme to generate interspecific hybrids between the cultivated okra and the tolerant species (*Abelmoschus pungense* var. *mizoramensis*, *A. enbeepeegeearensis*, *A. caillei*, *A. tetraphyllus* and *A. angulosus* var. *grandiflorus*). The F<sub>1</sub> plants of these crosses had varying degrees of sterility which was overcome by doubling the chromosome number of interspecific hybrids by applying 0.1%



colchicine at the seedling stage. In order to undertake generation advancement and preliminary characterization, a total of 113 crosses comprising amphidiploids in C 1 generation (30 nos.), amphidiploids in C<sub>3</sub> generation (15), BC 1 F<sub>1</sub>s (25), F 2s (01), multicross combinations (39), and subspecific cross at F 8 generation (03) were raised during *Kharif-2021* along with *A. esculentus* genotypes. All the cross combinations were morphologically characterized for two qualitative and six quantitative fruit characters. The *Abelmoschus amphidiploids* were the store house of many desirable genes with a considerable magnitude of linkage drag. Majority of crosses exhibited an intermediate fruit morphology, however, with hispid pods, stem, leaves, vigorous and perennial growth habit, and continued flowering and fruiting beyond four months, confirming the dominance of wild characters. The fruit morphology of three back cross progenies; Ruchi (*A. esculentus*) x AM24(C 2 /50/Mizo34), Ruchi (*A. esculentus*) x AM-6 (C 3 /50/Mizo24), and Arka Anamika x(C 2 /50mizo34 x Parbhani Kranti), exhibited high morphological resemblance to the cultivated okra, confirming geneflow from the cultivated okra to the amphidiploids and further, demanding confirmation of the virus tolerance in these genotypes. Generation advancement was done by selfing (71 nos.), back crossing (46) and bulking the open pollinated seeds (113), and were supplied for screening them at hotspots.

**Keywords:** *Abelmoschus*, Amphidiploids, Preliminary characterization, Generation advancement

## 261 (P-261)

### Sex Identification in a potential biodiesel plant *Simarouba* (*Simarouba glauca* DC)

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The polygamodioecious perennial *Simarouba* (*Simarouba glauca* DC) has gained popularity as a significant oilseed tree crop for cultivation. Only female plants are preferred in *simarouba* for the commercial production of fruits and seeds. However, it is crucial to identify the gender of male and female genotypes early on before planting because extra male plants can be eliminated at the seedling stage for successful plantation. In this view, 80 simple sequence repeats markers were used to screen male and female plants in order to differentiate male plants from the female ones. Among these primers SSR-34 has produced only male specific bands. This marker can be used to identify male plants among the female plants. These findings suggested that the male-specific marker SSR-34 may be employed to characterise sex in *Simarouba* at an early stage of plant development. Also, this marker can be used for accurate and rapid identification of the male plants during certification and determination in mass multiplication.

**Keywords:** Biodiesel, *Simarouba*, Sex Identification, SSR



## 262 (P-262)

### **High oil yield in sesame (*Sesamum indicum*) is shaped through sustained gene expression during seed development**

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Sesame is a well-known and primordial oilseed crop. However, the genic foundation of sesame oil quantity as well as quality is still little understood. Recently high-throughput sequencing studies have concentrated on the understanding towards production of lipids and fatty acids (FA) in sesame plant. Here, to understand the transcriptional regulation of the oil biosynthesis during sesame seed development, we analysed a publicly available transcriptome dataset for three sesame genotypes contrasting for oil yield. We identified a total of 501 genes that are significantly differentially expressed in the developing seeds of the high oil yielding sesame genotype when compared to the low oil yielding genotypes. Furthermore, 27 genes of those were found to be associated with oil biosynthesis. The higher expression levels for previously reported key genes of oil biosynthetic pathway were recorded in the transcriptome of high oil yielding genotype. The expression level of oil biosynthesis genes decreased towards later developmental stages in low oil yielding genotypes while the expression pattern in high oil yielding genotypes is sustained at comparatively higher levels than the low oil yielding genotypes. Also, an early onset and sustained expression of certain oil biosynthetic genes until seed maturity was observed in high oil yielding genotype. Hence, for higher oil yield, expression of genes of the oil biosynthesis pathway to be to be sustained from initial seed developmental stage to the seeds that are progressing towards maturity. Typically, the high oil yielding genotype accommodates a broader window of time for active oil accumulation when compared to the low oil yielding ones. These findings will speed up the analysis of the genetic basis of sesame oil production for its utility in enhancing oil yield.

**Keywords:** High oil yield, Gene expression, Sesame, Transcriptional regulation

## 263 (P-263)

### **Genetic diversity assessment using SSR markers in the prospective progenitors of sesame (*Sesamum indicum* L.)**

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The sesame (*Sesamum indicum* L.) is an ancient oilseed crop with the presence of its wild relatives distributed across Africa, South Asia, Indonesia, New Guinea and Australia. The cultivated sesame is known for its high quality and highly nutritional edible oil and belongs to the Indian centre of origin while most of the wild relatives belong to African centre. *Sesamum indicum* subsp. *malabaricum* is known to be the prospective progenitor of the cultivated sesame, with *Sesamum mulayanum* being synonymized with the former. However, our studies indicated a contrasting phenotypic feature that distinguishes these two. To test this hypothesis, we subjected the 188 wild sesame accessions comprising *S. malabaricum*, *S. mulayanum*, and *S. indicum*, along with few inter-specific derivatives among them for molecular level assessment using simple sequence repeat (SSR) markers. Here, we report the evaluation of the extent of genetic diversity among the 188 wild sesame species using thirty SSR markers. Also, these were used to assess the grouping pattern for the known taxonomical identities among these progenitors for an understanding on the molecular level differences between *S. malabaricum* and *S. mulayanum*. Of the thirty primers studied, we obtained amplicons ranging from 140 bp to 300 bp. The present study provides an overview of the differences at molecular level between the taxa studied and its association with the phenotypic distinguishing features. The degree of grouping of the inter-specific derivatives with the parental taxa, the generic grouping pattern between the accessions of different taxa aids in deciding on the phenotypic distinction made especially between *S. malabaricum* and *S. mulayanum*. Also, our study will also provide preliminary evidences on to the degree of closeness of the present day cultivated sesame with the above-mentioned taxa to identify the prospective progenitor.

**Keywords:** Genetic diversity, Progenitor, Sesame, SSR

264 (P-264)

**Transferability of cultivated sesame SSR markers to the closely related wild species – an assessment**

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Family *Pedaliaceae* is harbored with an important oilseed crop, sesame (*Sesamum indicum* L.) being widely cultivated across the tropical regions of the globe and originated from India. There are 31 accepted species in the genus *Sesamum*. Except few species, information on the chromosome number, genome size estimates, genome grouping, is scanty for many of the wild relatives and forms as a key bottleneck for the genome scale studies in those wild species. Existence of synteny relationship and possibility of using comparative genomics approach, information from the cultivated crop can be taken for its best utilization in the closely related wild species. As a first step, we tested for the cross-species transferability of simple sequence repeats (SSRs) markers that were initially identified and reported for its polymorphism in the cultivated sesame. Particularly, SSRs are the targeted molecular marker system due to its higher degree of polymorphism, better reproducibility, and present both in genic and inter-genic regions. Identified transferrable SSR markers can be used in the wild species for molecular diversity assessment and to gain population structure information, without much cost in marker development. Here, we report the assessment of cross-species transferability of 43 SSRs that were earlier identified and documented in cultivated sesame, for the eleven wild taxa of sesame. The wild species used in our study comprise, *S. alatum*, *S. angolense*, *S. angustifolium*, *S. laciniatum*, *S. latifolium*, *S. indicum* subsp. *malabaricum*, *S. mulayunum* (although synonymized with *S. malabaricum*, due to consistent phenotypic differences, we included for molecular level assessment), *S. prostratum*, *S. radiatum*, *S. triphyllum*, and *Pedaliium murex*. These were tested along with the cultivated sesame (cv. Swetha and TMV-3) and few inter-specific cross derivatives.

**Keywords:** Cross-species, Sesame, SSR, Transferability

## 265 (P-265)

### Genetic diversity among oat (*Avena sp.L.*) germplasm accessions

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Genetic divergence was studied for 294 oat germplasm accession belonging to ten different *Avena* species including six checks (RO-19, JHO-822, OS-405, JO-1, JHO-851 and UPO-12-1). Experiment was conducted in augmented design in *Rabi* 2019-20. Observations were recorded on five randomly selected plants in each genotype for quantitative traits. Non-hierarchical Euclidean cluster analysis grouped oat genotypes into ten clusters indicating presence of substantial genetic diversity in the evaluated germplasm. Cluster VIII comprised by highest number of genotypes followed by cluster V, cluster VII, cluster VI, cluster III and cluster II. Four cluster I, IV, IX, X had lowest number of genotypes. Wide range of intra cluster distance obtained. Highest intra cluster distance obtained by cluster VII represent the high genetic diversity among the genotypes. Traits *viz.*, plant height, leaves length, leaves width, number of tillers per plant, number of leaves per plant, leaf stem ratio and seed yield per plant contributed highest towards genetic divergence. The highest inter cluster distance found between cluster V and cluster VII



(7.91). Cluster I and II had better cluster means for many characters. Germplasm accession could be used as parent in further hybridization programme in oat.

**Keywords:** Genetic diversity, Germplasm, Oat, Euclidean cluster

## 266 (P-266)

### **Maize germplasm exchange in India: significance of quarantine regulatory measures**

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The success of any crop improvement programme depends on identifying the availability and augmenting the potential crop genetic resources from other countries. However, global exchange of germplasm also poses risk of entry of exotic pests. ICAR-NBPGR is the nodal authority for quarantine processing of crop germplasm under exchange. The Regional Station of NBPGR, located at Hyderabad facilitates quarantine processing of germplasm meant for the Southern part of the country. During the past twelve years (2010-2022), the Hyderabad Station processed about 82,000 imported accessions of maize genetic resources from 14 different countries meant for international organization, public organizations, private industry etc. The material consisted of breeding lines, segregating material, inbreds, varieties, hybrids, restorer lines etc. All the accessions were exposed to various seed health protocols, which resulted in the interception of several important pests of quarantine significance thereby preventing the entry and spread in our country. The important pathogens were *Bipolaris maydis*, *Stenocarpella maydis*, *Pestalotia* spp., *Lasiodiplodia theobromae*, *Rhizoctonia bataticola*, *R. solani*, and insect pests such as *Sitophilus oryzae* and *S. granarius*. There are four different races, 'T', 'O', 'C' and 'S' of *B. maydis* across the world, while race T is seed borne and highly virulent and is a Quarantine pest for India. This pathogen was intercepted from nine countries and almost every year during the reporting period. Although identification up to race level could not be done in the above instances, necessary salvaging procedures were followed using fungicidal seed treatment prior to the release and conducting rigorous post-entry quarantine inspections during active crop growth stage. All precautions were taken to uproot and incinerate the pathogen infected and virus suspected plants during post-entry quarantine inspection. Similarly, about 1,23,727 healthy accessions of maize germplasm were exported from India for research purpose. Pre-export crop inspections were also carried out from time to time for facilitation of providing additional declarations specified by the importing country during the Phytosanitary certification. Significance of these interceptions was studied by assessing the yield losses that would have occurred had they not been intercepted, thereby emphasizing the role of quarantine regulations under implementation in germplasm exchange. Further, the challenges in preventing the entry and spread of maize exotic pests of quarantine significance are discussed.

**Keywords:** Exchange, Germplasm, India, Maize, Quarantine, Regulatory measures



**267 (P-267)**

**Utilization of GM diagnostics in monitoring adventitious presence of transgenes: Checking unauthorized genetically modified events for regulatory compliance**

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*Bt* cotton is the only approved GM crop in India, which is considered as authorized. Rest of the GM events approved in other countries may be considered as unauthorized GM events (UGM) in the Indian context. The unauthorized entry of UGM needs to be monitored in the imported consignments of seeds and food products for regulatory compliance using GM diagnostics. ICAR-NBPGR, New Delhi is the nodal organization for import of germplasm for research purposes. As in some of the countries of export, several GM crops/events are approved so it is necessary to check the selected imported material for confirming the GM-free status. A case study to reflect the restriction of UGM in the country is being highlighted employing GM diagnostics in the imported accessions of flax (linseed) and soybean as a precautionary measure. For ensuring GM-free conservation, adventitious presence of transgenes was also monitored in the selected genebank accessions of cotton and mustard collected from the states where confined field trials of GM events of these crops were conducted. For carrying out systematic GM detection, Polymerase Chain Reaction (PCR)/ real-time PCR-based screening tests targeting commonly employed promoters, terminators and transgenes were employed. These diagnostics were also utilized to check GM ingredients in domestic and imported food products available in the marketplace. Based on the tests conducted, none of the samples were found positive for transgenic elements tested. ISO/IEC17025:2017 accredited GM Detection Research Facility at ICAR-NBPGR being a designated National Referral Laboratory for GM detection under sub-section (1) of Section 4 of the Seeds Act, 1966 in a Gazette of India: Extraordinary Notification (Department of Agriculture, Cooperation and Farmers Welfare) dated 15.11.2017, is providing GM testing services to public and private sector to track the unauthorized entry of GM seeds in the supply chain for regulatory requirement.

**Keywords:** Adventitious presence, Real-time PCR, Regulatory requirement, Unauthorized GM (UGM) detection

**268 (P-268)**

**Studies on morphological characterization in Pigeonpea [*Cajanus cajan* (L.) Millsp] germplasm of Chhattisgarh**

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Pigeonpea [*Cajanus cajan* (L.) Millsp] ( $2n = 22$ ) is an important pulse crop that provide food fodder and variable sources of proteins for poor smallholder farmers in the semi-arid tropics and it can survive in dry environments. In this study 104 germplasm were evaluated and morphological characterization were carried out by visual observation on the basis of DUS characterization, which was conducted in Augmented Randomized Complete Block Design (ARBD) with 4 blocks during kharif 2020-2021 at College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. Data were recorded on five randomly selected plants in each genotype for 15 qualitative traits viz, anthocyanin colour on hypocotyls, flower pattern of streaks on petal, pod constriction, pod pubescence, plant branching pattern, Stem colour, Pod colour, leaf shape, Leaf pubescence on lower surface of the leaf, pod surface stickiness, colour of flower base of petal, plant growth habit, seed colour, seed colour pattern seed shape. The qualitative characters showed wide variation and the potential germplasm may be utilized for further breeding program.

**Keywords:** Characterization, Germplasm, Pigeonpea, Variation

**269 (P-269)**

**Access and Benefit Sharing (ABS) issues in genomic resources**

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India is a land of diversity in terms of flora and fauna. Genetic and genomic resources are enormous while comparing many countries of the globe. There are thirty-six wild life hot spots in this world; of which six are from India, representing almost 1/6<sup>th</sup> of the world's wild resource under threat. Focused conservation efforts may be required save over 1500 unique species from these hot spots. Human intervention is high due to anthropogenic activities and exploration from these confined regions is a threat to the biodiversity. Further, use of resources from such areas as well as other sources needs to be critically seen where the robust Access and Benefit Sharing (ABS) and Material Transfer Agreement (MTA) is not in place. Genomic resources are the part of research results published in open access journals by researchers worldwide. The public databases are enriched by research results from scientists across the world; without which the databases cannot exist. Although these results are considered as resources and are provided by the custodians viz.; The Salk Institute for Biological Studies (SALK), The *Arabidopsis* Information Resource (TAIR) etc. which charge the users for the resources which actually is the Intellectual Property Right (IPR) of the researchers. The robust system for benefit sharing through MTA and Standard Material Transfer Agreement (SMTA) needs to be developed for this area also. Also, it's worthwhile to mention that the researchers are paying substantially for publication in these open access journals. In light of the above a system needs to be put in place for benefit sharing arising out of the



use of such genomic resources in light of the Convention of Biological diversity (CBD) and other international agreements w.r.t access and benefit sharing issues.

**Keywords:** Access and Benefit Sharing, Conservation, Databases, Genomic resources

## 270 (P-270)

### Genetic diversity study in cotton through DNA profiling using molecular markers

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Cotton, also known as white gold, is widely cultivated all over India. DNA profiling method by molecular markers is considerably utilized in many crops to have a look at diversity, gene identity and identifying markers linked with desired traits. Existence of genetic diversity is a vital requirement for a good hybridization program. An estimate of genetic range among maternal and paternal is an essential device *via* which a breeder can choose suitable parents for a sound hybridization program. In this study, 21 RAPD markers were used to analyze the genetic diversity of 30 cotton genotypes procured from MCRS, Surat, Gujarat. DNA extraction was done using CTAB method followed by standard PCR protocol and agarose gel documentation. Further, a dendrogram generated by UPGMA cluster analysis based on Jaccard's similarity coefficient, was used to form clusters. The percentage of polymorphism ranged from 29 % to 100 % with an average of 76 % polymorphism per primer. The Jaccard's similarity coefficient ranged from 0.61 to 1.0. In dendrogram, 30 cotton genotypes were divided into 2 main clusters. Further clusters are subdivided into two sub clusters, resulting in 4 sub clusters (cluster 1A, cluster 1B, cluster 2A and cluster 2B). Out of which cluster 1A consisted of seven genotypes, Cluster 1B includes eight genotypes, 2A consisted of eight genotypes and cluster 2B consisted of seven genotypes. Genotypes falling within the same cluster are considered to be more similar compared to genotypes falling in different clusters. More genetic diversity is observed between the clusters, so we have to go for hybridization between the genotypes of different clusters to exploit more heterosis.

**Keywords:** Cotton, Dendrogram, DNA profiling, Molecular markers, Clusters

## 271 (P-271)

### Inheritance of leaf rust and stripe rust resistance genes transferred into bread wheat from tetraploid progenitor *Triticum dicoccoides*

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Wild emmer wheat, *Triticum dicoccoides*, the tetraploid progenitor of wheat is an



important source for novel disease resistance genes. *T. dicoccoides* acc pau 14716, showed resistance to the predominant leaf rust and stripe rust races in India. An introgression line (IL<sup>dic</sup>) was developed in the background of *T. aestivum* cultivar WL711(NN). To examine the genetics of these transferred resistances, a F<sub>4</sub> mapping population was generated by crossing the IL<sup>dic</sup> with leaf rust and stripe rust susceptible cultivar HD2967. The mapping population was screened against highly virulent *Pt* leaf rust pathotypes at seedling and adult plant stages, *Pst* stripe rust pathotypes at the adult plant stages and genetic ratios were calculated. Inheritance studies segregated for a single dominant LR and YR resistance, as indicated by the theoretically expected ratio of 3 Resistant (R):1 Susceptible (S) plants. For mapping leaf rust and stripe rust resistance genes in the F<sub>4:5</sub> mapping population bulk segregant analysis in combination with whole-genome resequencing (BSA-seq) was performed. BSA-seq analysis in combination with QTLSeqR identified a candidate region on chromosomes 2B,1B for leaf and stripe rust resistance respectively. Around 300 genes were found to be annotated in the 10Mb candidate region on chromosome 2B. It was observed that out of 300 annotated genes, 81 genes were involved in the defense mechanism against diseases. Similarly, a 10Mb region identified on chromosome 1B to be associated with stripe rust resistance was identified to carry 149 annotated genes. Out of 149 annotated genes, 13 genes were found to be involved in defense mechanisms against diseases in which three genes had an NBS-LRR domain and therefore considered as candidate putative genes.

**Keywords:** Rust resistance, Introgression lines, Whole-genome resequencing, Bulk segregant analysis

## 272 (P-272)

### Screening diverse cowpea germplasm for identification of *Bean common mosaic virus* (BCMV) resistance sources and confirmation through serological and molecular methods

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Cowpea (*Vigna unguiculata* L. Walp.) is a multipurpose crop grown throughout India for its long green pods as a vegetable, seeds, foliage and fodder. Cowpea is susceptible to a number of viral diseases including Bean common mosaic virus (BCMV) which is a major threat for production. BCMV belongs to Potyvirus genus and it has a wide host range can cause economic yield losses in common beans from 35 to 98%. Screening of germplasm against BCMV will provide a source of resistance that can be utilized to develop resistant cultivars. A total of 85 cowpea germplasm was screened against BCMV with one susceptible check, C-152 and one resistant check, CP-55 and shown various symptoms



like mosaic, blistering, puckering, leaf rolling and stunting. EM revealed the flexuous rod viral particles of 725 nm in infected leaves. RT-PCR protocol standardized with three primer sets (BCMV1, BCMV2 and BCMV3). The amplified PCR products were sequenced and blast analysis revealed 92.75%, 90.68% and 92.5% nucleotide similarity with previously reported BCMV in GenBank. No cross reactivity was observed during specificity tests against a panel that included BCMNV, BYMV, CABMV, SMV and PeMoV. The assay is sensitive enough to detect 0.14 ng/ $\mu$ l of BCMV cDNA. Among the 85 accessions screened by artificial inoculation, 24 accessions were immune, 31 were highly resistant, 25 were resistant, 5 were moderately resistant to BCMV. DAC-ELISA of embryo and seed coat of 24 immune accessions revealed the presence of BCMV in seed coat of four accessions. However, these need to be further evaluated under BCMV hotspots, for different strains and under multi-location to know the genotype and environment interaction to further assure the quality of resistance exhibited by the immune germplasm accessions.

**Keywords:** Cowpea, Germplasm, Immune, Screening, Viral diseases

## 273 (S-05)

### **Development of Pre-breeding genetic sources for trait discovery and gene mapping in bread wheat: Indian perspectives**

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Pre-breeding populations are vital for trait-discovery and fine mapping of QTLs for complex quantitative traits like yield and tolerance to abiotic stress. Terminal-heat stress during grain filling is the major abiotic stress affecting wheat productivity globally and the production is affected the most in Indo-Gangetic plains the wheat bowl of India. In order to create pre-breeding populations with enhanced resilience to heat-stress, we used exotic lines to further augment heat-stress tolerance in the well-adapted bread wheat germplasm. In this endeavour the crosses were made to develop a 5-parental MAGIC (Multi-parent Advanced Generation Inter-Cross) and five bi-parental mapping populations. MAGIC has more power for high-resolution QTL mapping due to high frequency of recombination and reshuffling of genome. Unlike a panel of diverse germplasm, this population is tailor-made for plant breeders with a combination of useful traits derived from multiple parental lines. For MAGIC development in bread wheat, we crossed five founder parents selected based on component traits to create three F<sub>1</sub> hybrids (Ipace Robe  $\times$  NW1014, HD2864  $\times$  UP2338 and DL788-2  $\times$  HD2864) using HD2864 (founder line) as reciprocal parent. Each F<sub>1s</sub> crossed in a full diallel pattern to produce six double crosses during 2016-17. The two-way crosses were further hybridized in all possible combinations in 2017-18 to reshuffle the genomes of founder lines. The MAGIC population stabilized by natural self-pollination, and 4<sup>th</sup> cycle selfed seeds of 1930 MAGIC RILs and F<sub>8</sub> seeds of 1090 RILs of five biparental populations harvested during 2021-22. These mapping populations were exposed to 35-38°C during grain development stage to



screen for terminal heat-stress tolerance and to impart adaptation to elevated temperature under extremely late-sown conditions. The promising 510 RILs of 5-parental MAGIC population would be evaluated in multi-environment for fine-mapping of QTLs for heat-stress tolerance in bread wheat.

**Keywords:** Bread wheat, Genetic resources, MAGIC, Pre-breeding, Trait discovery

## 274 (P-274)

### Extent of genetic variation and character association in okra

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The present investigation was carried out with 28 okra genotypes at Horticulture experimental farm, Assam Agricultural University, Jorhat during the Summer season of 2021. The objective of the investigation was to study variability, heritability, genetic advance, correlation coefficient, direct and indirect effects of interrelated characters. Analysis of variance revealed substantial genetic variation present among the genotypes for each observed character. High genotypic and phenotypic coefficient of variation was recorded for the number of fruits per plant, fruit length, fruit diameter, internode length, fruit weight, number of seed per fruit, seed yield per fruit, and fruit yield per plant, which indicates the existence of broad genetic diversity. The estimated heritability was high for fruit length, fruit diameter, leaf blade length, leaf blade width, number of fruits per plant, number of branches per plant, seed yield per fruit and fruit yield per plant. High heritability accompanied with high genetic advance was observed for fruit length, fruit diameter, number of fruits per plant, fruit weight, number of branches per plant, seed yield per plant and fruit yield per plant. These characters could be improved through direct selection since these characters are controlled by additive gene action. The fruit yield per plant was found to be positively correlated with fruit length, internode length, number of fruits per plant, hundred seed weight and seed yield per fruit at both phenotypic and genotypic levels and with plant height at genotypic level only. Hence selection for such positively associated characters could result in direct improvement of yield. Path coefficient analysis revealed that characters namely fruit length, plant height, number of fruits per plant, first flowering node number, hundred seed weight and number of seed per fruit had positive direct effects on yield. So direct selection for such characters will be effective for further yield improvement.

**Keywords:** Variability, heritability, genetic advance, correlation, okra

## 275 (P-275)

### Genetic variation and character association in Brinjal

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Present investigation comprised of 16 genotypes of brinjal which were evaluated in order to estimate variability, heritability, genetic advance, correlation coefficient, direct and indirect effects of inter-related characters. The experiment was conducted at Horticulture experimental farm, Assam Agricultural University, Jorhat during the Summer season of 2020-2021 following Randomized Block Design with 3 replications. The analysis of variance revealed high genotypic and phenotypic coefficient of variation for number of fruits per plant, fruit length, fruit girth, fruit weight and fruit yield, which indicates the existence of broad genetic base among the genotypes. High heritability was estimated for fruit length, fruit girth, fruits per plant, primary branches per plant, duration to first harvest and fruit yield. High heritability accompanied with high genetic advance was observed for fruit length, fruit girth, fruits per plant, fruit weight, branches per plant, duration to first harvest and fruit yield suggesting that these characters could be improved through direct selection. Correlation studies revealed significant positive correlation of fruit yield per plant with fruit weight, plant height and fruit girth at both phenotypic and genotypic level and fruit length, root length, root dry weight and first flowering node at genotypic level only. Hence genetic improvement of fruit yield could be obtained by direct selection of these traits. Path coefficient analysis revealed direct effect of fruit length, fruit girth, fruits per plant, primary branches per plants on yield. So direct selection of such characters will be effective for further yield improvement.

**Keywords:** Genetic variation, Heritability, Genetic advance, Correlation, Brinjal

**276 (P-276)**

### **Genetic diversity studies in Brinjal (*Solanum melongena* L.)**

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Present investigation comprised of 16 genotypes of brinjal which were evaluated in order to estimate genetic variability, and diversity present among the genotypes for yield and component characters. The experiment was conducted at Horticulture experimental farm, Assam Agricultural University, Jorhat during the Summer season of 2020-2021 following Randomized Block Design with 3 replications. The analysis of variance revealed high genotypic and phenotypic coefficient of variation for number of fruits per plant, fruit length, fruit girth, fruit weight and fruit yield, which indicated the existence of broad genetic base among the genotypes. Analysis of genetic diversity based on Mahalanobis  $D^2$  statistics indicated presence of significant genetic diversity among 16 brinjal genotypes. The genotypes were grouped into 4 clusters. Cluster I consisted of maximum genotypes (7) followed by cluster II (6), cluster III (2) and cluster IV (1). Maximum intra cluster distance was obtained in cluster III (363.258) followed by cluster II (219.629) and cluster I (145.747). High degree of divergence among the genotypes within a cluster would produce more segregating material. Maximum inter cluster distance was obtained between the cluster III and cluster IV (6340.559) followed by cluster I and cluster II



(4026.446), cluster I and cluster IV (266.973), cluster I and III (1566.423) and cluster I and II (1141.384). This clustering helps the breeders to choose the diverse parents for hybridization programme which leads to recombination of non-identical genes. Within the cluster the genotypes are more homogeneous but the genotypes between different clusters are more or less diverse depending upon the cluster distance. The genotypes belonging to the clusters which are widely distant may be selected as parents for hybridization programme.

**Keywords:** Genetic diversity,  $D^2$  statistic, Cluster distance, Hybridization, Brinjal

## 277 (P-277)

### Use of bio-formulations for improving seed quality and yield in garden pea (*Pisum sativum* var. *hortense*)

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Pea (*Pisum sativum* L.) is an important annual legume crop belonging to family leguminosae (*Fabaceae*). It is a protein rich, self-pollinated cool season vegetable crop grown throughout the world. There are two subspecies: *Pisum sativum* var. *hortense*, the garden pea and *Pisum sativum* var. *arvense*, the field pea. It is the third most important pulse crop at global level. Seed is a vital input in crop production and key to agricultural progress. A good quality seed is essential for successful crop production. Synthetic chemicals used in agriculture has a detrimental effect on agro-ecosystem. Hence use of bioformulation is the alternative strategy to improve seed quality and yield. The present investigation was therefore carried out during *rabi* season of 2021-22 in ICR farm of Assam Agricultural University, Jorhat to study the use of bio-formulations for improvement of seed quality and yield in garden pea. The laboratory analyses were conducted in Complete Randomized Design for seed vigour characteristics whereas the field experiment was laid out in factorial Randomized Block Design for assessing plant growth and yield attributing characters. The present study involved two varieties of garden pea *viz.*, Arkel and DS-10, each having seven treatments with three replications. All the priming treatments had significantly influenced in early germination, seed vigour and yield attributing characters. Biopriming with *Trichoderma viride*, *Pseudomonas fluorescens*, *Rhizobium* and PSB gave better results in both the varieties for seedling emergence, early initiation of flowering, pods per plant, seeds per pod, seed yield per plant as compared to control. Among all the treatments, seed priming with combined application of *Rhizobium* @ 20 g/kg + PSB @ 10g/kg gave the best results for almost all the parameters under laboratory and field conditions. The variety DS-10 performed better as compared to Arkel. Correlation analysis revealed significant positive, correlation of seed vigour with seed yield and yield attributing characters such as pods per plant, seeds per pod and seed yield per plant. Among the laboratory parameters, germination percentage showed positive and significant correlation with seedling length, seedling dry weight, seed vigour index-I and seed vigour index-II. From this investigation combined application of *Rhizobium* @ 20 g/kg + PSB @ 10g/kg may be promoted for



future recommendation as a seed priming treatment in pea and for this purpose the variety DS-10 is better than Arkel.

**Keywords:** Bio-formulation, seed quality, yield, correlation, garden pea

## 278 (P-278)

### **A chemometrics approach based NIR modeling studies for nutritional enrichment in potato**

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Potato is the staple food on the globe and majority of the population is consuming as a source of nutrition in daily diet. Potato tubers the commodity of commerce is rich source of protein and on dry weight basis the percentage is more than cereals. Besides, a high-amylose potatoes has potentially interesting for nutritional properties especially among starch foods. Earlier, for screening large and diverse germplasms aimed at nutritional profiling was assessed with conventional approaches that are not only laborious but also time consuming. For mass germplasm screening, a Near-infrared reflectance spectroscopy (NIRS) approach can be implemented that uses near-infrared sections of the electromagnetic spectrum for precise and speedy determination of biochemical parameters. In our studies, we focused on MPLS (Modified Partial Least Squares) regression based NIRS prediction models for assessment of protein and amylose for high throughput screening of diverse potato germplasms. The mathematical treatments executed by permutation and combinations for calibrating the model, where 2<sup>nd</sup> derivatives produced the best results. Treatments "2,4,4,1" were finalized for protein and amylose estimation in potato. Furthermore, treatments highest  $RSQ_{internal}$  (coefficient of determination) values and lowest SEP(C) (standard error of performance) were classified for subsequent validation. The prediction of accuracy of external validation were based on  $RSQ_{external}$ , RPD (residual prediction deviation) and low SEP(C). NIRS prediction model is calibrated and validated for protein with  $RSQ_{internal}$  0.96 and  $RSQ_{external}$  0.94, respectively. whereas, for amylose content  $RSQ_{internal}$  was obtained 0.73. This finding can be further streamlined into breeding nutritionally rich potato cultivars for aiding sustainable development goals towards combating zero hunger and nutrient dense tubers in the era of climate change.

**Keywords:** Chemometrics, Nutritional variability, MPLS Regression model,  $RSQ_{external}$ ,  $RSQ_{internal}$ , RPD

## 279 (P-279)



## ***In situ* conservation of old tea seed jats in North East India**

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Tea is a cross pollinated, self-incompatible and highly heterozygous plant. Species or an old seed jat plant population, particular of its genetic variation can be conserved and maintained through *in situ*. *In situ* conservation method has accelerated the preservation of the old tea seed jats and the evolutionary processes that enable the population to adapt the natural state or within their normal range. The large old seed grown sections of tea ecosystems may be remain unaffected and survive as protected reserve areas with minimal intrusion or alteration by the humans. Till date Tocklai has covered about 19 tea estates under *In situ* conservation program with estimated area about 7.5 hectares. It aims to maintain target species and the collective jats and genotypes that represent under evolution. The conservation of tea seed jats has developed theoretical and methodological focus and achieved significant on the ground progress in the last 13 years. Tea growing regions summaries on *In situ* seed jats conservation activities are presented and recommendations are made for future action. After the development of clones for tea plantation area, most of the old seed grown sections of tea estates of N.E India are uprooting extensively without thinking the importance of tea genetic variability. Old seed jats are the 'gold mine' of Indian tea gene pool system. Tocklai is the pioneer tea research institute and it has initiated a scheme under the umbrella of Tea Board, Government of India, "In situ conservation of old seed jats and its seeds production" in the year of 2009 to avoid the rapid loss of exclusive old seed jats as a first and foremost priorities. In situ conservation technique is highly essential to protect the genetic loss of tea plant and availability of diverse tea germplasm for various research activities.

**Keywords:** Germplasm, *In situ* conservation, Old seed *jats*, Plant gene pool, Tea, Variability

## **280 (P-280)**

### **Evaluation of hybrid rice for yield and quality traits suited to eastern plain zone of Uttar Pradesh**

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A Field experiment was conducted to evaluate yield and quality traits among 31 rice hybrids (including check) for which data was recorded for 13 quantitative and 7 quality characters to study genetic variability, heritability and genetic advance. Analysis of



variance among rice hybrids showed highly significant differences for all the characters indicating the presence of substantial amount of genetic variability. On the basis of mean performance for grain yield per hill, early maturity, no of tillers per plant, hulling %, kernel length and Kernel width, highest GCV and PCV was observed for grain yield per hill followed by spikelets per panicle indicating that these characters could be used as selection for crop improvement. High estimates of heritability were observed for plant height, spikelets per panicle and biological yield followed by days to 50% flowering and days to maturity. High heritability coupled with high genetic advance was observed for spikelets per panicle indicating predominance of additive gene effects and the possibilities of effective selection for the improvement of these characters.

**Keywords:** Heritability, genetic advance, variability, GCV, PCV

## 281 (P-281)

### **Genetic variability, heritability and genetic advance in Okra (*Abelmoschus esculentus* (L.) Moench)**

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Okra (*Abelmoschus esculentus* (L.) Moench) is an important vegetable and annual herbaceous crop. It is grown in subtropical and tropical parts of the world for its immature green fruits and fresh leaves. *Abelmoschus esculentus* is the only species which is known to be cultivated extensively as commercial vegetable among 34 species of *Abelmoschus*. In determining the potential of genetically different lines and cultivars, breeders have to observe various traits that influence yield. The estimates of the heritability and genetic advance are the important parameters on which the success of selection line depends. The present investigation was carried out during *kharif* 2020 at experimental farm, Department of Agricultural Botany, VNMKV, Parbhani. The experimental material consists of forty-two genotypes (including two checks) of which forty genotypes were the derivatives of segregating generations *i.e.*, F<sub>2</sub> and Back crosses of Parbhani Kranti × VROR-159, Parbhani Kranti × Kashi Pragati, Kashi Satadhari × BO-2, Kashi Satadhari × VROR-159. These genotypes were evaluated for twelve traits in RBD design with two replications and data was recorded. The experiment has revealed that PBNLF 4, PBNLF 5, PBNLF 6, PBNLF 13, PBNLF 15 and PBNLF 33 genotypes were found superior for yield and yield attributing characters over rest of the genotypes and checks. The traits *viz.*, plant height (cm), internodal length (cm), number of nodes on main stem, number of branches per plant, 100 seed weight (g) and fruit yield per plant (g) have recorded the moderate values of GCV, PCV and high estimates of heritability along with high genetic advance, while the trait number of seeds per fruit have shown moderate estimate of GCV and PCV only. Hence characters showing high to moderate values of PCV, GCV and high estimate of heritability and genetic advance as per cent mean were



considered as most important characters and selection of these traits will be more effective in improvement of fruit yield per plant.

**Keywords:** Okra, Genotypes, Genetic variability, GCV, PCV, Heritability, Genetic advance

## 282 (P-282)

### **Diversity studies in Buckwheat (*Fagopyrum esculentum* and *Fagopyrum tataricum*) based on morphological traits**

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Buckwheat is commonly grown in the hilly regions of India, especially the Himalayan districts. In the present study, carried out in RBD in the Rabi season of 2021-22 and grown in the crop research field at SHUATS, Prayagraj, 16 genotypes of buckwheat were analysed using 9 quantitative and 9 qualitative characteristics. It was discovered that *Fagopyrum tataricum* (tartary buckwheat) had a determinate growth type and had green coloured cleistogamous flowers that encouraged self-pollination, whereas *Fagopyrum esculentum* (common buckwheat) had open flowers that ranged in colour from white to pink and had an indeterminate growth type. The flowers of common buckwheat were also found to be self-incompatible. Some qualitative characters like leaf blade shape, leaf blade colour, stem colour, seed shape, seed coat colour showed considerable variations, both within and among the species. The characterization results revealed a wide variation in days to 50% flowering and days to 80% maturity showing that common buckwheat matures earlier than tartary buckwheat despite early flowering. Mahalanobis  $D^2$  analysis was performed on the 9 quantitative traits and the genotypes were grouped into 5 clusters, of which cluster 3 was the largest with 7 genotypes of tartary buckwheat and has the maximum intra-cluster distance of 12.88. The maximum intercluster distance was found between clusters 4&5. The tartary buckwheat genotypes were distributed in clusters 3&4 and common buckwheat genotypes were distributed in clusters 1,2&5. Tartary buckwheat being cleistogamous and common buckwheat being open pollinated and self-incompatible can mean that a cross between both might yield good results. Previous studies show that hybridisation between common buckwheat and tartary buckwheat is not compatible through conventional breeding. Based on the clustering pattern, we can suggest that hybridisation between late maturing but high yielding genotype in cluster 4 and mid late maturing but medium yielding tartary buckwheat genotypes in cluster 3 may prove beneficial.

**Keywords:** Buckwheat, diversity,  $D^2$  analysis, morphological traits

## 283 (O-08)

### **Exploration of diversity in pungent chilli genotypes from Arunachal Pradesh**



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North Eastern Region is one of the secondary centres of chilli diversity and in fact, it is home for some of the hottest peppers in the world, viz., Naga Chilli where diverse variation can be seen. Arunachal Pradesh possesses tremendous variation in chilli crop. So, study was conducted to explore the diversity of chilli from Arunachal Pradesh. Thirty (30) pungent chilli genotypes belonging *Capsicum annuum*, *C. chinense* and *C. frutescens* were studied for their biochemical parameters for their diversity in biochemical parameters. Capsaicin varied from 0.2% to 2.2%, capsaicin content which imparts red colour to ripe fruits ranged from 18.1 to 220.2 ASTA units. Ascorbic acid varied from 63.1 to 269.3 mg/100g fresh weight of fruit whereas TSS in fruit juice varied from 1.8 °Brix to 6.9 °Brix. The total chlorophyll content of the leaves varied from 1.4 mg/g to 2.4 mg/g fresh weight of leaf. Capsaicin had the highest values for GCV (60.4), PCV (60.6) and genetic gain (131.2%) whereas capsanthin was found to be the most heritable character with a heritability of 94.7. 5 clusters were found using D<sup>2</sup> analysis where, cluster I had 13 genotypes, cluster II had 2 genotypes, cluster III had 7 genotypes, cluster IV had 8 genotypes and cluster V had 3 genotypes. Cluster I and Cluster IV had highest inter-cluster distance whereas intra cluster distance was highest in cluster IV. Exploring and exploiting chilli diversity from North Eastern States of India can abolish low national average productivity.

**Keywords:** Arunachal Pradesh, Exploration, Pungent chilli, Genotypes

**284 (O-16)**

**Genetic diversity, population structure and trait characterization of Indian cauliflower germplasm**

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Cauliflower is an important vegetable crop which supplies dietary minerals and health-beneficial glucosinolates to consumers and provides livelihood opportunities to growers. In India, it was introduced as a winter vegetable in India in 1822 which later underwent major and minor mutations to evolve as tropical or Indian cauliflower. Since, cauliflower is thermosensitive for curd formation and in India it is grouped as Early (20-27 °C), Mid-early (16-20 °C), Mid-late (12-16 °C) and late snowball (10-16 °C). Over the years, a diverse set of germplasm has been generated with distinctive traits. New genes such as *Or* ( $\beta$ -carotene in curd), *Pr* (anthocyanin in curd), self-blanching, retentive white curd, cytoplasmic male sterility (CMS) systems (*Ogura*, *Can* and *Tour*) were deployed in different maturity groups. Resistant sources and genes responsible for resistance against black rot, downy mildew and Alternaria leaf spot have been identified and used in breeding hybrids. In the present study, 92 Indian cauliflower genotypes from all four



maturity groups were analysed using 100 SSR markers and performed genotyping by sequencing (GBS). The genotypes were also observed for 14 different morphological traits for 3 years. The experiments for morphological observations were undertaken in paired-row and augmented block design. The genotypes showed wide variation in observed morphological traits particularly plant and curd characters. The genotypes showing the earliest curd initiation were PM, DC-EK, DC-8, DC-7 and DC-108. The SSRs generated 1 to 9 with mean value of 2.16. Cluster analysis indicated that the genetic relationship of these cauliflower cultivars was tightly associated with its maturity groups but with slight admixture among the genotypes. The UPGMA dendrogram obtained from SSR markers divided all the 96 genotypes into 4 clusters. Cluster III had maximum number of genotypes. Most of the sub-clusters had genotypes from different maturity groups indicating admixture in genetic makeup among the genotypes. The STRUCTURE 2.3.4 based analysis using data from SSRs and GBS analysis divides the genotypes into 4 sub-populations and supported the historical performance-based classification of maturity groups, however, the genotypes showed introgression of genomic segments from other maturity groups.

**Keywords:** Cauliflower, Germplasm, Genetic diversity, STRUCTURE, SSR

## 285 (S-07)

### **A paradigm changes in on-farm conservation of mango genetic resources and the development of new varieties**

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India is widely renowned for its excellent mango diversity, preserved in field gene banks or orchards maintained by custodian farmers around the country. One cause for the abundance of genetic resources is the planting of mango orchards from seedlings and the crop's highly heterozygous nature. About a half-century back, mango cultivation was not undertaken for commercial purposes compared to today's scenario. Several varieties were cultivated and maintained as a hobby and for personal use. The seedling populations were used as a foundation for developing novel types and heirloom varieties that had little commercial value but were maintained by several generations of custodian farmers. Custodian farmers have played a significant role in conserving Indian mango genetic resources; nevertheless, their numbers are rapidly declining, and the next generation has less incentive to maintain these variations. No new orchard is planted with seedlings, and growers attempt to grow commercially popular types. As a result, the chances of getting a new type via seedling variability are diminishing. Nurserymen also promote commercial mango variety cultivation and prepare grafts based on demand. They have lost the collection of heirloom varieties that was formerly an indicator of a good nursery. Rare kinds are no longer propagated in nurseries since there is no market for them. The quantity of seedling populations is decreasing in the changing scenario, large multivariety old orchards are becoming rare, and grafted plants are replacing seedling trees. The variety in the seeding population had already been used to search for commercially viable types. As a result, the remaining seedling population has a limited



likelihood of producing a new variety. Farmers in many areas are removing traditional orchards and replacing them with high-return crops/varieties. The current research investigates the significance of existing traditional types, their on-farm conservation, and ways to increase the returns from these varieties. Mango seedlings must be planted along the highway, roads, and public land that is not utilised for cultivation. The seedling population developed in this area will act as a new population with the potential for new variations to evolve.

**Keywords:** Genetic resources, mango, On-farm conservation, varieties

## 286 (0-30)

### **Harnessing diversity of genus *Phaseolus* in Western Himalayan Kashmir: The journey of 15 years of breeding for yield, quality and resilience**

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Western Himalayan Kashmir valley is a hot spot of diversity of *Phaseolus* with *P. vulgaris* and *P. coccineus* being major two species found in various parts of valley. There is huge diversity of beans across all use categories, growth habits and market classes. Despite its importance in terms of food and nutritional value it has not received the just attention. In J&K's Kashmir valley, a strong breeding effort in *Phaseolus* especially the common bean covering basic studies pertaining to the origin and domestication, population structure based on Phaseolin marker as well as germplasm characterisation and trait identification has resulted in identification of a large array of diverse germplasm as well as development of high yielding and stress resilient varieties. During last 15 years our major focus has been the conservation of bean genetic resources as well as identify novel trait sources for yield, quality, plant type and resilience to diseases and pests. A large number of genotypes that have shown consistently higher yield in research station trials, state adaptive trials as well as national testing programmes have been identified (WB-1634, WB-341, WB-185, WB-1492, WB-1446, WB-401, WB-1282, WB-N-1). In addition to yield, a huge diversity has been recorded for parameters related to abiotic stress tolerance such as root architecture, canopy temperature depression, relative water content, biomass production as well as in vitro parameters such as response to PEG6000. Among diseases, our focus has been on identifying sources of resistance to Bean common mosaic virus, anthracnose and angular leaf spot and has led to identification of stable resistance sources such as WB-216, WB-1129 and WB-206. Among quality parameters, we have characterised germplasm for seed cooking quality as well as biochemical parameters including antioxidants. This paper discusses the progress made in last 15 years in breeding *Phaseolus* for marginal farming systems of Kashmir valley.

**Keywords:** Diversity, *Phaseolus*, 15 years, Western Himalayan Kashmir

287 (P-287)

**Effects of soluble salts on seed germination of aromatic marigold (*Tagetes minuta* L.)**

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Aromatic marigold (*Tagetes minuta*L.) is an essential oil-bearing plant that is being commercially cultivated due to great demand in flavour and perfume industry. The species have worldwide spread due to its broad adaptations. Although, limited information is present in the literature regarding its salt tolerance. Understanding the germination requirements is important for its establishment in new saline habitats. The present investigation evaluated the effects of five different soluble salts (CaCl<sub>2</sub>, KCl, MgCl<sub>2</sub>, Na<sub>2</sub>SO<sub>4</sub> and NaCl) on seed germination, germination velocity and salinity tolerance index. The five different concentrations of soluble salts (0 - 200 mM) were given in a two-factor factorial, completely randomized design. The experiment was performed in a programmed culture room of IHBT at 25 °C (16 h of light and 8 h dark). The seed germination inhibition under different soluble salts recorded, follows the order Na<sub>2</sub>SO<sub>4</sub>>KCl> NaCl > CaCl<sub>2</sub>> MgCl<sub>2</sub>. Significant decrease in germination velocity and salinity tolerance Index were observed with the increasing concentrations of salinity. The concentration resulting in 50% inhibition *i.e.* IC<sub>50</sub> value of ~ 80 mM was recorded for aromatic marigold. The study also found that few seeds germinate even at highest concentration of MgCl<sub>2</sub>. There is strong sign that aromatic marigold can tolerate moderate salinity. The germination even beyond 200 mM salt concentration provides an opportunity for future research of salt tolerance in aromatic marigold by identifying salt tolerant breeding lines at seed germination stage.

**Keywords:** Aromatic marigold, soluble salts, salt tolerance, Seed germination

288 (P-288)

**Genetic diversity analysis of released cotton varieties using microsatellite markers**

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Cotton is India's most important fibre-yielding plant that contributes significantly to India's textile industry and plays a pivotal role in its economy. This study analysed the genetic diversity in cotton varieties released from the years 2000 to 2020. The study used one hundred and thirty-nine cotton varieties released over the years, sourced from the National genebank. Microsatellite markers that are well known for their reproducibility, co-dominant inheritance and multi-allelic nature compared to other markers were selected as the marker of choice for this study. Forty microsatellite markers having high PIC (Polymorphic Information Value) and distribution throughout the cotton genome



were used in this study. Out of the 40 microsatellite markers used, 15 primers gave polymorphism, and the rest were monomorphic. Based on statistical parameters such as percent polymorphism, PIC, Resolving Power (RP) and Marker Index (MI), primers, namely NAU1230, BNL834, BNL2709, CGR6022, DPL0135, JESPR 153, JESPR270, MGHE573, MUCS443 and NAU4926 were found to be quite informative. The average Polymorphism Information Content (PIC) value of the SSR primers was found to be 0.37. The number of alleles amplified by the 15 polymorphic primers ranged from 2 to 4. The average genetic similarity of the 139 released varieties revealed by the set of polymorphic SSR markers was 74%. A dendrogram was constructed based on genetic similarity matrix obtained from the allelic data using software NTSYS PC. Cluster analysis was carried out, and two major clusters, Cluster I and Cluster II was observed at 74 percent genetic similarity. Further, principal co-ordinate analysis (PCoA) employing the Jaccard's coefficient of similarity substantiated the cluster analysis findings.

**Keywords:** Genetic diversity, Microsatellite markers, NTSYS PC, Jaccard's coefficient

## 289 (P-289)

### **Genetic variability and diverse array analysis of sorghum (*Sorghum bicolor* (L.) moench) germplasm lines for shoot fly resistance**

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Shoot fly is a major insect pest of cultivated sorghum. Host plant resistance is itself excellent pest controlling method. knowledge of major resistance contributing components is of paramount significance in formulating an effective selection programme. Genetic variability for shoot fly resistance in plant exists in sorghum germplasm. Therefore, the present study was carried out to study genetic variation, heritability and genetic diversity in sorghum accessions for shoot fly tolerance traits and grain yield. 116 sorghum germplasm lines along with four checks (One resistant check IS-18851, one susceptible check DJ-6514 and two varietal checks SPV-1411 and PVK-801) were evaluated in randomized block design during rabi 2017-18 at Sorghum Research Station, Vasantnao Naik Marathwada Krishi Vidyapeeth, Parbhani to assess genetic variability and genetic diversity. Phenotypic and genotypic coefficients of variation were calculated according to Burton (1952). The genetic divergence was estimated by  $D^2$  statistics for 18 quantitative characters. Wide range of variation was observed for shoot fly resistance and yield contributing characters. GCV ranged from 3.49% (days to maturity) to 111.53% (abaxial trichome density). Higher GCV along with high heritability and genetic advance exhibited by traits dead hearts at 14 and 28 DAE, trichome density (abaxial and adaxial) and plumule & leaf sheath pigmentation indicating the scope for improving shootfly resistance through selection of these traits. 120 genotypes including 4 checks were grouped into sixteen clusters with variable number of entries. revealing the presence of considerable amount of genetic diversity in the material. Among the sixteen clusters, Cluster III was the largest involving 40 genotypes. Out of the 18 characters studied, trichome density (adaxial and abaxial) contributed maximum



(43.42.%) and (39.06.%) towards genetic diversity followed by plant height (8.03%), leaf angle (2.98%) and chlorophyll content (1.50%). Cluster II, VI, IX and X has good scope for future breeding programme, exhibiting shoot fly tolerant sources as high mean for shoot fly resistant parameters. Genotypes IS 17757, IS 33770, IS 33746, PVR 658 and IS 40269 with less dead heart per cent and shoot fly resistant parameters may be used as promising sources for breeding shoot fly resistant genotypes.

**Keywords:** Sorghum, Genetic variability, Genetic Diversity, Shoot fly resistance, D<sup>2</sup> statistics

## 290 (P-290)

### **Exploiting BMR genes for forage quality improvement in Sorghum (*Sorghum bicolor* (L.) Moench)**

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The value of a crop plant as forage is primarily determined by the digestibility and biomass production per unit area. Presence of brown midrib gene in sorghum is bringing an attention to utilize this crop in manipulating forage quality due to its low lignin content. Therefore, efforts were made to improve fodder quality parameters along with grain and fodder yield in 30 sorghum F<sub>1</sub> hybrids derived from crossing with Bmr sorghum derivatives. 30 F<sub>1</sub> hybrids were produced through hand emasculation and pollination in line x tester mating design using Bmr sorghum genotypes. These 30 hybrids along with their parents and two checks viz., CSH 15 R and CSV 22 R were evaluated in Randomized Block Design with three replications. Observations were recorded on randomly selected 5 five plants in each replication for grain yield and its contributing characters. heterosis was calculated as per the procedure suggested by (Fonseca and Patterson, 1968). Results evidenced *that* significantly highest all three types of heterosis and *per se* performance was recorded by CSV 29R x Pbmr 3, Parbhani Moti x Pbmr 4, Phule Anuradha x Pbmr 4 for grain yield and Parbhani Moti x Pbmr5, PMS 71 B x Pbmr5 and CSV 29 R x Pbmr 5 for fodder yield per plant. For fodder quality parameters viz., in-vitro digestibility and lower lignin content hybrids; MS 104B x Pbmr 2, Parbhani Moti x Pbmr 5, Phule Anuradha x Pbmr 3, MS 104B x Pbmr 3 and PMS 71B x Pbmr 5 possessed high *per se* performance and significant all three types of heterosis. In addition, these crosses showed low NDF, ADF and cellulose values and higher metabolisable energy. Overall, amongst 30 crosses, six F<sub>1</sub> hybrids; MS 104B x Pbmr 3, MS 104B x Pbmr 2, PMS 71B x Pbmr 3, Parbhani Moti x Pbmr 5, Phule Anuradha x Pbmr 3 and ICSR 196 x Pbmr 3 identified as potential crosses for grain yield, fodder yield coupled with improved fodder quality in terms of digestibility and crude protein. These crosses may be utilized in future breeding programme to improve the fodder digestibility along with the higher yield and protein content.

**Keywords:** Brown midrib, Sorghum, Heterosis, Fodder quality parameters, IVOMD



## 291 (P-291)

### **Evaluation and identification of high yielding genotypes for varietal development in *Amaranthus* (*Amaranthus* spp.) under hilly region of Uttarakhand**

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Evaluating *Amaranthus* genotypes is a key task for *Amaranthus* improvement programs. Generally, the genotypes that were found as being steady and high yielding are often recommended for cultivation at the farmer level. For this purpose, 20 *Amaranthus* genotypes were subjected to stability analysis to determine the nature and extent of genetic stability for across locations, village Pakh, Ghansali, Tehri garhwal district for grain yield and yield components. A randomized complete block design (RCBD) was used in this study with three replications for the identification of stable and high yielding genotypes. The results showed that genotype (Gat a 0.05% probability level of 0.05 significantly influenced the grain yields of *Amaranthus* genotypes. Genotypes IC-340943 (43.03g) and IC-317517 (39.49g) with more than unity regression indicated the genotype's suitability for favorable conditions. Genotype IC-340943 was stable. Thus, to improve the production of *Amaranthus* in the mid hill environments Uttarakhand, this genotype was put forward for release as a variety.

**Keywords:** *Amaranthus*, genotypes, high yielding

## 292 (P-292)

### **Detection of plant parasitic nematodes in exotic germplasm and salvaging for safegermplasm introduction**

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ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR) plays an important role in quarantine processing of introduced plant germplasm to prevent introduction of exotic pests. Plant parasitic nematodes are one of the important agricultural pests those cause significant yield losses worldwide and spread along with seeds and other vegetative planting material. All the imported samples were subjected to visual inspection and specialized detection techniques were used for suspected samples for nematode isolation. Nematodes were identified using morphological and molecular



methods. During past ten years, total of 2,557 samples of imported germplasm were found infected with nematodes. Out of these samples 2,175 samples were infected with white tip nematode of rice, *Aphelenchoides besseyi*. This nematode was intercepted in paddy seeds imported from Bangladesh, China, Japan, Philippines, USA and Vietnam. All the imported paddy samples were subjected to hot water treatment (HWT) at 52°C for 30 min. After HWT, the seeds from infected samples were again water soaked, split opened and observed for presence of *A. besseyi* and to see the efficacy of HWT in salvaging of *A. besseyi* infected paddy. None of the sample was found with live nematode which proved efficacy of HWT in salvaging of infected paddy samples. Among vegetative propagules and rooted germplasm, 400 samples were found infected with nematodes. Major nematode species identified were, *Helicotylenchus dihystera*, *Pratylenchus penetrans*, *Rotylenchus minutus*, *Tylenchulus semipenetrans*, *Meloidogyne incognita* etc. Among vegetative propagules, bare rooted plants were most infected with nematodes. The genus *Pratylenchus* was most intercepted nematode as it was identified in 209 samples (52%). All these infected samples were salvaged effectively by 0.2-0.25% formalin dip treatment and post-entry quarantine inspections. Therefore, successful detection, identification and salvaging of nematode infected germplasm are important in prevention of entry of exotic nematodes into the country and safeguarding the agri-horticultural crops from nematode pests.

**Keywords:** Detection, exotic germplasm, plant parasitic nematodes, salvaging

**293 (P-293)**

**Assessment of morphological variability and diversity analysis in *Abrus precatorius* (L.) germplasm conserved at National Gene Bank, NBPGR**

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*Abrus precatorius* (L.), commonly known as Ratti, is a perennial herb native to Indian sub-continent. Indian National Gene Bank (NGB), National Bureau of Plant Genetic Resources (NBPGR) conserves 152 accessions (august, 2022) of Ratti collected from the diverse agro-ecological zones of India. The plant has wide range of usage especially in pharmacological industry. In the Indian subcontinent, various parts of this plant are traditionally used in ayurvedha and siddha system of medicines. Various Vedic literatures of ancient India had mentioned its importance in measuring the weight of gold. The present investigation was carried out to assess the morphological variability and analyse the diversity of Ratti germplasm. The seeds were sown as main crop at Issapur whereas it was intercropped with Bael (*Aegle marmelos*) at Ranchi. The experimental design used was augmented block design in which the checks were replicated in each block while the entries were not replicated. Totally, 95 entries and 4 checks were used. Commercial varieties were not available in this crop and therefore accessions itself was used as checks. These checks were IC0306236, IC376080, IC0469931 and IC0418097. The present investigation revealed wide range of morphological variability (for various traits



studied) in the Ratti accessions. The seed yield per plant of Ratti accessions as a sole crop and as an inter-crop was statistically on par. This shows the ability of the plant to adapt to inter-cropping system and give optimum yield. For seed yield, genotypic sources have revealed highly significant variation at 1% level of significance, whereas variations of environment and genotype  $\times$  environment (G $\times$ E) interaction were statistically non-significant. Thus, the mean seed yield per plant at Issapur (13.02 g) and Ranchi (10.13 g) were statistically similar. Best performing accessions with respect to seed yield per plant at Issapur were IC0385619 (32.416 g), IC0371792 (30.27 g) and IC0553727 (29.651 g) and at Ranchi were IC0322486 (27.626 g), IC0280795 (27.187 g) and IC0385619 (26.878 g).

**Keywords:** *Abrus*, diversity, germplasm, Ratti, variability

## 294 (P-294)

### **Correlation studies on screening of coriander (*Coriandrum sativum* L.) genotypes for drought tolerance and yield**

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A field experiment was carried out to screen the coriander germplasm for drought tolerance at various drought prone areas of Tamil Nadu viz., Agricultural Research Station, Kovilpatti, Regional Research Station, Aruppukottai, Agricultural College and Research Institute, Killikulam and Horticultural College and Research Institute, TNAU, Coimbatore. Preliminary screening was done with 240 accessions and 50 accessions were selected based on yield performance along with check CO (Cr)4 and were raised in main field in a Randomized Block Design in three replications. The crop was grown purely under rainfed condition. Morphological, physiological and biochemical parameters were measured during crop growth. The water deficit caused a reduction in morphological and growth characters except root length which was more in drought tolerant accessions (ACC18) than in susceptible accessions (ACC119). Genotypic correlation of all the traits, except 50% flowering showed positive and significant correlation with seed yield. Seed yield was highly correlated with all the biochemical parameters. In all the five environments, seed yield per plant at genotypic level was strongly correlated with all the characters.

**Keywords:** Coriander, drought tolerance, yield, correlation

## 295 (P-295)

### **A comparative study of morphological variability in selected wild *Ocimum* accessions in India**

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*Ocimum* (Basil) is one the important genus of the family Lamiaceae which comprises more than 160 species. In India, so far about nine species of *Ocimum* have been reported including three exotic species namely *O. americanum* L., *O. minimum* L., and *O. Africanum* Lour. The traditional system of Indian medicines utilizes different plant parts of *Ocimum* spp. viz. leaves, stem, flowers, seed or even whole plant to treat several ailments like skin diseases, bronchitis, bronchial asthma, malaria, arthritis, dysentery, painful eyes, fever, insect bite. The most widely studied species viz. *O. Basilicum* & *O. Tenuiflorum* have been found to possess various bio active compounds like eugenol, methyl eugenol, rosmarinic acid, methyl chavicol, beta caryophyllene, ursolic acid, linalool, oleanolic acid, limonene etc. which are found to be responsible for their therapeutic potential and major class of compounds present in essential oil of *Ocimum* spp. is terpenes. A total of 36 accessions of 7 wild species representing different phyto-geographical regions in India, were raised in the field during kharif seasons 2020-21 and 2021-22 to analyse the morphological variability and essential oil content. Minimal descriptors developed by ICAR-NBPGR, New Delhi were used for characterization and Clevenger apparatus used for extraction of essential oil. A wide range of variability observed in morphological descriptors viz. Plant height (54.2-84.3cm), Number of branches (40- >100), Leaf lamina length (1.8-7.0cm), Leaf lamina width (1.2-4.6cm), LLL and LLW ratio, Leaf petiole length (1-2.6cm), Inflorescence length (11.2-35.8cm), Essential Oil % (0.04-0.4%). Essential oil content was highest in *O. kilimandascharicum* species varying between 0.13 to 4.0% on fresh weight basis, followed by *O. Viride* (0.37%). Present work revealed the significant variation in morphology and essential oil content within and between *Ocimum* wild species which may be further explored for utilization in breeding high oil yielding varieties in *Ocimum*.

**Keywords:** *Ocimum*, Morphological variability, Indian medicines, Bio active compounds

296 (P-296)

### **Morphological, biochemical and molecular characterization of elite Indian Nutmeg varieties**

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Nutmeg (*Myristica fragrans* Houtt.) is an aromatic tree spice belonging to the primitive family Myristicaceae. It is also known as the "Twin spice", as it produces two commercially important spices: nutmeg (a kernel of seed) and mace. The term nutmeg comes from the Latin word nuxmuscatus meaning 'Musky Nut'. Nutmeg belongs to the order Magnoliales (Cronquist system 1981) and the genus *Myristica* which is one of the most primitive and basic genera in the Myristicaceae family. Among the 300 species in the family, *Myristica fragrans* is commercially most important species. An important



problem in nutmeg cultivation is the segregation of seedlings into male and female plants resulting in about 50% unproductive male trees. In addition to this the seedling progenies show high variations in yield and quality. Hence the earlier practice of seedling planting has now completely been replaced by vegetative propagation. Establishment of commercial plantations are now mostly through budded plants of proven varieties. Since the budded plants are priced high, queries are often received from the farmers to assure the varietal purity and authenticity of planting material sold in nurseries. Development of suitable morphological markers will help the farmers to identify the plants by visual comparison. On the other hand, development of molecular markers is highly needed to tackle the difficulty in distinguishing the morphologically resembling varieties and also to confront the variations seen in morphology due to the environmental and soil conditions. Present study aims to develop morphological and molecular markers for identification of four popular varieties of nutmeg viz IISR-Viswashree, IISR-Keralashree, Sindushree and a monoecious cultivar, besides the biochemical characterization. Morphological and molecular markers were identified for four commercially useful nutmeg varieties and biochemical characterization of these was carried out. Morphological characters like leaf length, leaf width, fruit width, fruit shape, and seed shape exhibited variations and similarity in characteristics like presence of stylar scar, mace covering pattern and seed colour were observed among the varieties. The biochemical characterization resulted in highest amount of nut oil in IISR-Vishwashree; mace and nut oleoresin in IISR-Keralashree; and nutmeg butter in the monoecious nutmeg. DNA finger printing was carried out using 35 ISSR primers and unique bands were identified using primers IS-02, ISSR 12, ISSR 05, ISSR 14, ISSR 01 and UBC 834. ISSR primers used for the study were accurate for distinguishing varieties like IISR-Viswashree, IISR-Keralashree, Sindushree, and monoecious nutmeg.

**Keywords:** Nutmeg, characterization, Molecular marker, ISSR

297 (0-04)

### **Conservation priority of *Buchanania lanzan* Spreng. (Chironji): A potential wild fruit tree of peninsula India**

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Wild fruits trees have been a valuable source of food for humans since time memorable. One such wild fruit tree *Buchanania lanzan* Spreng. (Synonym *B. latifolia* Roxb.), locally known as chironji is an important underutilized fruit crop found in dry tropical forests of India, Bangladesh, Nepal, Myanmar, Thailand, Malaysia, Sri Lanka, Australia and the Pacific Island. In India the species is sparsely distributed from Shiwaliks hills to peninsular region of MP, UP, Bihar, Orissa, AP, Chhattisgarh, Jharkhand, Gujarat, Rajasthan, Maharashtra and then extending to south in Tamil Nadu and Kerala. The nut fetches about Rs. 1500 -2000 per kilogram, edible kernels contain about 52% oil with abundant medicinal properties. Despite its immense potential for commercialization,



chironji still remains a minor fruit crop. NBPGR, New Delhi has a collection of about 127 accessions while, ICAR-CIAH, Bikaner at its Regional Station CHES, Vejalpur (Godhra), evaluated 30 promising genotypes and found Thar Priya and CHESC-2 as the most promising genotypes. Germplasm survey, collection and conservation work was carried at BUAT, Banda during 2020-21 and 2021-22 to identify and collect the promising genotypes with short juvenile period, regular fruiting, good quality fruits, kernels and to conserve diversity for promotion of socio-economically valuable species among the farmers. 74 accessions (BUAT C 1 to BUAT C 74) were collected from UP (Manikpur, Lalitpur, Kallinjer), MP (Chitrakoot, Majhgawan, Satna, Katni, Burhanpur), Gujarat (Godhra, Pancnchmahal, Dahot) and Bihar (Champaran). Variation was recorded in tree form, flower colour, bark, leaf shape, stone size and gestation period. Range of variation also noted for quality attributes of fruits (fruit length 8.86-23.0 mm; fruit weight 0.271-0.803g; stone weight 0.129-0.356g; kernel weight 0.08-0.13 g; pulp weight 0.108-0.526g; TSS 19.5-23.51<sup>0</sup> Brix; Vitamin C 46.44-63.31 mg/g pulp). Conservation programme is being supported by UPCAR, Lucknow and Bioversity International and CIAT funded projects.

**Keywords:** *Buchanania lanzan*, Chironji, Genotypes, Kernels

## 298 (P-298)

### **In situ evaluation and morphological characterization of naturally occurring wild pomegranate in southern Himachal Pradesh**

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Pomegranate wild types commonly referred by locals as 'Daru' are grown in the natural habitat across western Himalayan region. Wild pomegranate arils are widely utilised to make *Anardana*, a souring agent, with regional economic significance. A survey was undertaken in august 2017 to collect wild pomegranate types in Darlaghat-Solan region and characterize the variability for vegetative and fruit characters and incidence of pests and diseases. 25 accessions were collected from 22 locations along with passport data. Insitu evaluation data was recorded on plant growth habit, tree height, girth, vigour, flowering, fruiting and pest and disease incidence. Plants were robust, healthy with 2-5 stems. Voucher samples of twenty-five accessions collected were characterized for qualitative and 13 quantitative characters using DUS guidelines. Variability was observed for economically important traits such as fruit weight, aril weight and rind thickness as indicated by high coefficient of variation. Fruit weight ranged from 30 to 90 g, fruit width 3.1 cm to 5.6 cm; Aril size varied from 5.9 x 8.4 mm to 3.81 x 5.99 mm. TSS ranged from 14 to 20°B. Screening the voucher samples revealed that two accessions AS/NN 17 and AS/NN 27 were free from pest and disease incidence. Despite the fact that they are available in their natural habitat, more consideration must be given to document and conserve wild pomegranates as they could serve as root stocks for commercial varieties for biotic stress and as potential donor parents in breeding programmes.



**Keywords:** Wild pomegranate, variability, characterization, evaluation

**299 (P-299)**

**Morphological characterization and evaluation of Gunj (*Abrus precatorius* L.) germplasm**

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**Abstract**

*Abrus precatorius* L. (family Fabaceae), is a popular medicinal climbing herb. Common names of this plant are Gunj, Indian licorice, Coral bead, Coral pea, Rosary pea, Crab's eye, Ratti, etc. Based on seed coat colour, three common genotypes (Red, Black and White) had been reported in this crop. Apart from anti-tumour properties, plant parts have anti-diabetic, nephroprotective, neuroprotective, analgesic emetic, purgative, aphrodisiac, and anti-inflammatory properties also. However, the seeds are highly toxic due to the presence of a biochemical compound called *abrin*. As the leaves are low in *abrin*, they are used as oral medicine. Glycyrrhizin, another component of this plant, was reported to affect the replication of corona virus. The present study was conducted at the AICRP on MAP & B, Thrissur centre, Kerala Agricultural University, Vellanikkara. White grained gunj accessions (24 Nos.) were collected during 2018-19 and evaluated during 2019-22 in RBD with three replications. Observations were recorded on morphological traits viz., vine length (cm), length of first branch (cm), no. of leaves per branch, no. of primary branches, leaf length (cm), leaf breadth (cm), no. of leaflets per leaf, leaflet length (cm), leaflet breadth (cm), pod length (cm), pod breadth (cm), pod breadth (cm), no. of seeds per pod, 100 seed weight (g), and total seed yield per plant (g). The evaluated accessions exhibited significant variation with respect to vine length, height of first branch, number of branches, number of leaves, leaf length, pod length and seed yield. The vine length of accessions ranged from 31.30 cm to 164.70 cm and the mean length was 121.67 cm. 100 seed weight (g) ranged from 11.8 to 13.6 with a mean value of 12.5. Among the 24 lines, the highest total seed yield was recorded for the accession AP 9 (110.2 g) which had high vine length also (163.6 cm). Other promising lines with high yield were AP4 (108.2 g) and AP8 (106 g).

**Keywords:** Gunj, characterization, evaluation, germplasm

**300 (P-300)**

**How much is too much: An untold story of Indian *Arabidopsis thaliana* germplasms**

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India is one of the rich biodiversity hotspots of the world. It is the home to many important plant species and thousands of species have been documented from Himalayan region over centuries. Some of the most important plant species have been studied in details including diversity, genetics and genomics. However, there was no report of detailed work on Indian populations of *Arabidopsis thaliana*, the model species in plant science before 2015. The 1001 genome consortium was launched in 2009 to unearth the genetic and epigenetic variations in natural accessions spread across the globe. The major conclusions about the origin and demography so far have been derived exclusive of Indian populations. This might have restricted our current knowledge on the important species. We will be discussing the major findings including morphology, genetics, genomics and epigenetics of the species. We also analysed the genomes of 38 individuals of *A. thaliana* from eight West-Himalayan populations with earlier global and regional collections to clarify and re-investigate their evolutionary history. By incorporating Indian population with the largest existing global data, we show uniqueness of Indian population and clear existing doubt on the expansion of the species globally from the source to sink. The Indian populations of *Arabidopsis thaliana* are unique and may provide valuable information on its evolution and adaptation under different climatic conditions. Our findings reconfirm that unexplored natural variants of *Arabidopsis* may still help in discovering specific traits and functional alleles or in understanding basic biological processes.

**Keywords:** *Arabidopsis*, morphology, genetics, genomics

### 301 (P-301)

#### **Exploring genetic diversity of *Artemisia maritima* germplasm for essential oil content and its contributing traits**

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*Artemisia maritima*, commonly known as Sea wormwood, is a perennial herb that inhabits northern hemisphere. In India, it is naturally found in western Himalayas in between altitude of 2500 m – 3500 m. It is mainly used as digestive tonic, treating fever, anthelmintic and antiseptic, etc. *Artemisia* essential oil (EO) is a rich source of sesquiterpenes with numerous uses including antifungal and antibacterial properties. In the current study, a total of eight accessions available and grown at CSIR-IHBT Centre for High Altitude Biology (CeHAB), Ribling, Lahaul & Spiti, Himachal Pradesh were screened to evaluate the genetic variation for essential oil content and its related traits. Data was recorded for plant height (PH), plant diameter (PD), number of primary branches per plant (NPB/P), number of secondary branches per plant (NSB/P), number of leaves per secondary branch (NL/SB), leaf length (LL) and leaf width (LW). Oils was extracted from



each accession using hydro-distillation. Analysis of variance showed significant variation for the recorded traits except primary branch number. Oil content ranged between 0.253 - 0.333 per cent. PH, NSB/P and NL/SB recorded significantly positive correlation with PD, LL and EO content, respectively. Based on morphological traits, accessions were clustered to know the inter-accession relationship. This showed high number of secondary branches and the leaf number per secondary branch which directly contribute to the essential oil content. The accession number 1, 5 and 8 can be used directly for essential oil extraction. These accessions can also be used in other artemisia improvement programs too.

**Keywords:** *Artemisia meritima*, Germplasm, Biomass, Correlation, Essential oil

### 302 (P-302)

#### **Landraces and wild introgression lines as source of novel traits for climate smart rice varieties**

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Rice (*Oryza sativa* L.) has a renowned relationship with the human since ages and it is the most important staple food and India hosts a wide genetic diversity in case of rice with a spectrum of cultivars, landraces and wild and related species. Identifying the novel genes which are lost during the domestication helps in development of climate smart rice varieties with high yield and tolerance to various stresses. The present investigation was carried out at ICAR – Indian Institute of Rice Research, Rajendranagar, Hyderabad during *Kharif* 2021 to investigate diversity of rice cultivars landraces and wild introgression lines for seedling vigour and yield related traits. The investigation consists of released cultivars, landraces and wild introgression lines from ICAR-IIRR, Hyderabad, Telangana and SGCAR, Jagdalpur, Chattisgarh. Molecular screening for reported yield genes were also carried out in this germplasm. Significant genetic variation was observed in the germplasm for targeted traits under study showing their potential in further breeding programmes. High heritability was found for seedling vigour related traits. Trait association revealed that single plant yield had a positive significant correlation with productive tiller number, the total number of grains per panicle, tiller number, the total number of filled grains per panicle, plant height, flag leaf length and panicle length. High positive and direct effect with seedling vigour traits were observed with yield traits. The molecular screening was done for the genotypes under study linked markers to *Gn1a*, *Ghd7*, *GS5*, *SPIKE* and *SD1*. Based on genotypic data germplasm was grouped into 6 major clusters grouping genotypes based on seedling vigour traits and yield parameters like panicle weight and grains per panicle. This study indicates the potential of available germplasm in our country for simultaneous improvement of yield and seedling vigour traits for stress tolerance.

**Keywords:** Rice, Landraces, Introgression lines, Novel traits, Climate smart



**303 (P-303)**

**Screening of germplasm of minor pulses for resistance to root-knot nematode (*Meloidogyne incognita*)**

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Root-knot nematode (RKN), *Meloidogyne* spp. are one of the most important nematode pests of legume crops in tropical and sub-tropical regions including India, causing enormous economic damage to plants. RKN also breaks resistance in varieties, which are resistant to soil-borne fungal and bacterial plant pathogens. Nematode resistant accessions are one of the important alternatives which are not only eco-friendly but also economically feasible means for the management of RKN. During 2020-2022 a total of a total of 954 accessions of various minor pulses viz., urd bean (358 acc), mung bean (194 acc) and cowpea (402 acc) were screened for the source of resistance to root-knot nematode, *Meloidogyne incognita*. Preliminary experiments were conducted in plastic pots (10-cm-dia) filled with naturally *M. incognita* infected soil (500g/pot) collected from a nematode sick plot, which contained two 2<sup>nd</sup> stage juveniles per gram of soil (1000 J2/pot). After six weeks of sowing, plants were uprooted and observed for root galls and egg-mass formation. Host status was designated based on number of root galls induced by *M. incognita*, which is the main characteristic of the RKN infection. Those accessions showing <10 root galls/root system were considered as resistant, and re-evaluated twice with artificial inoculation in pots filled with 500g sterilized soil for confirmatory test, each pot was artificially inoculated with 1500 freshly hatched 2<sup>nd</sup> stage juveniles of *M. incognita*. Based on two years data, three accessions of cowpea (IC397455, IC381584, and EC472264) and five accessions of urdbean (IC355588, IC326077, IC485645, IC530615 and IC423034) were confirmed as resistant to *M. incognita*. These accessions can be further used in nematode resistance breeding programmes.

**Keywords:** *Meloidogyne incognita*, Inoculation, Nematode resistant, Minor pulses

**304 (P-304)**

**Multivariate evaluation of Giloi (*Tinospora cordifolia*) under semi-arid conditions of Haryana**

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The medicinal advantages of *Tinospora cordifolia* have been identified in Indian Pharmacopoeia as an important constituent in several of medicinal formulations. The plant parts i.e., leaf, stem, bark, and fruit have been used for the treatment of a diverse



disorder. Genotypes vs. traits bi-plot analysis, multivariate methodology, have assessed genotypes based on multiple traits and proved useful in identification of promising genotypes. Sixteen promising collections were evaluated under fields at CCSHAU during cropping season of 2019-20 and 2020-21. Significant effects have been mentioned by analysis of variance. Values of PCV were more as compared to corresponding GCV values for morphological traits and advance as percent of mean along with heritability were more for number of leaves and ranches for first year of study. PCV were more as compared to GCV for all studied morphological traits while heritability and advance as percent of mean was more for number of leaves and branches. Multivariate hierarchical clustering of genotypes exhibited two clusters with 13 and 3 members respectively. Number of leaves partitioned leaf length, leaf width from vine length, vine yield, vine girth traits in two way clustering pattern of genotypes vis-à-vis traits of giloi. Vine length, Vine yield, branches, number of leaves observed as major contributors for first principal component whereas leaf length, leaf width, number of leaves for the second one. Both components accounted for more than 90% of variation in morphological traits. Second year found Vine yield, Vine length, lead width, leaf length were major contributors for first while number of leaves, leaf length, and leaf width accounted towards second principal components as nearly 86.7 % share by both.

**Keywords:** Giloi, Evaluation, Morphological traits, Hierarchical Clustering

### 305 (P-305)

#### **Transfer of mutant *sugary1* gene from unadapted genetic stock to elite lines through molecular breeding**

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Sweetcorn is popular in shopping-malls, multiplex-theatres and tourist places as snacks. It is also consumed as vegetable worldwide. Two recessive mutant genes viz., *shrunken2* (*sh2*) and *sugary1* (*su1*) are commonly used in sweetcorn breeding programme. *sh2*-based sweetcorn has higher shelf-life and possesses more sweetness, whereas *su1*-based sweetcorn is preferred due to attractive looks and flavour of kernels caused due to increased levels of water-soluble phytyglycan. Two *sh2*-based released sweetcorn hybrids viz., Pusa Super Sweet Corn-1 (PSSC-1) and Pusa Super Sweet Corn-2 (PSSC-2) were targeted for introgression of *su1* gene for elevating sweetness along with combining attractive looks and flavour to the kernels. However, the source of *su1* gene was a poorly-adapted genetic stock (MGU-1- *su1su1* and MGU-2-*su1su1*) which could not be used directly as parent in the breeding programme. Thus, *su1* gene from these donors was introgressed into the parental lines of PSSC1 (SWT019×SWT020) and PSSC2 (SWT016×SWT017) using molecular breeding. Gene-based markers viz., SNP\_TC2 (for *sh2*) and SuDel36 (for *su1*) were used for foreground selection in BC<sub>1</sub>F<sub>1</sub>, BC<sub>2</sub>F<sub>1</sub> and BC<sub>2</sub>F<sub>2</sub> generations. More than 100 SSRs were employed for background selection which



led to >90% recovery of recurrent parent genome (RPG). The mean sucrose among double mutant versions (*su1su1/sh2sh2*) was 43.2%, with an increase of 39% over the original *sh2*-based versions (mean: 26.0%). These hybrids also showed high degree of similarity with their original versions for agronomic, yield and other morphological traits. The multi-environment analysis showed that yield potential of improved hybrids was similar to original hybrids (10.0-12.0 tonnes/ha). The reconstituted *su1su1/sh2sh2*-based hybrids are first of its kind of hybrids in India. These new hybrids possessed more sweetness, outstanding tenderness, creamy texture, flavour of *su1* as well as extended longevity of the *sh2* type. These improved inbreds with *su1su1/sh2sh2* genetic constitution would serve as donors in sweetcorn breeding programme.

**Keywords:** *Sugary1* gene, Genetic stock, Elite lines, Molecular breeding

### 306 (O-05)

#### IoT based E-solution for safeguarding tree germplasm against physical damage, misidentification and mistracking in field Genebanks

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National Active Germplasm Sites (NAGS) of India networked with ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), maintain a large number of perennial tree germplasm such as *Mangifera indica*, *Moringa oleifera*, *Dalbergia sissoo*, *Azadirachta indica*, *Aegle marmelos* etc. at different locations in the country. Their labelling has been one of the greatest challenges for any field worker engaged in maintenance, and evaluation. These trees are manually labelled, which often are lost and damaged. This necessitates a lot of manual work to do re-labelling. In the process, many times the individual trees get wrongly labelled, more so, if any accessions are missing in between. Long life cycle or gestation period makes the problem all the more difficult. This valuable tree germplasm many a times are quite vulnerable to damage by, natural weather disturbances, theft, nuisance etc. which is difficult to quickly monitor because of remoteness of the conservation sites and field genebanks. A tree accession misidentified or mistracked is as good as a tree germplasm lost. To address the problem, a pilot study was taken at three NAG sites: NBPGR, Delhi; CAFRI, Jhansi and IIHR, Bengaluru to devise a digital E-solution to reduce these risks substantially. Two systems such as active/real time monitoring with the help of Real time sensors (RTS), and passive monitoring through RFID tags were taken up. A total of 248 sample trees covering 15 multipurpose trees and fruit trees, were tagged with RFID (98) and RTS (150) sensors. Gateways were places in all the three locations to transmit data to the principal database. The RFIDs could be scanned from 2 to 12 m across all the three locations. Orientation of the tags significantly influenced the distance of scanning. In the scanner, which is internet



enabled, characterization and evaluation data of the specific germplasm were updated and uploaded to the principal database. An app was developed to use in the Scanner and populate the basic data of the trees. The tag id (both RFID and RTS) were linked to the unique accession numbers. In case of replicates of accessions, the accession number was hyphenated with numbers 1, 2 or 3. The RTS were programmed with an algorithm to detect any disturbance to the trees such as cutting, breaking, shaking etc. The RTS were successful in detecting the simulated disturbance. Sensitivities of the sensors and algorithm were also evaluated. None of the sensors gave false negative signals, but there were few false positives. For ensuring security, false negatives are more dangerous than false positives. The technology is in the process of refinement and further optimization. In this pilot study, the technology has produced encouraging results in managing the tree germplasm, in real time, sitting more than 2000 km away from the actual conservation site.

**Keywords:** RFID, RTS, IoT, Multipurpose tree species, Realtime monitoring, Germplasm conservation

### 307 (P-307)

#### **Evaluation of Buckwheat (*Fagopyrum* spp.) indigenous genotype under northern hilly region of Surguja**

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Buckwheat (*Fagopyrum esculentum* Moench) is one such underutilized crop, which holds tremendous nutritional benefits among the cereals. It is highly nutritive and unlike common cereals, which are deficient in lysine, buckwheat has excellent protein quality in terms of essential amino acid composition. It is mainly grown in Mainpat and some part of Samripat in Surguja and Balrampur district of Chhattisgarh state. A study has been conducted at Potato Research Station, Mainpat during 2018-2019 under GEF project entitled "Mainstreaming agricultural biodiversity conservation and utilization in agriculture sector to ensure ecosystem service and reduce vulnerability". Buckwheat is rich in various antioxidant plant compounds, which are responsible for many of its health benefits. Tau (Buckwheat) is regional denomination widely cultivated in the Mainpat region of Surguja. Complete grain is used as a nutritive supplement for different stews, while seed flour is used for making bread, cake, noodle, pakora, biscuit and seed is also used for making beverage. The total area of buckwheat in Mainpat block of Surguja district is 1390.0 hectare and production are 21517.20 metric tons. The total cultivated area per farm was observed to be 0.90 hectare at marginal farm, 1.30 hectare at small farms, 3.00 hectare at medium farms and 5.10-hectare at large farms along with 2.76 hectare as an overall average leading to a high yield. Buckwheat is less productive than true grain crops on good soils but is particularly adapted to arid hilly land and cool climates. Because it matures quickly, it can be grown as a late-season crop. Buckwheat



flowers provide both pollen and nectar for bees and can be used as a common honey crop. The plants improve conditions for the cultivation of other crops by smothering weeds and fostering beneficial insects and may be planted as a green manure crop that is plowed under to improve the soil.

**Keywords:** Buckwheat, Baseline Survey, Farm, GEF, Mainpat, Nutrition

### 308 (S-04)

#### **Towards harnessing soybean germplasm diversity in the National Genebank for summer season cultivation**

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India is importing edible oil worth more than Rs.70, 000 crores annually. Soybean has potential to be exploited as a summer season crop intercropped with sugarcane in both Northern as well as Southern parts of India, where sugarcane remains in vegetative stage for 4-5 months during spring-summer season. Cultivating soybean during this spring season offers an opportunity for productivity enhancement of oilseed crops in India. However, there is meager information on the availability of suitable and adaptable soybean varieties and germplasm for this season. Therefore, 8029 accessions encompassing 6000 lines from National Genebank, ICAR-NBPGR, New Delhi and 2029 from ICAR-IISR, Indore, were evaluated for their performance during summer season (Feb-July,2021) at ICAR-NBPGR Issapur farm in augmented block design (ABD) along with 5 check varieties. Based on their performance, a set of 251 early lines maturing earlier than the checks were selected. Of these, 45 accessions were distinctly earlier by one week to one month than the best early checks (Pusa9712, SL955 and PS1347). While 8 accessions were revealed as very early maturing (92 days), 14 accessions were categorized as early maturing (111 days) as compared to the checks (123 to 126 days). These genotypes were further validated for earliness and characterized for their agromorphological traits during *Kharif* 2021 and 2022. Thus, the accessions identified as early and very early maturing types may further be tested over locations so that these may serve directly or as donor to enhance soybean yield during summer season in conjunction with sugarcane inter-cropping system for crop diversification and additional income.

**Keywords:** Soybean, Summer season, National Genebank, Early maturity

### 309 (P-309)

#### **Fingerprinting profiles for sesame cultivars (*Sesamum indicum*) using SSR markers**

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Sesame (*Sesamum indicum* L.) is an ancient oilseed crop known for its seed and high-quality edible oil. It is a crop with a significant commercial value and is popularly known as the "queen of the oilseeds" due to the qualities of its oil. Additionally, the seeds are utilised in diverse cooking preparations across a range of cultural foods. Among the various molecular markers system available, simple sequence repeats (SSR) are widely accepted and reliable as they are abundant, co-dominant, reproducibility and can be analysed by a convenient PCR- based method. These advantages make it easy to screen a large number of samples at shorter time point with lesser cost. For development of fingerprinting profiles, highly polymorphic SSR markers are chosen. Distribution across all the chromosomes and robustness were the prime criterion to choose the SSR markers for fingerprinting studies. Here, a total of 43 simple sequence repeat (SSR) markers that were known to be highly polymorphic in sesame were selected and used for development of fingerprinting profiles. Most popularly cultivated sesame cultivars were subjected to DNA profiling using SSR markers and are discussed in detail here. In brief, these 43 primers had generated amplicons ranging from 150 to 300 bp with a total of 75 alleles. Among these 43 primers tested for, our study reveals 23 of them are highly polymorphic across various cultivars and could be used to distinguish the cultivars studied for and can be potentially used for cultivar distinction, molecular diversity assessment and population structure assessment studies in sesame.

**Keywords:** Fingerprinting, Sesame, SSR, Amplicons

### 310 (P-310)

#### **Effect of different soil media mixtures on seedling survival and growth of *Ferula assafoetida* accessions introduced in India**

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*Ferul aassafoetida* L. is a perennial plant of Apiaceae family used as spice in all households of India and component of several ayurvedic medicines in pharmaceutical industry. *F. assafoetida* seeds are difficult to germinate and take a long time period to germinate seed due to seed dormancy. After standardization of seed germination method at CSIR-IHBT, it was required to maintain and grow the seedling in suitable media mixture for hardening till transplanting to open field conditions. The present study was conducted to evaluate the effect of different media mixture on seedlings of six *F. assafoetida* accessions survival and growth. A total of six media mixture i.e., M<sub>1</sub> {Soil + Farmyard Manure (1:1)}, M<sub>2</sub> {Soil + Farmyard Manure + Cocopeat (1:1:1)}, M<sub>3</sub> {Soil + Fine river sand + Farmyard Manure (1:1:1)}, M<sub>4</sub> {Soil + Fine river sand + Farm Yard Manure + Cocopeat (1:2:2:1)}, M<sub>5</sub> {Soil + Fine river sand + Farm Yard Manure + Cocopeat (1:1:1:1)}, M<sub>6</sub> {Soil only (Control)}



were prepared for evaluation. The seedling survival and plant height observations were recorded. The results of different media mixtures showed that media M<sub>4</sub> had the best performance for seedling survival among all the accessions. Media mixture M<sub>4</sub> also recorded highest plant height, the number of leaves, leaf length, leaf width, root length and root diameter as compared to control. It showed that the combination of soil, sand, Farmyard Manure, and cocopeat in 1:2:2:1 ratio was the best mixture to attained maximum survival of *F. assa-foetida* seedlings. Hence, as a result, the media M<sub>4</sub> had been used to raise the *Heeng* nursery at CSIR-IHBT and could also be used as base media for hardening of '*Heeng*' plantlets raised through mass multiplication method.

**Keywords:** Germination survival, media mixture, genotypes, *Ferulaassa-foetida*

### 311 (P-311)

#### **Indigenous traditional knowledge (ITK) and ethnobotanical importance of crop diversity in Kota Ramachandra Puram and Polavaram of Papikonda National Park, Andhra Pradesh**

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Eastern Ghats is an abode of rich biodiversity with mixed deciduous forests. Papikonda National Park (Papikonda or Papi hills) falls in northern Eastern Ghats, covers an area of 1,012 km<sup>2</sup> and lies between 18°49'20"–19°18'14" N, 79° 54' 13"–83° 23' 35" E. The PNP is distributed on the banks of the Godawari River, spread across the Alluri Sitharama Raju and Eluru districts of Andhra Pradesh. Traditionally, people in many tribal communities worldwide are extremely knowledgeable about plants and other natural resources on which they are dependent. Inhabiting diverse tribal communities and ethnic groups like Chenchus, Koyadoras, Sugalis, Yerukulas and Yanadis living in small hamlets called Gudems or Tandas, across the National Park. There is several ITK aspects are followed in and around PNP for a long back by local farmers and people. Most people are from farming communities, especially Horticulture and livestock (Integrative farming). Several indigenous designs have a wealth of knowledge on traditional crops, cultural practices, pest and disease management in agriculture, cropping systems, seed storage methods ethnobotanical importance followed by the farmers and the local people. Traditional practices like hanging maize cobs from the roof for seed storage, planting *Jatropha* sp. and *Chrysanthemum* sp. around the fruit plants to protect them from external enemies, the decoction of tobacco leaves as insecticide and storage of grains in big baskets made with bamboo materials were documented from this region. Rice panicles are hanging outside of house roofs for feeding birds believed as well-wishers for farmers. Tribal inhabitants living in this region are using botanical-based drugs for ailments of a lot of disorders and diseases. Local people have identified semi-dried leaves of Palmyrah locally known as "Tadi Chapa" is strong and long-lasting for making traditional mats and others. Local women usually made local toys and flower pieces with thin bamboo sticks. These methods have adopted a new vision of eco-friendly approaches. It has helped many farming communities, especially women's, earn supplementary revenue for their livelihood.



**Keywords:** ITK, Tribal inhabitants and livelihood

**312 (P-312)**

**Multi-location evaluation of wheat germplasm under drought stress for identification of trait specific germplasm**

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Wheat crop provides about 20% of daily calories intake to humans. With an area of more than 200 mha, wheat is the most widely grown cereal crop in the world and thirteen percent of the world's total wheat production is produced in India. Only one-third area under wheat in India receives full irrigation while the remaining is cultivated under partial irrigation often affected by drought which is further aggravated due to climate change and vagaries of weather. Drought affects plant health and ultimately reduction in yield via effect on relative water content, chlorophyll content, degenerated membranes, reduction in leaf area, biomass, tillering and grain weight. Breeding for drought tolerant genotypes by integrating crop morphology, physiology, genomics and breeding approaches is the plausible solution to mitigate effects of water scarcity on wheat productivity. Evaluation of diverse and unique set of germplasm for the identification of novel sources for drought stress tolerance is essential for incorporation in breeding programmes. In the present study, ~7500 wheat accessions from National Genebank, ICAR-NBPGR, New Delhi and other sources were characterized for agro-morphological traits during *rabi* 2019-2020 at two locations namely, Delhi and Pune. Based on this study, ~3100 selected unique wheat accessions were evaluated for drought tolerance during *rabi* 2020-2021 in Augmented Block Design with five checks at three locations (Delhi, Pune and Ludhiana) using 18 morpho-physiological traits. Subsequently, selected panel of wheat accessions (475 accessions) based on selection index for drought tolerance were evaluated for drought tolerance during *rabi* 2021-2022 in Augmented Block Design at five locations. Based on BLUP value estimation, IC128386, IC082167, IC336648, IC531505, IC598726, and IC611310 were found promising accessions for high and stable grain yield and IC118721, IC252928, IC477973, IC582710 and IC309875 were promising for thousand grain weight under both irrigated and drought conditions over the locations and years. These accessions can be utilized for trait discovery, allele mining and introgression in wheat improvement programmes for drought tolerance.

**Keywords:** Wheat, Evaluation, Germplasm, Drought, Trait discovery



313 (P-313)

**Kiwifruit- potential for fruit diversification and nutritional security**

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Kiwifruit has gained popularity in the past two decades in many countries of the world. It is also known as China's miracle fruit and the horticultural wonder of New Zealand as it has revolutionised the horticulture sector there. In fact no other fruit has gained so much popularity in such a short period in the history of commercial production. In India, this fruit was introduced in 1960's and it was first planted in Lalbagh garden of Bangalore as ornamental as well as fruit plant where it did not fruit. Later on, in the year 1963 under the leadership of late Dr Harbajan Singh it was introduced from U.S.A. by the Plant Introduction Division of Indian Agricultural Research Institute located at Phagli, Shimla (HP) now known as National Bureau of Plant Genetic Resources, Regional Station, Phagli, Shimla. After cultural practices standardised the propagating material distributed among research institutes and progressive farmers for further evaluation. Late 90's the acreage started increasing under kiwi cultivation but it was not much appreciating due to the less demand and market issues. During the last two decades the area has increased substantially to around 4000 ha with the production of 11,000 MT. The Indian states like Arunachal Pradesh, Nagaland, Sikkim, Meghalaya, Himachal Pradesh, Uttarakhand, and Jammu & Kashmir are mainly kiwi growing states. The kiwifruit cultivation helped in fruit diversification as well as nutritional security as the fruit is very rich in vitamins and minerals and antioxidants. Earlier only seven cultivars with two male parents were grown in India and in 2019 new introductions were made and it was encouraging to report the colour fleshed cultivars which will be available for cultivation soon.

**Keywords:** Cultivation, Kiwifruit, Nutritional security, Shimla

314 (P-314)

**Introgression of the genes governing resilience for climatic change into *Brassica juncea* from *Sinapis alba***

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Wild relatives of *Brassica* serve as a gene bank for traits controlling resilience to changing climatic conditions. An allied genus of the Brassicaceae family called *Sinapis alba*, also known as white mustard, possesses the ability to withstand biotic and abiotic stresses brought on by various climatic conditions. These stresses include *Alternaria* blight,



Sclerotinia stem rot, heat stress, drought, and pod-shattering. Due to the two genera's cross incompatibility, it was difficult to introduce the genes from *S. alba* that were responsible for these traits into *B. juncea* cultivars. With this in mind, we performed PEG-mediated protoplast fusion and subsequently developed five stable and viable somatic hybrids. Four of these are symmetric allohexaploid Brassicas with seeds in three distinct hues; two of them were discovered to be brown like *B. juncea*, another to be yellow like *S. alba*, and the final one was mottled in colour. Out of them, two brown-seeded allohexaploid *Brassica* (H1 and H2) were high-temperature tolerant and resistant to Alternaria blight. However, in addition to *A. brassicae*, yellow-seeded allohexaploid Brassica was also discovered to be resistant to Sclerotinia stem rot. As a result, we developed 154 BC<sub>2</sub>F<sub>3-4</sub> introgression lines to introduce the Alternaria blight resistance by successive backcross breeding, and we were able to understand the quantitative inheritance of the Alternaria blight resistance in the crop Brassica for the first time. The QTL introgressions on chromosomes 5 and 11 that contain a total of one (Abr-01) and two (Abr-02 and Abr-03) quantitative trait loci identified by ICIM-ADD mapping have been identified in this order. In addition, by synthesizing *S. alba*-specific microsatellite markers, we have established a marker-trait association between the resistance to Alternaria blight and the *S. alba*-derived marker number Sa25102. Furthermore, by utilizing a set of 94 *S. alba*-*B. Juncea* introgression lines, we conducted a single marker analysis to demonstrate a marker-trait association between the resistance to *Sclerotinia sclerotiorum* rot and a specific marker for *S. alba*. By locating several (>2000) HSPs in the allohexaploid *Brassica* (H1), we were able to corroborate our earlier findings about heat tolerance at seed maturity and unravel the genes causing heat stress tolerance.

**Keywords:** *Brassica juncea*, Introgression, Resilience, *Sinapis alba*

### 315 (P-315)

#### **The food system and environment: a study on cucurbits**

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The interplay between and within biophysical, geophysical, and human contexts, which shape a range of activities, is referred to as the food system. Food systems around the world are predicted to be profoundly impacted by global environmental change. Horticultural crops contribute significantly to food systems at a global scale. Cucurbitaceae is an important horticultural crop whose production is significantly affected by environmental variables. In this study, four cucurbit crops were sown in the field on three different dates sowing date (SD) 1, 2, and 3, and the variation in the phenology of cucurbit plants was quantified. Ridge gourd plants grown on SD1 took 27-45% days more for germination when compared to those grown on SD2 and SD3. Bottle gourd grown on SD1 requires 50% and 25% fewer days for germination than the plants grown on SD2 and SD3 respectively. Sponge gourd grown on SD1 requires 35% and 78% days more to germinate when compared to those grown on SD2 and SD3. Cucumber plants grown on SD1 required 34% more than SD2 and 4.3% fewer days than SD3 to germinate. The cucurbits grown on SD3 show a trend of better morphological parameters



e.g., vine length, root length, higher root-to-shoot ratio, and higher total chlorophyll content, pH and plant biomass of cucurbits grown on SD3 were only a bit higher than those grown on SD1 and SD2 but relative water content had an opposite trend. The study finds out that environmental variables have a significant effect on various parameters of cucurbits but the responses differ significantly. These changes may affect their production at a large scale which in turn will adversely affect our food system.

**Keywords:** Cucurbit, Phenology, Food system, Variation

### **316 (P-316)**

#### **Screening of bread wheat genotypes for drought and heat tolerance under field conditions**

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A field experiment was conducted in the Research Area of Wheat and Barley Section, Department of Genetics and Plant Breeding, CCSHAU, Hisar during the *Rabi* 2019-2020 to evaluate 62 bread wheat genotypes under normal, drought, heat and combined stress conditions. The experiment was conducted in four different environments, *viz.*, normal sown-irrigated (normal), normal sown-rainfed (drought), late sown-irrigated (heat) and late sown-rainfed (combined stress) and was laid out in RBD with two replications in each environment. Analysis of variance revealed highly significant variation among the genotypes for all the characters studied. Moderate estimates of GCV and PCV were reported for traits- early vigour, spike weight, number of grains/spike, grain weight/spike, grain yield/plant, harvest index and CTD, accompanied by moderate to high heritability and genetic advance as per cent of mean in all four environmental conditions, which suggests that still there is scope for further improvement of genotypes for these characters. Grain yield per plant reduced by 24.8%, 14.8% and 36.4% due to drought, heat and combined stress, respectively. Grain yield had a positive and significant correlation with number of productive tillers/plant, grain weight/spike, spike weight, number of grains/spike, 1000-grain weight, biological yield, harvest index, chlorophyll content, CTD and NDVI. Path coefficient analysis revealed that harvest index had the highest positive direct effect towards grain yield per plant, followed by biological yield per plant in all four environments. Grain weight/spike in normal and drought stress and number of grains/spike in heat and combined stress had high positive direct effects on grain yield. Thus, these traits may be used as selection criteria for respective environments. Clustering using Ward's method grouped 62 genotypes into 6, 8, 6 and 7 distinct clusters under normal, drought, heat and combined stress respectively. Genotypes P 13855, P 13841, P 13666, P 13633, P 13821 had low DSI, genotypes- P 13789, WH 1025, P 13633, P 13644, P 13858 had low HSI and genotypes- DBW 187, HD 3086, P 13815, P 13789, P 13841 had low CSSI values, subsequently they were categorised as drought-tolerant, heat tolerant and combined stress tolerant genotypes, respectively.



**Keywords:** Bread wheat, Drought, Heat, Genotypes, Screening

### 317 (P-317)

#### **Molecular characterization of *lpa1* (low phytic acid-1) gene governing kernel phytic acid accumulation in maize for alleviating iron and zinc malnutrition**

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Maize is a valuable source of micronutrients in addition to being an important food, feed, and fodder crop. Minerals such as iron (Fe) and zinc (Zn) are inaccessible to monogastric animals due to several anti-nutritional factors like phytic acid. Phytic acid is an effective chelator of positively charged mineral cations that are essential for nutrition. The mutant *lpa1* (low phytic acid-1) gene-based maize genotypes enhances the bioavailability of essential minerals. The *lpa1* gene located on chromosome-1S is 5139 bp long with no intronic sequences and here, we characterized the *lpa1* gene sequence to define it at the molecular level. Three *lpa1* based-mutants and seven wild-type inbreds were sequenced to find allelic variation and phylogenetic relationships with 26 selected orthologues. The number of exons ranged from 1-11 in maize; whereas it varied from 1-14 among orthologues. Sequence alignment revealed 662-InDel sites that categorized 11 haplotypes among 11 maize inbred lines. Nucleotide diversity in maize inbreds was found to be 0.02399; and there were 549 polymorphic sites across the 11 maize *lpa1* sequences. Motif prediction revealed eight motif sites in the *lpa1* sequence, with three best motifs (the range of motifs was 6-50 amino acids). Major functional motifs were ABC transporter trans-membrane region and ABC transporter. Phylogenetic tree using nucleotide and protein sequence showed closer relationship of maize *lpa1* sequence with *Eragrostis curvula*, *Setaria italica*, *S. viridis*, *Panicum hallii* and *Sorghum bicolor*. This study offered new understanding of the genetic diversity of the *lpa1* gene, which can be used to improve the nutritional value in breeding programme.

**Keywords:** Maize, Malnutrition, *lpa1*, Iron, Zinc

### 318 (P-318)

#### ***In vitro* clonal propagation and genetic fidelity assessment of black pepper (*Piper nigrum*)**

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Black pepper (*Piper nigrum* L.) called to be the “King of spices” is a highly commercial, much traded and valuable spice crop in the world. The black pepper is originated in Western Ghats region of southern India. An efficient and reliable *in vitro* clonal propagation protocol is attempted, which can be utilized for multiplication of elite genotypes of black pepper using nodal segments as explants which are free of endogeneous bacteria. Shoot regeneration was induced on Murashige and Skoog (MS) and Woody Plant Media (WPM) media in 30 combinations using BA and Kn hormones used individually and in combination. Nodal explants cultured in MS media supplemented with 0.5 mgL<sup>-1</sup> BAP formed 6.5 nodes per plant with longest shoots (10.42 cm) after 12 wk. Rooting was attempted on MS media supplemented with 2.0 mgL<sup>-1</sup> IBA, yielding about 15 roots per plant with an average root length of 3.40 cm within 4 wks of culture. The primary hardening of the rooted plantlets was achieved under a mist chamber conditions (25±2°C, 70-80% RH) yielding 100% survival after acclimatization. Genetic stability analysis of the micropropagated and mother plants as done using 48 ISSR markers yielding monomorphic bands indicating genetically fidelity when compared with mother plants. A ratio of 1:6.5 numbers of nodes is obtained on the MS medium supplemented with 0.5 mgL<sup>-1</sup> of BAP within 3 months. This research presents an improved and efficient *in vitro* clonal propagation protocol with good rate of multiplication, free of endogeneous bacteria and genetically stable plants that are easily acclimatized to the field conditions.

**Keywords:** Clonal propagation, *Piper nigrum*, Black pepper, Field acclimatization

0319 (P-319)

### **Genome-wide identification and characterization of trihelix gene family in Asian and African *Vigna* species**

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Trihelix transcription factors play crucial role in varied stress responses as well as in the growth and development of plants. Role of trihelix transcription factor in the non-shattering phenotype in domesticated rice is known. *Vigna* group of crops have different degrees of shattering phenotypes in different species. Here, genome wide identification



and characterization of trihelix gene family in four *Vigna* species including cowpea (*Vigna unguiculata*), greengram (*V. radiata*), adzuki bean (*V. angularis*) and ricebean (*V. umbellata*) have been performed. A total of 41, 39, 52 and 50 genes have been identified in adzuki bean, cowpea, mung bean and ricebean, respectively. The trihelix genes in each of the four *Vigna* species were classified into five sub-groups: GT, GT $\gamma$ , SH4, S1P1 and GT $\delta$ . The members of each subgroups shared similar pattern of gene structure and motifs across the four species. The cross-species positional relationships of cowpea, adzuki bean, mung bean *Vis-a Vis* rice trihelix gene have been studied. Further, Ka/Ks ratio for the trihelix genes in four *Vigna* species indicated purifying or stabilizing selection of the family. Gene expression analysis was performed for trihelix gene family in cowpea. Based on detailed bioinformatics analysis, potential targets for gene editing towards possible non-shattering phenotype in the four important *Vigna* crops have been discussed.

**Keywords:** Characterization, Genome-wide identification, trihelix, Vigna

### 320 (P-320)

#### **Molecular characterization of *Anthocyanin1 (A1)* gene governing anthocyanin accumulation in maize kernels**

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Blue maize rich in anthocyanins has emerged as a popular food worldwide. Anthocyanins are water-soluble flavonoids having anti-cancer and anti-diabetic properties. *Anthocyanin1 (A1)* gene encoding dihydroflavonol-4-reductase (DFR) is one of the major structural genes involved in anthocyanin biosynthesis pathway. *A1* present on chromosome-3L is 4467 bp long and codes for 357 amino acid proteins. Here, *A1* gene in maize was characterized among five wild type (*A1*) and five mutant (*a1*) maize inbreds, and was compared with 23 orthologues of grasses, legume, fruits, flower and *Arabidopsis*. Complete gene sequence of *A1* in maize revealed a total of 291 InDel sites with an average length of 2.83 bp. Seven haplotypes of *A1* were identified in maize. Number of exons in *A1* gene ranged from 3-5 in maize, while it was 1-7 among orthologues. Epimerase domain of NAD-dependent epimerase/dehydratase family was predicted as a major functional domain. Homology modeling of *A1* protein showed Q score of 0.83, with NAP and DQH as major ligands. *A1* protein of maize and its orthologues had alanine as the major amino acid (8.4-13.2%). Thermostability was predicted from aliphatic index in the range of 75.04-90.11. Phylogenetic analysis revealed that maize *A1* gene is more close to *Sorghum bicolor* followed by *Setaria italica*. The information generated here would help in assessing the evolutionary relationship of *A1* gene, and provide insight into the nature of *A1* protein in maize and its orthologues.

**Keywords:** Maize, *A1* gene, *a1* gene, Haplotypes, Molecular characterization



### 321 (P-321)

#### **Peaceful applications of radiation techniques in germplasm conservation, crop improvement and food processing**

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Over the time, human population is growing significantly and arable lands are decreasing which may threaten the human civilization on earth. To meet the global food requirements, higher productivity with sustainable utilization should be the prime objective. Several techniques have been developed for increasing the food productions and their sustainable utilization. Interestingly, nuclear radiation based techniques are important among them. Nuclear techniques are not only acknowledged for developing atomic weapons but also well-known for their peaceful application in the field of agriculture and food processing. Now days, radiation techniques are being utilized for crop improvement; extension of shelf life of fruits, vegetables and RTE/ RTC food products; disinfection of food grains and spices; control of fungi & bacterial infestation in food products etc. Moreover, they are also useful in making colorful diamonds which cost higher than original. In this way, excellent work for the improvement and revival of traditional landraces through radiation induced mutation breeding was performed. More than 50 rice mutant varieties have been developed from more than 90 traditional rice landraces by using radiations. Of which five rice mutants *viz.*, TCDM-1, Vikram-TCR, CG Jawaphool Trombay, TCVM and TCSM have been released by SVRC and notified by Government of India. In addition to this, with the help of nuclear techniques, flower colour have been changed in many varieties of chrysanthemum, gladioli and tube rose; sexual morphology has been changed in spine gourd; disease resistance has been developed in wheat; seed size and leaf width of Lathyrus has been increased; oil content of safflower variety has been increased etc. Besides the crop improvement, more than 25 nutritionally enriched ready to eat/ ready to cook food products have been developed from IGKV developed bio-fortified crop varieties with extended shelf life which will be channelized in mid-day meal scheme of state government. In this way, radiations can be utilized peacefully for plant architect improvement, food processing, developing ready to eat products, enhancing food quality and many more. This would be beneficial for many farmers, self help groups, industries and researchers.

**Keywords:** Radiation techniques, Germplasm, Conservation, Food processing

### 322 (P-322)



## **Improvement and revival of traditional rice landraces of Chhattisgarh through radiation induced mutation breeding**

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Chhattisgarh is popular as 'Rice bowl of India' due to its rich heritage of rice landraces. More than 23250 rice germplasm have been recorded in the state which is conserved at IGKV, Raipur. Interestingly, several traditional rice landraces have premium grain quality, special aroma, therapeutical properties, nutritional values etc. Unfortunately, many of these rice landraces have not been grown in farmers' field due to poor yield potential (2-3 t/ha), late maturity duration (150-175 days) and tall plant height (150-180cm); therefore they are at edge of getting extinct. To overcome this, mutation breeding could offer a simple and quick approach for improvement of these landraces through radiation induced mutagenesis without altering their original features. IGKV, Raipur and BARC, Mumbai started a joint program for the improvement and revival of about 100 traditional rice varieties of Chhattisgarh through radiation (gamma rays, electron beam, X-rays, proton beam and thermal neutrons) induced mutation breeding in 2013. The major aim of this collaborative work is to develop dwarf to semi-dwarf (100-120 cm), early to medium maturity duration (105-125 days) and good yield potential (4.5 to 6.5 t/ha) mutants by maintaining their original grain quality features/ nutritional values/ medicinal values. Till now, five rice mutant varieties *viz.*, TCDM-1, Vikram-TCR, CG JawaphoolTrombay, TCVM and TCSM have been released and notified by Government of India. TCDM-1, CG JawaphoolTrombay and TCVM are aromatic fine grain mutant varieties whereas Vikram-TCR and TCSM have non- aromatic but high yield potential. More than 50 stable rice mutants are under evaluation at station, state and national multi-location trials. In addition, about 550 mutant lines in the background of 35 rice landraces are in various mutagenic stages of confirmation, stabilization and evaluation. Interestingly, the mean percentage reduction in plant height was 7% to 55% and days to maturity was 6% to 40% whereas the mean percentage increase in grain yield per plant was 10% to 65% in various rice mutants with respect to parent, which indicated the potential of radiation induced mutation breeding. Currently, it is the World's largest active mutation breeding program for the improvement and revival of traditional rice landraces. The success of this collaborative work indicated that radiation induced mutation breeding is one of the most viable tools for improvement and revival of the traditional rice landraces and could be applied in other crops also to improve one or two major drawbacks with retained original

**Keywords:** Rice, Landraces, Induced mutation breeding

**323 (P-323)**



## Genetic improvement in plant architecture, maturity duration and agronomic traits of three traditional rice landraces through gamma ray based induced mutagenesis

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Rice landraces are the important source of several valuable genes for crop improvement except with few lacunae *viz.*, poor yield potential, tall plant stature, late maturity duration which restrict their commercial cultivation. Radiation induced mutation breeding offers simple, fast and efficient way to rectify these major defects without altering their original identity. The present study deployed the radiation (gamma rays @ 300Gy) induced mutation breeding for improvement and revival of three traditional rice landraces *viz.*, Samundchini, Vishnubhog and Jhilli. Desirable mutants identified were evaluated based on 13 agro-morphological and 16 grain quality traits in M<sub>4</sub>, M<sub>5</sub> and M<sub>6</sub> generations along with their parents and three checks. Further SSR markers based genomic similarity and genetic diversity study was also performed. All the mutants of the three landraces showed reduction in maturity duration and plant height compared with their parents. Furthermore, two, six and three mutants of Samundchini, Vishnubhog and Jhilli have increased yield potential over their parents, respectively. Interestingly, Samundchini Mutant-18-1 (22.45%), Vishnubhog Mutant-74-6 (36.87%) and Jhilli Mutant-13-5 (25.96%) showed highest yield advantage over their parents. Further, ANOVA based on RCBD revealed ample variations among the genotypes for studied traits. In addition, all the traits consistently showed high to moderate PCV and GCV and slightly difference between them in all the three generations. Moreover, in association analysis, the traits *viz.* fertile spikelets/panicle, panicle length, total tillers/plant, spikelet fertility percent and 100 seed weight with grain yield/plant whereas the traits, hulling (%) and milling (%) with HRR (%) were consistently showed high direct effects and significant positive correlation. SSR marker based genome similarity in rice mutants and corresponding parents ranged from 95.60% to 71.70% (Vishnubhog); 95.62% to 89.10% (Samundchini) and 95.62% to 80.40% (Jhilli), indicating the trueness of the mutants. Moreover, UPGMA algorithm and Gower distance based dendrogram; neighbour joining tree and PCA scatter diagram assured that mutants were grouped with their respective parents and fell into separate cluster showing high similarity between mutants and parents and dissimilarity among the 24 genotypes. Results revealed that irradiation could generate a considerable amount of genetic variability, and provide new avenues for crop improvement and diversification.

**Keywords:** Plant architecture, Agronomic traits, Rice landraces, Gamma mutagenesis



## **On-farm conservation of traditional biodiversity in Central Western Ghats of India**

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Conservation in nature's original form is very sporadic nowadays except in remote areas/tribal belts. However, in Karnataka, farmer's awareness and passion has motivated for on-farm conservation of biodiversity in Western Ghats, UNESCO World Heritage Site & hotspot of biodiversity Central Western Ghats lie in Karnataka state in the total of 1,600 km (990 mi) stretch. Three rivers Aghanashini, Tunga, Netravathi enrich the soil and increases urban settlements rapidly. In spite of urbanization, highly variegated topography restricts the mono-cropping and heavy rainfall facilitates and accommodates more crops and increased diversity. Awareness of farmers on the rich biodiversity and natural farming, hence conservation of traditional varieties through organic farming is continued out of personal interests; the famous local cuisines of these region, specially of rice, jackfruit and mango varieties; Religious importance; maintaining values of forefathers, young farmers maintain the legacy through generations; special endemic traits like good keeping quality (pepper-karimunda, mango-Neerukukku), specific uses pickling purpose (appemidi mango), puffed rice (Bangaradagundu, Bilidivaalya), aromatic rice, tolerance to pests and diseases (pepper-Gejehipli, rice-Bar Rathnachoodi), medicinal (Rice-Athikaraya, Sorata), khaira tree for pan masala etc.; the social status attached to conservation of biodiversity has encouraged some farmers to get noticed in the society; communities, NGOs and others help promotion of local diversity through facilitating exchange of traditional varieties and marketing; conserving traditional biodiversity is made sustainable by promoting local eco-tourism, local markets, fairs etc.; With all these, support from external source is limited to few farmers. A good intervention of support, recognition and value chain/marketing will facilitate many farmers to grow and conserve the diversity of crops in this region.

**Keywords:** On-farm conservation, Western Ghats, traditional storage structures

**325 (P-325)**

### **Genetic variability and diversity analysis in Potato (*Solanum tuberosum*) genotypes for yield and yield attributing traits**

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Potato (*Solanum tuberosum* L.) is widely regarded as the 'King of vegetables' due to its enormous utility and occupies a pre-eminent place amongst the vegetable crops. Potato exhibits considerable variation for a number of traits which provide greater scope for improving this crop through selection. The magnitude of genetic variability and extent heritability and association among quantitative characters are essential in crop improvement programme and for effective screening of superior genotypes in the



available germplasm. This study was carried out among thirty three diverse genotypes of potato in Jorhat, Assam in randomized block design with three replications during *Rabi* season of 2021-2022 to determine the extent of genetic variability and identify superior genotypes with high yield potential and high quality seed tuber. Analysis of variance for 17 characters showed that there existed highly significant differences among the genotypes, indicating an ample amount of genetic variability among the genotypes. High genotypic and phenotypic coefficients of variation were observed for characters like leaf area index, stem diameter (cm), number of tubers/plant, average tuber weight(g), tuber yield/plant(g), marketable yield/ha(q), tuber volume (cm<sup>3</sup>), shoot dry weight (g/plant), tuber dry matter content (%), and total yield/ha (q). High heritability coupled with high genetic advance as a percent of mean for the above mentioned characters was recorded, suggesting preponderance of additive gene action, thus paving the way for direct selection. Total yield/ha was positively and significantly associated with tuber yield/plant and average tuber weight, suggesting that these traits are the prime traits that could be considered for selection to increase tuber yield. The high positive effect on tuber yield through the number of tubers/ plant and average tuber weight suggested good scope for improvement of tuber yield by selecting plant types bearing a greater number of tubers with a higher tuber weight. The D<sup>2</sup> analysis delineated three different clusters of potato genotypes, which might be useful for breeding better varieties. Evaluation of genetic divergence is important for an efficient choice of parents for breeding and to ensure genetic variation for successful potato improvement.

**Keywords:** *Solanum tuberosum*, Genetic variability, Heritability, Potato, Yield

### 326 (P-326)

#### **Development of novel ornamental interspecific hybrid in okra - a success story for harnessing genetic diversity in CWRs**

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Crop improvement mediated through distant hybridization requires hybridization of elite cultivated varieties with their allied species so as to introgress novel traits and rectify some of their inherent problems which lead to poor yields. Such interspecific or intergeneric hybridization can lead to broadening the genetic base of the crop. With recent advances in plant tissue culture, molecular biology, biotechnology and scientific instrumentation, the importance and scope of distant hybridization has widened and the potential of distant or wide hybridization in crop improvement seems more promising than ever. A cross was made between two wild species of okra viz. *A. moschatus* and *A. moschatus*subsp. *tuberosus* (IC 470750) and an intersubspecific hybrid was developed. About more than 2000 of the crosses were attempted through hand pollination and five



crosses were set out of which three seeds showed germination. The only germinated seed out of total three could be successfully raised in the field up to a mature stage. The morphological features of the F1 hybrid being promising in context of its beautiful red flowers and an ability of the plant to propagate vegetatively paved a way out for its release as an ornamental variety in Gujarat which is probably a type of first such example in world to exploit CWRs of Okra as an ornamental variety for commercial release. The trueness of interspecific hybrid plant obtained through hybridization between two wild species of okra was confirmed by morphological and molecular characterizations. The two parents and F1 hybrid developed were characterized morphologically using DUS parameters set for okra. The results in this research have surfaced a way further for gene introgression for YVMV resistance through distant hybridization in okra.

**Keywords:** interspecific hybridization, YVMV, *A. moschatus* subsps. *tuberosus*, DUS, CWRs

### 327 (P-327)

#### **Characterization of *Curcuma caesia* germplasm for qualitative and quantitative traits**

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*Curcuma caesia* Roxb. is an erect, perennial, medicinal rhizomatous herb belonging to Zingiberaceae family, commonly known as black turmeric due to its bluish-black rhizome and is native to North-East and Central India. It is of immense therapeutical potential having pharmaceutical and industrial applications. *C. caesia* is now classified as an endangered species due to which, conservation of this species is of utmost importance. Therefore, hundred *C. caesia* germplasms were characterised for twenty-six agromorphological traits in accordance with DUS testing procedure as described in the Protection of Plant Varieties & Farmers' Rights Act. Characterization consisted of the recording of those characters which are highly heritable, can be visually detected and are expressed in all environments. Two of the 26 characters were found to be monomorphic, twelve each were found dimorphic and polymorphic in nature. In general, the germplasms were observed to be of tall height, long lamina length, medium lamina width, medium duration, medium primary rhizome length, and with high dry recovery percentage. They were mostly of compact pseudostem habit, semi-erect leaf disposition, close venation pattern, even leaf margin with compact rhizome habit. Genotypes had anthocyanin colouration on pseudostem, with strong blue colour rhizome, curved rhizome, coloured coma bract and rose bract tip colour. Vigour of the plant viz., tall plants, long petiole & lamina length were considered as a morphological characters for selection of adoptable genotypes RRL J – 51, RRL J – 61, RRL J – 69, RRL J – 74, RRL J – 79, RRL J – 84, RRL J – 88, RRL J – 89, RRL J – 95, RRL J – 98) to local conditions. The variations observed using DUS characters offer a bright scope for selection based on desirable



morphological traits, which can be potential for further crop improvement and conservation.

**Keywords:** Characterization, *Curcuma caesia*, Germplasm, DUS

### 328 (P-328)

#### **Determination and comparative study of total soluble solids, sugar content and acidity of tamarind germplasm collected from Jharkhand**

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Tamarind (*Tamarindus indica* L.) is an economically important tree, grown across India. The fruit pulp is the richest source of tartaric acid and find application in various Indian cuisines as flavouring agent. The taste of ripen tamarind pulp is attributed to acid and sugar content and combination thereof which further decide the quality of products made after processing tamarind pulp. Considering this various parameter responsible for unique flavour of tamarind viz. total soluble solid, titratable acidity, total sugar, and reducing sugar is determined for 28 accessions conserved in field genebank. The total soluble solids were determined by using portable hand refractometer and the reading recorded were expressed in °Brix. Acidity of tamarind pulp was calculated by titrating the diluted pulp against the standard N/10 NaOH solution using phenolphthalein as an indicator. Total sugar and reducing sugar were determined as per "Lane and Eynon" titration method as described by Ranganna (2003). Where as pH was determined using pH meter. Significant difference for these traits were recorded for 28 accessions of tamarind. Titratable acidity ranged from 7.79% (IC-594345) to 21.16% (IC-594321) with an average value of 14.46 %. Reducing sugar ranged from 6.48 (IC-594323) -15.15% (IC-209883) with an average value of 10.81 and total sugar ranged from 13.89 (IC-594343) - 40% (IC-209890) with an average value of 21.23. Whereas TSS ranged from 19.33 (IC-594336) to 29.37 (IC-594337) °Brix. pH ranged from 2.5 (IC-285280, IC-312361)-2.9 (IC-594329) with an average value of 2.67. further, A comparative study for these parameters were also made with the Thailand sweet tamarind, a table purpose variety. Some of the accessions were at par with sweet type for TSS and TA however Thailand type showed substantially high value for total sugar and reducing sugar content which may be responsible for its excessive sweetness. Further germplasm augmentation and genetic improvement is needed to develop a sweet type tamarind variety.

**Keywords:** Tamarind, Germplasm, TSS, Sugar, Acidity content

### 329 (P-329)

#### **Genetic diversity analysis in Rice (*Oryza sativa*) for reproductive phase cold tolerance and yield attributing traits grown in late *Sali* season**

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Genetic diversity study among thirty three rice genotypes was assessed for reproductive phase cold tolerance and yield attributing traits at Assam Agricultural University, Jorhat during late *Sali* 2020-2021 under rainfed condition. The genotypes were grown in Randomized Block Design (RBD) with three replications. Thirty three genotypes grouped into five different clusters under late *Sali* rainfed condition by the genetic diversity studies. Grains per panicle followed by 1000 seed weight contributed maximum towards diversity in late *sali* season. Inter cluster average  $D^2$  values ranged between 919.2 and 5577.73. Cluster III was identified to be the most divergent cluster among five. In the late *Sali* season, genotype Jalashree, Moinajan, Mashuri, Solpona, Prafulla, Johingia, KutkutiSali from cluster I, KolaSali, Manohar Sali, Ronga Bordhan, JR-16, Swarna sub-1, Dolkachu, Biriabhanga, BR-11 sub-1, Dhanshri, Jalkunwari, MemSali, Betguti from cluster III, genotype Ranjit from cluster V were identified to be superior and they were from genetically divergent clusters so, they could be used to produce transgressive segregants in future hybridization programmes.

**Keywords:** Autogamous, Clusters, Late sali, Pollen fertility, Transgressive segregants

### 330 (P-330)

#### **Genotypic screening for heat use efficiency and related traits in cultivated rice of Assam**

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More than 55% of the world's population consumes rice (*Oryza sativa* L.), which is the most important cereal crop in the world. By 2050, it is predicted that 50% more rice would be needed to feed the growing population. This has been a difficult challenge with the current selection methodologies, especially in light of the current rate of productivity growth. In order to increase selection efficiency, attention has recently been placed on a few physiological and related climatic indices in addition to conventional yield component qualities. The purpose of this work was to screen 58 rice germplasm from Assam for variables connected to temperature indices. Estimation of mean sums of square (MSS) indicated that it was significant for all the characters. This means, there were highly significant differences among all the fifty-eight genotypes of rice under study and there was ample scope for the selection of desirable genotypes. The phenotypic variance (PV) for all the characters was higher than the genotypic variance (GV). This might be due to some environmental effect on expression of those characters. High heritability (more than 90 %) was observed for all the characters. High heritability coupled with high genetic advance per cent of mean was observed for trait heat use efficiency. Selection thus, would be effective for this trait. At both genotypic and



phenotypic level, highly significant association of all the characters with grain yield was observed. Among the genotypes Maizubiron had the highest value for heat use efficiency on the other hand Boga joha had the highest GDD and HTU and Rabjit had the highest yield performance. These varieties can be promising for undertaking hybridization programme. Efficient hybridization programme formulated among these parents are expected to yield desirable segregants for their further utilization in breeding programme.

**Keywords:** Assam, Rice, Heat use efficiency, Temperature indices

### 331(P-331)

#### Seed storage behaviour and cryopreservation of Date palm (*Phoenix* sp.)

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The date palm (*Phoenix dactylifera*) is one of the oldest cultivated fruit trees on earth. The closely-related, wild date palm of India (*P. sylvestris*) has apparently existed from prehistoric times in the region and is widely occurring in Indian subcontinent in wastelands and disturbed areas. The date palm diversity in India, maintained in the form of *in-situ* or on-farm conservation, is facing threats of loss due to overall pressure on agrobiodiversity. Morphological characterization using 11 quantitative and 7 qualitative fruit and seed characters in 23 date palm accessions of wild and cultivated species showed occurrence of wide variation and this variation was comparatively more in *P. sylvestris* than *P. dactylifera*. Fresh seeds of both species with a moisture range of 35-40% recorded more than 90% seed germination, highest being 100% for 10 out of 23 accessions. To understand the seed storage behaviour for long term conservation of the *Phoenix* species, seeds of the two edible species alongwith one ornamental species; pygmy date palm (*P. roebelenii*) were subjected to desiccation and cryo-exposure. Reduction in vigour indices of desiccated and cryo-stored seeds was reported compared to fresh control. Seeds of both *P. sylvestris* and *P. dactylifera* species could tolerate desiccation upto 8% moisture content, with loss of germinability upto 3-20% before and upto 10% after cryoexposure. However, further reductions in moisture content to less than 5% adversely affected germinability of both species after cryoexposure. On the other hand, small seeded species *P. roebelenii* showed 90% germinability before as well as after LN exposure of desiccated seeds at less than 8% moisture level and seeds could maintain high viability after 12 months of storage at RT. Thus, *P. sylvestris* and *P. dactylifera* may consider to exhibit as intermediate seed storage behaviour and that of *P. roebelenii* as orthodox seed storage behaviour. In the present study, the feasibility of *Phoenix* species for their cryobanking for long-term conservation have been investigated.

**Keywords:** *Phoenix*, Cryo-exposure, Storage behaviour, Seed desiccation



### 332 (P-332)

#### **Glimpses of vegetable improvement research in Assam Agricultural University, India - a review**

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Vegetable plays an important role in human nutrition. They are very rich in precious nutritional components like vitamins, minerals, antioxidants and a series of micronutrients, indispensable for human health. They are very essential in human diet not only in the developing countries but also all over the world. A number of vegetable crops belonging to different groups like tuber crops, leguminous crops, root and bulb crops, solanaceous crops, leafy vegetables, cole crops and cucurbitaceous vegetables are grown not only in India but throughout the world also which are used by the people in diversified ways. The production of vegetable crop was handicapped by shortage of high yielding varieties with tolerance to biotic and abiotic stresses. The earliness and quality aspects are also very important from marketing point of view. In North East India, although lot of germplasm are available but proper study for the development of improved varieties was not systematically done till the establishment of AICRP Centre at AAU, Jorhat in 1972. The research programmes undertaken afterwards in the project geared up the varietal development works since 1987 onwards. The programmes involved application of standard breeding strategies starting from collection of germplasm to multilocation testing in the state and national trials and on farm demonstration in KVKs and farmers' fields. The exhaustive study and research finally led to the development and release of many high yielding varieties of different vegetable crops for cultivation by the farmers. The detailed characteristics of the newly developed varieties are described in this paper. These included JC-1, JC-2, ABU, BHUPENDRA in brinjal; MAMONI in tomato; AAUOKHYB-1 and AAUOKHYB-2 in Okra; BIREEK-1 and BIREEK-2 in Chilli; SHYAMOLI and RODALI in Amaranthus; SPG 09-01, GB 09-16-1, GB 09-18-8 in Spine gourd; JORMLG-1 and JORMLP-2 in Lai patta, RG 09-05 in ridge gourd; RS 09-01 and RS 10-02 in Roselle which were developed at Assam Agril. University, Jorhat. Some other high yielding varieties developed elsewhere were UTSAV and VNR-218 in brinjal, 09/TLCVRES-1 in tomato; 09/CHVAR-6 and IVR-338 in chilli; VRO-6, VRO-21, HOK-152, PRERANA and JOH 05-09 in okra; ARKA ANUP and ARKA SUBIDHA in French bean which were recommended for the state of Assam. Apart from high yield, the varieties were having additional advantages such as resistance to bacterial wilt in brinjal, leaf curl virus in tomato, little leaf in chilli, YVMV in okra and fruit rot in ridge gourd. The varieties of spine gourd and leafy vegetables were having additional advantage of earliness, tenderness and good consumer preference. These varieties have become very popular not only in Assam and North East but in West Bengal, Bihar, Telangana, Karnataka, Kerala, Haryana and Himachal Pradesh also.

**Keywords:** Vegetable, varieties, yield, disease resistance, consumer preference

### 333 (P-333)



## Morphological characterization studies in oat (*Avena* sp.) germplasm

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Oat (*Avena sativa* L.) is an important annual crop of rabi season, ranked 6<sup>th</sup> in the world cereal production. Genus *Avena* 70 species is very large and diverse and includes diploid, tetraploid and hexaploid species (Kaur and Kapoor, 2017). Oat's production in worldwide belongs to the hexaploid species: *Avena sativa* L. (widely cultivated white oat) (2n=6x=42. AACDD) and *Avenabyzantina* C. Koch (red oats) (2n=6x=42. AACDD). Other minor cultivated species includes *Avena abyssinica* (Ethiopian oats) (2n=4x=28, AABB) and *Avena strigosa* (Black oats) (2n=2x=14, AsAs) (Gorash *et.al.*, 2017). Two ninety-four oat genotypes belonging to ten different *Avena* species procured from NBPGR. There is tremendous variability available in oat germplasm studied to characterize and evaluate genotypes excluding checks using DUS guidelines for thirteen different nonmetric traits. Observations were recorded on five randomly selected plants in each genotype for traits *viz.*, early plant vigour, growth habit, leaf colour, leaf sheath pubescence, flag leaf attitude, panicle attitude, awn per spikelet, seed colour, stem solidness, primary floret pubescence, spikelet shattering, hullness and biotic stress susceptibility at Research cum Instructional Farm, Department of Genetics & Plant Breeding, IGKV, Raipur during *Rabi* 2019-20. Coefficient of variation and principal component analysis revealed variability among the genotypes for the qualitative traits evaluated. Highly significant positive correlation showed among traits *viz.*, seed colour (black) and biotic stress susceptibility (very low). PCA analysis showed that genotypes namely EC0004456, EC0099165, EC0178761, EC0104007, EC0537811 were very different from each other. Cluster analysis separated genotypes into four sub cluster: genotype EC0022023 with erect flag leaf attitude and brown seed colour (*Avena sativa*) present in different cluster and 23 genotypes with brown seed present in one cluster, all belongs to *Avena sativa* only one genotype IC0282934 belongs to *Avena byzantina*. Genotype namely EC0108477, EC0039402, EC0039915 (*Avena sterilis*) showed black seed. The genotype EC0178761 having compact panicle attitude.

**Keywords:** Oat, Germplasm, Morphological characterization, PCA

### 334 (P-334)

#### Standardization of long-term pollen cryopreservation of *Lathyrus sativus* to facilitate wide hybridization

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Grass pea (*Lathyrus sativus* L.) is a miraculous pulse crop, commonly known as chickling pea, 'khesari' or 'sabberi'. The crop has its origin in Mediterranean region and it possesses a high protein content (28%). To facilitate wide hybridization studies, pollen cryopreservation was attempted in 20 accessions of *L. sativus*. Among the different sucrose concentrations, Brewbaker and Kwack's medium with 15% sucrose was optimal for *in vitro* pollen germination. Fresh pollen viability ranged from 83.58% to 90.23%. Pollen viability at different storage regimes *viz.*, 25, 4, -20 and -196°C at different storage duration (1, 3, 5, 7, 9, 24 h, 1 wk, 2 wk and 6 months) was assessed. Ideal pollen moisture content of 14-16% for long term pollen cryopreservation was attained by desiccating the pollen for 10 min in laminar air flow chamber. Significant negative correlation was found between pollen viability, storage duration and temperature (25, 4 and -20°C) in all the accessions. Cryopreserved (-196°C) pollen showed significantly higher viability compared to all the other storage conditions. The cryopreserved pollen viability ranged from 65.53 - 85.60%. The cryopreservation protocol standardized was applied to 20 accessions of *L. sativus* for conservation up to six months without significant loss in its pollen viability. Successful pollination, fruit and seed set was observed in cross combinations attempted using cryopreserved pollen.

**Keywords:** Grass pea, Pollen germination, Pollen storage, Pollen cryopreservation

### 335 (P-355)

#### Evaluation of different sesame varieties in Telangana state

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Sesame (*Sesamum indicum* L.) is one of the world's oldest oilseed crops and is under cultivation in Asia for over 5000 years. Globally, sesame is produced over an area of 11.74 million hectares and annual production around 6.02 million metric tonnes with average productivity of 512 kg per hectare during 2018 (FAO 2020). India is still leading country with maximum (25.8 %) production from the largest (29.8 %) area and highest export (40 %) in the world. In India, sesame is being grown over an area of 16.25 lakh hectares with production of 0.83 lakh tonnes and productivity of 500 kg/ha (Annual report 2020-21 of AICRP on sesame and Niger). In Telangana, it is grown over an area of 0.23 lakh hectares with an annual production of 0.1514 lakh tonnes and productivity 636 kg/ha. In districts of northern Telangana, *viz.*, Adilabad, Jagtial, Karimnagar and Nizamabad, it is grown as summer crop. (Department of Agriculture reports 2021). In recent years, its



performance as a catch crop in *rabi* and after Bt cotton and turmeric in *summer* season particularly in area under cultivation is encouraging. Its oil content generally varies from 46 to 52%. During *summer* 2019, the experiment was conducted on sesame crop at Regional Agricultural research station, Polasa, Jagtial with sixteen entries viz., 3m length and width in three replications. The entries JCS 3 898 (1063 Kg/ha) and JCS 3970 (1052 Kg/ha) recorded highest yield than the local variety, Hima 879Kg/ha. If these entries performs well at different locations of Telangana for three years at different locations. Then we can recommend this variety for farmers during summer season.

**Keywords:** Evaluation, Sesame varieties, Telangana, Summer season

### 336 (O-07)

#### Large scale phenotyping of pea germplasm for discovery of resistant sources against powdery mildew (*Erysiphe polygoni*)

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Keeping potential threat of *Erysiphe polygoni* DeCandolle causing powdery mildew and significant yield losses in pea (*Pisum sativum* L.) in view, the present study was aimed to identify resistant sources through large scale phenotyping under field epiphytotic conditions at Research Farm, ICAR-NBPGR, New Delhi during *Rabi* season, 2021-22. A total of 1136 pea germplasm accessions consisting of indigenous as well as exotic collections were phenotyped. Based on disease scoring using standard rating scale, entire germplasm accessions were classified into different categories. Out of 1136, only 25 accessions (IC258401, IC262762, IC262849, IC267174, IC267180, IC274039, IC310074, NC-60761, IC552779, IC613133, IC267727, IC311066, IC629544, IC629687, IC208327, IC220109, IC220378, IC274040, IC345548, IC424898, EC598669, EC598709, EC598710, EC598713 and P-1541-19) were found to be highly and 76 accessions were found to be resistant and rest of the accessions were either susceptible or highly susceptible. For better understanding of the basis of resistance, the highly resistant and resistant accessions were also analysed biochemically for host defence chemicals such as total protein, phenol, peroxidase, catalase and hydrogen peroxide which contribute in showing resistance in host plant. During biochemical analysis, the highest level of hydrogen peroxide level was recorded in P-1541-19 (0.412 H<sub>2</sub>O<sub>2</sub> mM/g fresh leaf), soluble protein in IC345548 (0.0527 protein g/g fresh leaf), phenol in IC345548 (0.657 phenol mg/g fresh leaf), peroxidase in IC274040 (0.0787 absorbance change min<sup>-1</sup> g<sup>-1</sup>) and catalase in IC629687 (0.256 absorbance change min<sup>-1</sup> g<sup>-1</sup>). Quantitative biochemical estimation confirmed that four accessions, namely IC220378, IC274040, IC345548 and IC424898



are the most resistant ones. Since developing resistant varieties is the most effective and economical viable strategy for the disease management. Therefore, all these accessions identified as highly resistant may have potential of utilizing as resistant donor in the crop improvement programme for breeding of resistant/high yielding varieties and also for mapping and tagging resistant gene(s) against powdery mildew

**Keywords:** Germplasm, Phenotyping, Pea, Powdery mildew, Resistance

### 337 (S-09)

#### **Vista of opportunity for On-farm conservation of native crop diversity: on a cutting edge knowledge perspective**

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Agriculture and agrobiodiversity have linkage to all, 17 global Sustainable Development Goals (SDGs). Therefore, to ignore a dynamic harnessing of the conventional agricultural vertical, particularly the disruptive on-farm management of a protectable, resilient, profitable, protected, and branded mix; could be too late. Options to promote organised in-situ/ on farm conservation of native agricultural biodiversity, for availing a long-term benefit of its dynamic, evolutionary state remains lesser studied or under-prioritized. Some old experiments (1984-1989) on upland paddy and bamboo germplasm conducted at Basar (District West Siang), Arunachal Pradesh had led to suggesting a preliminary model for on-farm conservation of diversity of local rice and bamboos in the state. A few prominent, conventional/historical on-farm conservation practices in rice-based cropping systems across the country include, Zero Valley of Apatani Plateau, Arunachal Pradesh, Jaypore Tract of Orissa, Wynad District of Kerala, etc., which need systematic promotion and opportunity based replication too. The then proposed on-farm conservation model for Arunachal Pradesh suggested to; (i) earmark few superior local varieties having good farmer' preference, productivity, and local adaptability traits vis-a-vis premium value, (ii) encourage farmers to increase cultivated area under such elite varieties, covering 2/3rd to 3/4th of their holdings; to get more yield and higher produce/ incomes, (iii) farmers must not ignore rest of their conventionally grown varieties, and must grow them in at least 1/3rd to 1/4th of their cultivated area, and (iv) seasonal, multi-crop and varietal mosaics may have to be an essential feature of all such on-farm conservation practices to help foster resilience and endurance. A state-wide adoption of such on-farm conservation model could be dynamic, evolution-friendly, farmer-friendly, and competitive at a basic economic/ business level. Similarly, on-farm conservation of local bamboo diversity through use as agroforestry species assumes significance since bamboo is already de-notified from regulatory control of forest laws. Farmers may openly adopt, conserve, and fetch higher income from bamboos. A drastic change in the regulatory and farmer' welfare regimes over the time as well as an increasing complexity in farmers' coping up due to lack of awareness on empowerment



could constrain and complicate holistic promotion of on-farm conservation/management model(s), which needs to be addressed. Also, understanding and incorporation of further knowledge on farmers'/community participatory actions, and new welfare options could help in advancing a systematic adoption of on-farm management practices, up-scaling of remunerative options in medium term, and promotion of competitive farm business in the long term.

**Keywords:** Agrobiodiversity, On-farm conservation, Management

### **338 (P-338)**

#### **Grass biodiversity and its utilization in context of Chhattisgarh, India**

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Chhattisgarh is central most part of India and known for biodiversity not only for geographical landforms but also diverse form of cultivated as well as wild species and their close relativity to commercial plants. Distributions within state are compiled from a broad range of sources only some of which included specimen citations to support their claims of geographical distribution. All distribution records should thus be considered provisional. The objective of the overall work is to produce an authenticated and authoritative list of grasses of Chhattisgarh, both native and naturalized. This list is to include all taxa of seed plants with their accepted names, synonyms, details, habit, and distribution different locations. Grasses are placed as staple cereals and fodder, apart from their consumption the grasses serve as ornamental landscape, soil conservation, oil extraction and daily uses. Most common types of grassland prevails in Chhattisgarh are Aritida-Dicanthium, Dicanthium-Anthraxon, Anthraxon-Aristida etc. which are dominant grass species. Total 225 grass species belong to 75 genera were studied during grass survey trips in Chhattisgarh. Among 226 grasses, 81 were waned and 75 were wanless they grouped as excellent fodder, good fodder and average quality fodder habituating in diverse landforms and topography. Utilization of grasses in brooming, thatching, live fencing, mat preparation are often seen in villages and forest fringe habitats.

**Keywords:** Biodiversity, Grasses, Palatability, Topography, Uses

### **339 (P-339)**

#### **Screening of *Luffa* germplasm against ToLCNDV and identification of ToLCNDV resistant lines**

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*Luffa* is a popular indigenous cucurbitaceous vegetable on the Asian sub-continent. Tomato Leaf Curl New Delhi Virus (ToLCNDV), belonging to the genus Begomovirus in the family Geminiviridae, is a severe threat for *Luffa* production worldwide. In *Luffa*, ToLCNDV can be transmitted through sap inoculation or by whiteflies and cause a yellow mosaic disease, which is characterized by the presence of yellow spots on newly-emerging leaves, followed by mosaic patterning and upward curling of the upper leaves. In the event of a severe attack, ToLCNDV results in small, distorted leaves, and misshapen fruit causing devastating damage to resource poor farmers. Considering the practical problems of viral disease management, the identification and use of resistant germplasm lines for development of varieties is the most significant and practical approach to achieve higher yields and quality. Therefore, more than 200 germplasm accessions from the medium term storage of National Gene Bank were screened under natural epiphytotic conditions in the rainy season during 2021 & 2022, when the proliferation of whiteflies results in a high incidence of ToLCNDV disease symptoms. The experiments were laid in augmented block design with three susceptible and two resistant checks (DSG 6 & DSG 7). Three plants per accession were scored in the field 60 days after sowing for ToLCNDV severity using a six-scale scoring (0-5). Out of 200 accessions, 11 were highly resistant, 23 were moderately resistant and four were susceptible, 35 were highly susceptible and 12 were moderately susceptible; while 119 accessions were highly susceptible, It was found that accession IC 092624-A, IC 354863-A, IC 538150-A, IC 284899-A, IC 340430-A, IC 284957-A, IC 394720-A and D SAT 102 were highly resistant in both the seasons. The resistant lines were selfed in kharif 2022 and screened under challenge inoculation experiment. The ToLCNDV resistant lines identified herein provide an opportunity for the development of virus resistant varieties and study of inheritance of resistant trait.

**Keywords:** Germplasm, *Luffa* spp., Resistant, ToLCNDV

### 340 (P-340)

#### **Characterization of grasspea (*Lathyrus sativus*) germplasm for agro-morphological traits along with protein content**

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Grasspea (*Lathyrus sativus* L.,  $2n=14$ ) is an age old cool season legume which has been grown mainly for food and fodder. It is a climate resilient crop which requires only minimal inputs but having high biomass with an interesting nutritional profile like high folic acid content and the only known dietary source of L-homocystine which is used to treat cardiovascular ailments and hypoxia- Alzheimer's disease. A crop having multifaceted values had been given the status of 'Orphan' or 'Undermined' crop probably due to the presence of  $\beta$ -ODAP (L- $\beta$ -N-oxalyl- $\alpha,\beta$ -diaminopropionic acid) an antinutritional factor. Identification of lines having low  $\beta$ -ODAP and high biomass, high protein, early maturity and other agro-morphological traits can meet the challenges of grass pea improvement programmes in India. The present study involves the characterization of diverse set of 180 grass pea germplasm (131 from ICARDA and 49 from ICAR-NBPGR genebank) along with four checks for 39 agro-morphological traits and leaf protein using Kjeldahl method and seed protein by Dumas method. Experiment was carried out at ICAR-NBPGR farm, New Delhi during rabi 2019-2020 and 2020-2021 in augmented block design. Significant variability was observed for the traits- earliness, days to 50% flowering, plant height, 100 seed weight, pod length, single plant yield and leaf and seed protein which ranged between 15.46 to 37.13 mg/100g 22.01 to 32.90 mg/100g on dry weight basis respectively and the leaf protein is way higher than the earlier reports. Accessions BK-31-1-1, N/08-78, BK-15-4 and IFLA-220 showed high leaf protein and IC-347378, BK-10-1, IFLA 2750 and BANG-206 showed high seed protein content with appreciable agronomic traits. Further validation of the accessions for  $\beta$ -ODAP and various other biochemical parameters along with other traits will help in rediscovering its lost potential.

**Keywords:** Characterization, Germplasm, Grass pea, Protein

### 341(P-341)

#### Assessment of Cryo-fitness for Bitter gourd seeds

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Bitter gourd (*Momordica charantia*) also known as bitter melon, balsam pear or karela is an important cucurbit crop grown widely in Asia mainly in India, China and South East Asia for its immature fruit consumed as vegetable. The crop is well known for its hypoglycemic activity on diabetes mellitus. The seeds of bitter gourd even though classified as orthodox are expected to survive long-term dry storage at subzero temperatures. Cryo-conservation is a preferred method of storage for conservation of germplasm for posterity. The cryo fitness of four bitter gourd varieties Arka Harit, Co 1, Preethi, Bitter Gourd Long were assessed by the seed viability tests upto six months of cryo-conservation in the vapour phase of liquid nitrogen. The impairment in the fitness during cryo-conservation were studied by the morphometric parameters and biochemical proximates. There was no germination in the varieties Co 1, Preethi and Bitter Gourd Long whereas a minimal reduction of 6.15% was observed in Arka Harit



after six months of cryo storage. Studies on seedling injury for cryo-treated Bitter Gourd seeds revealed that there was a significant reduction of 18-20% in shoot length of Co 1, Preethi and Bitter Gourd Long varieties. The root length recorded a minimal reduction of <5% in Preethi and Arka Harit. SOD activity of cryo stored seeds has exhibited an increasing trend in the first four months and then recorded a reduction in up to sixth month of cryo storage in all the varieties. POX activity of cryo stored seeds has exhibited a decreasing trend throughout six months of cryo storage. The total lipid content gradually reduced in all the four bitter gourd seeds after six months of cryo-storage with the maximum reduction after six months of cryo storage. From this investigation, bitter gourd seeds which lost their vigour after cryo treatment can also be related with lipid breakdown that might be the cause of free radicles production by stress made on seeds during desiccation or freezing injury that occurred at low temperature storage.

**Keywords:** Bitter gourd (*Momordica charantia*), Cryo-conservation, Morphometric and Biochemical Parameters

### 342 (P-342)

#### **A rapid screening of brinjal for resistance to bacterial wilt in early seedling stage**

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The most significant disease of brinjal and other solanaceae crops in tropical climates is bacterial wilt caused by *Ralstonia solanacearum*. Thirty different genotypes of brinjal, including collection from North Kerala and cultivars released by the Kerala Agricultural University, were examined for disease response. Four weeks old seedlings of the genotypes were screened by artificial inoculation using *Ralstonia solanacearum* inoculum at a concentration of  $1.0 \times 10^8$  cfu/ml (O.D 600nm = 0.8-1.3) for a period of 24 hours. Thirteen genotypes including released varieties were found to be resistant to bacterial wilt of which SM-6, SM-15, SM-25, SM-28(Haritha), SM-29(Surya), SM-30(Ponni) were found to be highly resistant The genotype SM-1 was resistant whereas SM-2, SM-5, SM-7, SM-11, SM-17, SM-24 and Neelima (F1 hybrid) were moderately resistant. Seventeen genotypes were found to be susceptible, with SM-9, SM-10, SM-12, SM-18, SM-20, SM-21, SM-22, SM-23, SM-26, and SM-27 being found to be highly susceptible. In upcoming breeding initiatives, these resistant lines can serve as parents for hybridization.

**Keywords:** Brinjal, Bacterial wilt, *Ralstonia solanacearum*, genotypes

### 343 (P-343)

#### **Genome editing *vis-a-vis* conservation of plant genetic resources**



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The recent emergence of the novel plant breeding technologies like genome editing has opened up new doors for precise modification of the plant genomes without the introduction of foreign DNA. Their successful application in number of agricultural crops appears promising for developing climate-resilient plant varieties. Genome editing creates DNA modifications such as deletions, insertions, single nucleotide substitution (SNPs), and large fragment substitution. The site-specific nucleases (SSNs) that bring about nucleotide excision include engineered homing endonucleases or mega-nucleases (MNs), Zinc-Finger Nucleases, Transcription Activator Like Effector Nucleases (TALENs), and CRISPR-associated protein (*Cas*). Conservation strategies for genome-edited crops can be at par with the strategies adopted for conserving genetically modified (GM) crops in the *ex-situ* collections in gene banks. However, *in-situ* on farm conservation efforts need to be looked into carefully in the light of these gene editing products. With gene-edit options, domesticating new plant species might give farmers more options for growing diverse crops well-suited to changed climatic conditions such as stresses like heat, cold, salinity, nutritional etc. Each cell of the plant ought to have the same edit in order to benefit fully from the technology and to pass it down to future generations. It also needs to be made sure that these tools edit only the targeted gene(s) before it would be a viable option for conservation purposes. Conservation efforts need to protect not only one gene-edited species but also several other related and wild species. Since all species cannot be gene-edited, conservation needs to focus on the whole ecosystem. Gene drives, capable of addressing ecological problems by altering entire populations of wild organisms, have become more plausible with the advent of gene editing and could offer an efficient way of managing invasive populations and protecting the species they endanger. RNA-guided gene drives could hopefully prevent the spread of disease, support agriculture by reversing pesticide and herbicide resistance in insects and weeds, and control damaging invasive species and hence would offer substantial benefits to humanity and the environment. Unwanted ecological effects, spread across political borders, alignment with the socio-cultural values and indigenous knowledge might demand thorough public discussion to explore the responsible use of genome editing technologies.

**Keywords:** Genome editing, plant genetic resources, conservation

**344 (P-344)**

**Global millets genetic resources for enhancing productivity and nutrition in the context of climate change**

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A sustainable food system in the context of climate change requires diversification of agriculture in terms of both crops and varieties. The potential of millets to address climate change and food and fodder security is not being realized in full, despite that millets have the potential for higher productivity with minimal inputs, adapting to diverse ecologies, and the grains are more nutritious than major cereals. As an example, finger millet grains contain exceptionally high calcium (>350-500 mg per 100g), and all millets are rich in Fe and Zn, with a maximum in pearl millet (Fe 35-116 ppm, Zn 21-80 ppm), all the millets are rich in protein (6-18%) and fibre content (2-13%). Because of these characteristics, millets are collectively called 'future smart-food crops'. Globally over 479,000 accessions of millets have been conserved in the Genebanks, including sorghum (>259,000 accessions) and pearl millet (>73,000 accessions) which constitute the major portion of the global millets germplasm collections while all the minor millets need focused germplasm-collecting missions to conserve before we lose them forever. The ICRISAT Genebank conserves the largest collections of sorghum (42799), pearl millet (24663), and also global collections of finger millet (7519), foxtail millet (1542), proso millet (849), barnyard millet (749), kodo millet (665) and little millet (473), and distributed over 776,000 seed samples of these crops globally. Germplasm diversity representative subsets such as core and mini-core collections have been established in these crops, which serve as a gateway for use of novel diversity in crop improvement. Extensive evaluation of germplasm and subsets resulted in the identification of promising trait-specific sources for yield, quality (Fe, Zn, Ca, Protein etc.), and stress tolerance (drought, salinity, blast, etc.) traits, and these can be accessed through the ICRISAT genebank (<http://genebank.icrisat.org/>) and Genesys-PGR (<https://www.genesys-pgr.org/>) databases. Minor millets need a focused breeding effort to hasten millets advancement to fulfil the increasing food and fodder demands. With the availability of genome sequences of most millets and germplasm resources, a large-scale high-throughput phenotypic and genomic characterization and trait discovery could support breeding improved cultivars in millets. Researchers can obtain seed samples of millets accessions from the ICRISAT genebank (<http://genebank.icrisat.org/>) following the Standard Material Transfer Agreement.

**Keywords:** Climate change, millets, germplasm

**345 (P-345)**

### **Shrinking forests and dwindling health care plants**

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It is a well-known fact that medicinal and aromatic plants (MAPs) play an important role in health care system. Indian agro-climatic conditions are conducive for the growth of variety of MAPs. Moreover, it is one of the ten most forest-rich countries in the world, hence 70% of MAPs are still exploited from the forests. According to Niti Ayog, presently India has a 21.23% land under forest cover against 33% as recommended in the national forest policy. As per UNFCCC, 48% of deforestation is caused by subsistence farming; 32% by commercial agriculture; 14% by logging, and 23% by wildfires and impacts of climate change. About 275 million people depend on forests for their livelihoods, while MAPs offer the only available treatments to them. The gradual shrinking of forest wealth of the country is a critical problem and now attracting the attention of researchers. Habitat destruction for the export of MAPs lead to severe loss of genetic stock of many of these species. The MoEF has, therefore, notified 29 species including *Rauwolfia serpentina*, *Pterocarpus santalinus*, *Picrorrhiza kurroa*, *Gentiana kurroo*, *Swertia chirayita*, *Nordostachys grandiflora*, *Aconitum spp.* are banned for export. As per IUCN criteria, red listed important MAPs of India are 195. In the present paper, need for drafting a list of MAPs that are categorized as: (a) plants in demand of export value, (b) plants required for manufacture of most important Ayurvedic classical formulations and (c) plants required for processing proprietary medicines. So, the slogan “Wild to cultivation” must be adopted to prevent the depletion of M&AP resources. Several Boards and Councils have been formulated to overcome the problems pertaining to lack of coordination among various stakeholders. Even then, it is necessary to intensify the efforts to conservation (in situ and ex situ) and cultivation. Besides, creation of field gene bank/herbal gardens and imparting training to the farmers as per recommended practices has also been discussed.

**Keywords:** Medicinal and aromatic plants (M&AP), habitat destruction, export

346 (0-27)

### Elucidating the seed storage behaviour of Makhana (*Euryale ferox*)

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*Euryale ferox* Salisb, also known as “Makhana”, “Fox Nut” and “Gorgon nut”, is a nutritionally enriched agricultural crop. Makhana contributes enormously to the income security of farmers belonging to flood affected regions of Bihar and North eastern states of India. Due to production of good quality of makhana seeds and also realizing economic importance, Mithila region of Bihar has got GI status recently. *E. ferox* is a monotypic species in the genus *Euryale* belonging to Waterlily family, Nymphaeaceae. The crop’s aquatic ecological habitat puts forth an apparent non-orthodox implication of its seed storage behavior and there is no supportive scientific evidence for the same. Hence, in this context, this study was undertaken to elucidate the seed storage behavior of *E. ferox*.



Germination in Makhana seeds was studied in six different accessions, under ambient and controlled conditions, with reference to seed moisture content (fresh seeds, 9%, 7%), temperature (ambient, 4°C, -18°C) and germination period (0, 20, 40, 60 days). The initial viability percentage ranged from 75-90%. The moisture testing protocol was standardized and validated to be 130°C for two hours. Since the duration required for standard germination test in Makhana is very high, a quick viability testing protocol was also standardized using Tetrazolium (TTZ) test. It requires 24 hr soaking, followed by staining with 0.1% TTZ at 30°C, for 2 hours. Makhana seeds that were scarified and treated with KNO<sub>3</sub> and GA<sub>3</sub> showed considerably lesser Mean Germination Time (MGT). Germination was superior under submerged condition, (MGT 18 days). We found that seeds can be dried up to 6-7% without loss of viability and also seeds can be conserved for long-term (at -18°C) without losing viability, thus confirming its orthodox storage behavior.

**Keywords:** Makhana, Seed storage, germplasm

**347 (P-347)**

**Studies on seed morphometry and desiccation-freezing tolerance in Indian Madder (*Rubia cordifolia*)**

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*Rubia cordifolia* Linn., commonly known as Indian madder or *Manjishtha*, is a perennial climber species belonging to the coffee family, Rubiaceae. It is distributed across Africa, Asia and Europe. In India, it is found in the state of Kerala, Karnataka, Maharashtra and Tamilnadu. The economic value of *Manjishtha* is due to red pigments extracted from its roots. The red colour of the pigment is due to the presence of an anthraquinone 1,2,4-Trihydroxyanthraquinone, called as purpurin. Root extract is used as textile dye and colourant in paints. Besides, its roots are used in traditional medicines of different countries. In Ayurveda, *R. cordifolia* is used as colorant of medicinal oils and for external application to ulcers, fractures and inflamed areas. A preliminary study on seed morphometric parameters and desiccation-freezing tolerance was conducted on accession IC0637929 to understand the seed storage behavior and optimize a cryo-conservation protocol for the species. The seeds are round in shape with a diameter of around 3.5 mm with a hilum end of 1.3 mm. The thickness of seed coat was found to be 0.69 mm. The initial moisture content of seed was 59.66% and germination percentage of fresh seeds was 70%. Gradual desiccation of seeds on silica gel for 2 h, 4 h, 6 h, 8 h, 10 h and 12 h resulted in a moisture content of 55.82%, 50.33%, 47.32, 18.07%, 12.69% and 10.51%. Viability testing using TTC staining revealed retention of viability up to 18.07% moisture content. Further desiccation resulted in complete loss of viability. The germination percentage of *Rubia cordifolia* seeds at critical moisture content was observed to be 50%. Freezing tolerance studies revealed 37.5% germination of seeds



having a moisture content of 18.07%. These studies indicated the non-orthodox seed storage behavior of *Rubia cordifolia* that needs to be further validated using some more accessions of the species.

**Keywords:** *Rubia*, Indian Madder, *Manjishtha*

**348 (S-10)**

### **Plant Diversity, Indigenous Traditional Knowledge and local food system in achieving Food and Nutritional Security, Sustainability and resilience**

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Plant diversity and indigenous traditional knowledge (ITK) comprise an inimitable universal heritage, and their conservation and utilization are of instantaneous concern. Both play a crucial role in maintaining and enhancing genetic diversity, which reduces agricultural risks, and increases resilience to climate change. Innovation-based ITK provide climate smart alternatives that can significantly increase productivity and incomes, while ensuring sustainability. Plant genetic resources (PGR) are the heritable materials contained within and among plant species, and ITK is the outcome of intellectual practice in a traditional perspective. Both protect biological resilience that exists in a natural way. The problems of food security are of global significance and are further compounded by precedential increase in world population resulting in over-exploitation of genetic resources and diversity. Nevertheless, these resources are lost at alarming rates due to anthropogenic effects such as climate change, pollution, genetic erosion, gross mismanagement and population growth. Traditional knowledge of farmers in conserving and identifying useful biological material, embodied in biotechnological innovations, offers an effective strategy for achieving sustainable food and nutrition security. In order to meet current global challenges, it is obligatory to discover, collect and conserve potentially valuable PGR and traditional knowledge and utilise them sustainably. The CBD is engaged with the genetic erosion and waning use of agrobiodiversity in modern-day agriculture. This is perhaps the most comprehensive intergovernmental agreement concerning for conservation, proper utilization of genetic resources, and giving out the benefits arising out of exploitation in an equitable way. Additionally, local food helps reduce greenhouse gas emissions and contributes to improving carbon footprint. It benefits the local economy, including supporting local farmers and other producers. Concern about the looming accessibility of agricultural production, food and nutrition security, and environmental stability has encouraged the conservation of PGR and indigenous knowledge to the pinnacle of the international development strategies so that local tribes with their native practices facilitate in achieving SDG2, sustainability and resilience.

**Keywords:** Food security, genetic resources, indigenous people, CBD, traditional knowledge

349 (P-349)

**Phenotyping of Brassica germplasm for discovery of resistant sources against white rust (*Albugo candida*)**

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White rust, a serious foliar disease caused by the oomycete, *Albugo candida* is one of the most destructive disease of oilseeds and vegetable Brassica resulting yield losses ranging from 17-60% in India. Keeping potential threat in view the present study was aimed with an objective to identify resistant sources against White rust. Field screening of 62 accessions of *Brassica* under natural epiphytotic conditions of Delhi revealed that five accessions, viz., IC265495, EC206642, EC766193, NDN 125, NDN 126, NDN 128 and one introgressed line, i.e., RBJ 40 were identified as immune to white rust disease. Only three resistant accessions, namely IC313380, EC766136 and EC766164 showed per cent disease intensity (PDI) ranging from 5.00 to 7.50 per cent. Artificial screening of the same accessions under controlled environment was done using inocula i.e., *Ab-Del* (Delhi isolate) and *Ab-Png* (Pantnagar isolate) of *A. candida*. After 8-12 days of incubation, symptoms were observed and disease severity was recorded. More or less similar patterns were observed with some deviations at both the crop stages against both the isolates. Out of 62 accessions, five were observed with resistant reaction at cotyledonary stage showed PDI ranging from 2.50 to 10.00 and 5.00 and 10.00 per cent against *Ab-Del* and *Ab-Png* isolates, respectively. Whereas, PDI at true leaf stage ranged between 5.00 and 10.00 per cent against both the isolates. Since developing resistant varieties is the most effective and economically viable strategy for disease management. Therefore, all the accession identified as immune/ resistant could be utilized as resistant donor in crop improvement programme for developing resistant/high yielding varieties and also for mapping and tagging resistance genes against *A. candida*.

**Keywords:** Germplasm, Phenotyping, Brassica, White rust, Resistance

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