BOOK OF ABSTRACTS

National Seminar on

Plant Biodiversity for Food, Nutrition and Health Security in North-West Himalayas (PBFSNWH)

Shoolini University
Village Bajho, PO Sultanpur,
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November 27-28, 2023

National Seminar on Plant Biodiversity for Food, Nutrition and Health Security in North-West Himalayas (PBFSNWH)

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PREFACE

We are delighted to present the Book of Abstracts of the **National Seminar on Plant Biodiversity for Food, Nutrition and Health Security in North-West Himalayas (PBFSNWH),** held during Nov. 27-28, 2023. This event is projected to provide a roadmap to enhance food and nutrition security for improved health through optimal, efficient and sustainable use of Himalayan agro-biodiversity using innovations through interdisciplinary and inter-institutional scientific collaboration, as well as for ensuring enabling policies to conserve, use and mainstream the Himalayan agrobiodiversity for increased food and nutritional security and improved health of the people in Indian Himalayas.

The National Seminar comprises five Technical Sessions with >50 keynote/ invited lectures and oral presentations and >50 posters, one Plenary Session, an evening lecture and a Valedictory Session.

This publication carries abstracts based on the status of plant biodiversity in the N-W Himalayan region, their production potential, the current status of research relating to genetic improvement, their conservation through use, nutritional and medicinal values, value chain options, socio-economic dimensions (consumption pattern, cost and affordability), and enabling policy support relating to their promotion as alternative sources of food, nutrition and health security.

The abstracts included here offer a holistic view of the work in the area of PGR management in the North-West Himalayas. The Organizers acknowledge the contributors for the submission of the abstracts and the editors for compiling the publication by racing against time. It is hoped that this collation will be useful for students, faculty and researchers working in this area.

Core Organizing Committee

ACKNOWLEDGEMENTS

The National Seminar on Plant Biodiversity for Food, Nutrition and Health Security in North-West Himalayas (PBFSNWH), is a great opportunity for us, as both organizers and participants, to share mutual experience in such an important field of PGR management in North-West Himalayan region.

The delegates (> 175) comprise participants from the Indian Council of Agricultural Research (ICAR) and its varied crop-based institutes, Alliance for Bioversity International and CIAT, Central and State Universities, Council for Scientific and Industrial Research (CSIR) and Defence Research and Development Organization (DRDO), Himachal Pradesh State Government agencies, private stakeholders, progressive farmers and entrepreneurs etc.

We would like to express our sincere gratitude to Padma Bhushan Dr R.S. Paroda, President, ISPGR, for extended discussions and valuable suggestions. Support and encouragement by Dr Himanshu Pathak, Secretary, DARE and Director General, ICAR; Dr Trilochan Mohapatra, Chairperson, PPV&FRA; Dr Sanjay Kumar, Chairperson, ASRB are greatfully acknowledged.

Dr P.K. Khosla, Chancellor, and Dr Atul Khosla, Vice-Chancellor, Shoolini University, Solan, are profoundly thanked for the excellent technical and administrative support provided for organizing this Seminar. We also thank for the valuable suggestions and support by Dr Gyanendra Pratap Singh, Director, ICAR-NBPGR, New Delhi.

Special thanks to Dr P.L. Gautam, Chancellor, RPCAU, Pusa, Dr R.K. Tyagi, Vice President, ISPGR, Dr J.C. Rana, Country Representative, Alliance for Bioversity International and CIAT, New Delhi, Dr Mohar Singh, OIC, ICAR-NBPGR, Shimla, Dr Saurabh Kulshreshtha, Dean, Shoolini University for their critical inputs in developing the technical program and other support.

We duly acknowledge the financial support provided by Alliance for Bioversity International and CIAT, New Delhi, Protection of Plant Varieties and Farmers Rights Authority (PPV&FRA), New Delhi, Mahyco Pvt Ltd., H.P. State Council for Science Technology and Environment (HIMCOSTE), Shimla, Satluj Jal Vidyut Nigam (SJVN), Shimla, National Bank for Agriculture and Rural Development (NABARD), and Ambuja Cement Foundation. Knowledge partners are gratefully acknowledged especially Trust for Advancement of Agricultural Science (TAAS), New Delhi, CSKHP Krishi Vishwavidyalaya (CSHPKV), Palampur, Dr YS Parmar University of Horticulture and Forestry (YSPUHF), Solan,

We place on record the assistance received from the Core Organizing Committee, Local Organizing Committee, Technical Session Co-Chairs, Conveners and Rapporteurs, Poster Session Convener and Co-convener, for the smooth conduct of the Conference.

We express our sincere appreciation to public and private sector partners for joining hands with us in this endeavour. We draw our strength from the support of colleagues from different participating institutes in this Seminar. 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.

November 24, 2023 **Editors**

Abstracts

of

ORAL PRESENTATIONS

Technical Session - I

Status and Management of Plant Biodiversity of North-West Himalayas (NWH)

TSI-OP-01

Expedition of PGR diversity in North Western Himalayas of India

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The North Western Himalayas are spread in Himachal Pradesh, Jammu and Kashmir and Uttarakhand states of India. The region is enriched with plant diversity in cultivated as well as wild plant species. Systematic collection of PGR wealth of 53 accessions of different crops and crop wild relatives collected from remote and unexplored areas of this valley during 2021-22. Black gram, cowpea, French bean and wheat were collected from underexplored areas of this valley region of Kangra, Una (Himachal Pradesh) and Udhampur (Jammu and Kashmir). Of these, 14 unrepresented taxa belonging to minor economic groups were collected for the first time from the state of Jammu and Kashmir. Important collections were made in *Phaseolus vulgaris* [French bean] (04), *Vigna mungo* (05), *Sesamum indicum* (01), wheat landraces (06) and vegetables (14) with remarkable variability. Such valuable and unique germplasm can be utilized in future crop improvement programmes.

Keywords: Plant genetic resources, Diversity, North Western Himalaya

TSI-OP-02

Ampelographic characterization of grape genotypes from Himachal Pradesh

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For the first time, an exhaustive survey for collection, documentation, geotagging and characterization of grape genotypes was conducted in Kinnaur and Solan districts of Himachal Pradesh. The surveys were conducted in the areas spread between 30.840908 to 31.764121 °N (latitudes); 77.062697 to 78.593155 °E (longitudes); and 1188 to 2822 msl (altitudes) to collect 163 grape genotypes. For morphological characterization, 24 OIV descriptors were used to develop an ampelographic database of collected genotypes from Himachal Pradesh. Among them 17 were qualitative descriptors and 7 were quantitative descriptors. The first five axes of the PCA plot explained 56.67 % of the total morphological variation in the population. Phylogenic analysis separated all genotypes into two major clusters A and B having 65 and 98 genotypes, respectively. Both these clusters included genotypes from Kinnaur and Solan districts indicating that, there was no association of genetic diversity with geographic distribution and there might have been exchange of planting material among farmers of these two districts. Biochemical analysis was also conducted in 53 grape genotypes for 9 biochemical parameters. Anthocyanin, phenols and tannins were observed to be more in wild genotypes followed by genotypes having coloured berry skin and flesh. Biochemical evaluations of different genotypes from different elevations indicated low to significant +ve correlations between elevation, TSS, TA, carbohydrates, reducing sugars and phenols.

Keywords: Ampelographic characterization**,** Grape genotypes, Distribution, Biochemical parameters

TSI-OP-03

Interventions for conservation, productivity enhancement and nutrient assessment of medicinal and edible forest species

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Himachal is in a mountainous western Himalayas state which covers an area of 55,673 square kilometers. Most of the state lies on the foothills of the Dhauladhar Range. Himachal experiences three seasons: summer, winter, and rainy season. Summer lasts from mid-April till the end of June and most parts become very hot 28 to 32 °C (82 to 90 °F). There lower Dhauladhar Range is an abode of variety of trees with multiple produce. These not only sequester carbon but also yield many products for the lively hood of the people of rural and urban areas. Species like harar, baheda, aonla, lasura, kathal, dheu, jamun, reetha neem, tejptta etc. have good scope in the conservation of forests and lively hood enhancement. The studies were conducted at Regional Horticultural Research and Training Station, Jachh situated at 400 m above msl to standardize the modern techniques to conserve, propagate and multiply the rare and on the verge of extinction germplasm of these species. The techniques have been tried and standardized first time at this station to propagate the superior germplasm of above stated species. The survey of *Codia myxa* was conducted in the state to identify the superior genotypes and five strains with higher nutrient value and productivity were identified and mass technology to propagate at a faster rate was standardized. The species was adopted by the farmers as a crop and the fruit availability increased up to 20 per cent within four years and the quality planting stock demand increased from few hundred to 5000 thousand per year with in the span of the four years. Nutrient studies were conducted on the species to assess their nutritional value. *Cordia myxa* fruits and leaves exhibited a substantial amount of phenolics in the range of 9.65−26.22 mg GAE/g and 5.35−33.28 mg GAE/g, respectively, followed by appreciable flavonoid content. Higher antioxidant activity was detected in Shahpur leaf extract (SLE) (IC50ABTS 0.27 mg/mL) and Raja ka Talab fruit extract (RFE) (IC50ABTS 0.21 mg/ml) among different harvesting locations of C. myxa. A higher amount of vanillic acid and rutin was detected in Nagrota Surian fruit extract (NFE) by ultra-performance liquid chromatography quadruple time-of-flight ion mobility separation (UHPLC-Q-TOF-IMS) Similarly the Terminalia chebula improved stocks developed at the RHRTS, Jachh are being planted at the farmer's field and the farm productivity is increasing from the marginal lands. Because of this the germplasm which otherwise would have been lost is conserved and transplanted at the farmer's field to get early, high-value produce and production at the shortest possible time.

Keywords: Conservation, Productivity enhancement, Nutrient assessment, Edible forest species

TSI-OP-04

Reaching the unreached farming community through recent extension methods

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Agriculture has been the backbone of the Indian Economy and is a source of livelihood for a large chunk of the population. Though agriculture production has increased manifolds during the last six decades yet there is still a wide gap exists between the technology generated at the research station and its adoption by the farmers. There is no dearth of farm technologies generated by scientists but hardly 40 to 50 per cent of these technologies have reached the farmers' fields. To reach the farmers particularly small and marginal which constitute a large chunk of a farming community, an extension-workers needs to update his/her knowledge about the improved/ modern extension methods so that the same can be properly utilized in the task of transfer of farm technology. Most of our farmers have limited and fragmented land holdings. How to enhance production and income from this limited land holding is a challenge for our scientists. Diversification of agriculture and generating additional income from the allied enterprises like, floriculture, sericulture, poultry, apiculture, dairy, piggery, fishery, sheep & goat rearing, mushroom cultivation, horticulture, agro-forestry etc. is the only solution for doubling the income of farmers-a cherished dream of our Prime Minister. However the farmers need scientific information/ technical guidance with motivation to initiate these enterprises which can be possible only through well-planned and systematic extension approaches. Nowadays, a farmer is just like an entrepreneur who needs recent information on various aspects of agriculture and allied fields. In the present era of globalization, farmers will

have to transform themselves from mere producers in domestic markets to sellers/exporters in the global markets with a focus on high productivity, high-quality produce and low cost of production. The revolution in information and communication technology has made this task of transfer of technology quite easy and hence, the technical information can now be provided quickly by the extension workers in a cost-effective manner even without personally visiting the farmers. Various cost-effective and extension methods like Expert Systems, E-mail, Internet Browsing, Audio-Video Conferencing, Kisan Call Centres, Agri-clinics, Agri-business centres, Community Radio, SATCOM Networks etc. have been discussed along with a conceptual model developed by the authors for motivating the farming community to adopt these enterprises to improve their socio-economic status in the society.

Keywords: Farming community, Agriculture, Indian Economy, Livelihood

Technical Session-II:

Traits Discovery and Genomics in Plants of NWH

TSII-OP-01

Characterization and core set development of Amaranth using high-density 64K SNP Array

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Amaranthus hypochondriacus, a gluten-free pseudocereal commonly known as grain amaranth, native to the New World, has acquired increased attention due to its agronomic versatility, adaptability, and nutritional attributes as compared to cereal grains. It is considered a super food or millennium crop as it contains high-quality seed protein, unsaturated oils, tocopherols, flavonoids, dietary fibre, phenolic compounds, vitamins, and minerals. Amaranth can play a prominent role in food and nutritional security. Consequently, the gene pool of this significant crop needs to be characterized and genotyped to broaden its genetic base and enhance production. The functionality of the Single Nucleotide Polymorphism (SNP) markers in demonstrating the genomic structure of Amaranth genotypes offers valuable insights into the conservation, management, and utilization of Amaranth germplasm. A high-density SNP array technology provides an efficient method to analyze the genotypes of multiple loci in the whole genome scale. Here, we report the characterization of 917 amaranth genotypes and developed a core set (112 accessions) using an in-house developed 64K SNP array. Population structure analysis using quality-filtered 24,023 polymorphic SNP markers resulted in two subpopulations among the Amaranth accessions. Phylogenetic and principal component analysis showed clustering of genotypes irrespective of their geographical origin. Polymorphism Information Content and Minor Allele Frequency were observed in a range from 0.09 to 0.38 and 0.05 to 0.5 with a scoring mean of 0.23 and 0.15 across the genome respectively. Estimated Nei's genetic diversity index is 0.23 signifying high genetic variation within the population. The core set genetic diversity pattern corresponds to that of the whole population diversity pattern suggesting the reliability of the core set as the representative population of 917 genotypes for further genome-wide association studies and marker-assisted selection in crop breeding programs.

Keywords: Characterization, Core set, Single Nucleotide Polymorphism, Marker-assisted selection

TSII-OP-02

Search of novel donor germplasm for powdery mildew resistance in wheat minicore

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Developing effective and durable host plant resistance is crucial for controlling powdery mildew, a devastating disease caused by *Blumeria graminis* f. sp. *tritici* (Bgt). Smaller and diverse set from genebank serves the purpose of comprehensive and multi-environmental evaluation and identify novel and reliable source of resistance. In the present study wheat minicore comprised of 224 accessions developed at NBPGR were used for powdery mildew evaluation in augmented block design to identify sources of powdery mildew resistance. This minicore comprised three species of wheat, *Triticum aestivum* (162), *T. durum* (54) and *T. dicoccum* (8) were screened at the hotspot locations at two locations of Himalayan regions (Palampur and Almora) and one location of peninsular region, Wellington. Among the wheat species germplasm screened, 66 of *T. aestivum* (46%), 25 of *T. durum* (22%) and 5 of *T. dicoccum* (62%) were found to be resistant to PM with scores of 0 or 1. These accessions were also screened under controlled conditions at CSKHPKV, Palampur and promising accessions were subsequently screened for validation purposes. Based on screening under multi-location hot spots, we identified 15 accessions resistant to yellow rust, black rust and brown rust IC574388, IC539317, IC574476, IC554661, IC122726, IC527448, IC290195, IC582717, IC531969, IC532584, IC534538, IC464099, IC549388, IC128664, IC539267. Thus, wheat minicore proved to be a useful set for screening germplasm for searching novel multiple disease-resistant donors. The presence of PM resistance genes in these resistant accessions needs to be confirmed using molecular markers. The resistant accessions identified in the study will enhance the existing gene pool for PM resistance in wheat and will serve as a potential source for PM resistance in wheat.

Keywords: Novel donor germplasm, Powdery mildew, Resistance, Minicore

TSII-OP-03

Identification and development of yellow rust resistant sources in wheat using conventional, molecular and doubled haploidy breeding

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Wheat yield is affected by a plethora of biotic stresses, among which rusts are one of the most devastating fungal diseases causing severe losses and imperilling global food security. The worldwide prevalence of wheat yellow rust (*Puccinia striiformis* Westend. f. sp. *Tritici*) and its potential for long-distance migration and invasions into new areas may peril global food security. Protection from yellow rust requires the ingression of the resistant sources and their cultivation, which is a cost-effective and environment-friendly approach. Many wheat varieties have been released imparting resistance. However, conventional breeding is laborious, time-intensive, environment dependent, requires glasshouse and sometimes can lead to obscure results. Since, in conventional wheat breeding programmes, the isolation of homozygous and homogeneous breeding lines usually takes 6-7 years due to the requirement of several cycles of inbreeding and selection. This phase of breeding is most tedious, time-engrossing and expensive, thereby significantly delaying the cultivar development process. Hence, a need for speeding up the varietal development process by supplementing/complementing conventional breeding with biotechnological tools is highly anticipated. For this, the generation of doubled haploid (DH) plants and the use of molecular breeding tools are a boon. Molecular approaches and Doubled haploidy techniques via. cylindrica mediated chromosomal elimination techniques are used for gene identification, varietal improvement and development of new genetic stocks resistant to yellow and leaf rust diseases of wheat. By using Doubled haploidy technique, the DH-1 (HS 542 / China 84-40022), DH-4 (HD2997/KLEE/BER/2*FL8/DONSK-POLL), DH-7 (Jingdong X FLW3) and DH-8 (Jingdong X VL829) have been developed and were found to be resistant to yellow rust and brown rust at the seedling stage.

Apart from these, DH-1, DH-2, DH-4, DH-14, DH-15, DH-16 and DH-18 have also shown resistance to yellow rust at rust hot spots Dhaulakuan, Bajaura and Shimla at Adult Plant Stage. These DH are the potential future Genetic stocks for the rust resistance breeding programme of wheat in India. One doubled haploid line developed via this technique i.e. DH-1 (HS 542 / China 84-40022), a yellow and brown rust resistant genetic stock has been registered at NBPGR, New Delhi vide INGR 21119. DH-1 is resistance to all the prevailing pathotypes of stripe and leaf rust in the seedling stage (except for the 77-5 race of leaf rust) and is also resistant to both the rust in the adult plant stage. Therefore, conventional breeding supplemented with the molecular and doubled haploidy technology are highly efficient technologies for yellow rust resistance wheat breeding programmes.

Keywords: Yellow rust resistant, Conventional, Doubled haploidy breeding

TSII-OP-04

Morphological characterization of magic population reveals extensive genetic variation for morpho-physiological and yield-related traits in bread wheat (*Triticum aestivum* L.)

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MAGIC (Multi-parent advanced generation inter-cross) population provides a greater allelic polymorphism than the bi-parental crosses and enables a higher resolution mapping of complex quantitative traits. It has been effectively implemented in many agricultural crops. Bread wheat (*Triticum aestivum* L.) is one of the most important staple food crops and is vital for the food security of the global human populace. In bread wheat, a 5-parent MAGIC population was morphologically characterized using 23 morpho-physiological and yield-related traits. The MAGIC population consisting of 510 RILs (Recombinant inbred lines) were phenotyped under late (sown in mid of December) and extreme late (sown in mid of January) conditions for two consecutive *Rabi* seasons of the years 2021-22 and 2022-23 to dissect genetic variation under heat-stress. The morphological evaluation of MAGIC lines under late sown condition showed a wide range of variation for chlorophyll content index (CCI; 18.4 - 42.7), NDVI (0.39 - 0.77), plant height (PH; 55.7 - 146.8 cm), flag-leaf length (16.7 - 33.0 cm), flag-leaf width (1.6 - 2.7), spike length (8.2 - 15.6 cm), number of spikelet per spike (NSS; 15.2 - 24.0), thousand-grain weight (TGW; 24.1 - 50.5 g) and number of grains per plant (NGP; 226.5 - 692.1). However, under extremely late conditions, there was a significant reduction in all the traits with a maximum of up to 50.9% in TGW, 55.5% in CCI and 69.7% in NGP. Under extreme late conditions, the traits also showed a wide range of genetic variation viz., CCI (13.8 - 31.3), PH (44.5 - 131.8 cm), TGW (14.9 - 47.6 g) and NGP (82.6 - 483.3). TGW showed highly significant associations with grain width, grain length and NGP under both late and extreme late sown conditions. These MAGIC lines would provide useful germplasm resources with diverse allelic combinations offering a greater chance of detecting QTLs for different traits with enhanced precision.

Keywords: Morphological characterization, Magic population, Genetic variation, Yield-related traits

TSII-OP-05

Genome-wide association mapping of grain quality traits in rice using single-locus and multi-locus models

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Grain appearance and quality are crucial agronomic traits to meet the market acceptance of rice. Mining putative grain quality-related genes has been geared towards developing effective rice breeding approaches. Genome-wide association studies (GWAS) have become a powerful tool for dissecting complicated polygenic traits. Here, based on 5,53831 filtered SNP markers of a subset of 3K-RGP consisting of 198 rice accessions, we employed

GWAS for three grain quality traits using two single-locus models (MLM and CMLM), and three multi-locus (mrMLM, FASTmrMLM, FASTmrEMMA) models. 594 SNP markers were detected in overall by the MLM associated with grain quality-related traits.70 significant quantitative trait nucleotides (QTNs) were also detected across ML-GWAS models to be associated with grain aroma (AR), head rice recovery (HRR, %), and percentage of grain with chalkiness (PGC, %). mrMLM detected the maximum QTNs (65), followed by FASTmrMLM (37) and FASTmrEMMA detected the lowest number of QTNs (10). Finally, 39 common QTNs were simultaneously discovered by both single and multi-locus models. Of these 39 significant QTNs, 20 novel QTNs were discovered for the above-mentioned three quality-related traits. Gene annotations and previous studies unravelled four functional candidate genes *viz.,* LOC_Os01g66110, LOC_Os01g66140, LOC_Os07g44910, and LOC_Os02g14120 that might be closely related to AR, HRR (%), and PGC (%) in rice. These QTNs, haplotypes and putative CGs for grain quality provide invaluable resources for cultivating novel varieties with improved rice quality in the future.

Keywords: Association mapping, Grain quality, Multi-locus models

TSII-OP-06

Mapping and mining of major genomic regions conferring resistance to Bruchid (*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). It is a notorious storage grain pest that can cause full damage to seeds if not adequate care is undertaken during the storage period. In India, *C. maculatus* causes more yield loss up to 80 - 90%. The present study was employed in an F_2 bi-parental mapping population derived from a cross between susceptible (MDU 1) and resistant (TU68) genotypes. Phenotyping was carried out under an artificial bruchid screening procedure. QTL analysis was employed using QGene 4.4.0 software. The possible candidate genes associated with bruchine resistance were predicted using candidate gene analysis. 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 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 *qbr_Dev.T.* It explained 17.01 % of R^2 with an 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 bruchid resistance breeding program. Genome mining on the QTL regions harbours several possible candidate genes related to defence 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 the bruchid resistance breeding program.

Keywords: Mapping, Mining, Resistance, QTL

TS2-OP-07

Molecular and tepal morphology in delineating vegetable *Amaranthus* species complex conserved in Indian National Gene Bank

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Leafy vegetables are the most important component of the human diet. They are a rich source of vitamins and minerals, particularly the iron content. Consumption of leafy vegetables from cruciferous member is well known. However, leafy vegetables like leafy amaranthus are consumed seasonally and semi-domesticated. Though the consumption of vegetable amaranthus has increased in the past decades, the research and development on improving their quality and other agronomical traits are still not comparable with other leafy vegetable crops. The main reason behind the lack of development as a promising crop is frequent hybridization

and variation exhibits in different environmental conditions resulting in the description of more than 13 species of vegetable *Amaranthus* based on habit and geographical isolation. For effective utilization of these species for improvement programs, the identity of species needs to be clear. In the present study tepal morphological and sequence of nuclear ITS (inter-transcribed region) were used to identify and delineate 30 accessions of non-designated vegetables *Amaranthus* species from the National Gene Bank of ICAR- NBPGR. A morphological study revealed that the lanceolate shape of the tepal and acuminate tip belongs to the species *A. tricolor,* whereas the ovate shape and acute tip belong to *A. blitum*. DNA-based barcoding using ITS sequence was used to establish the identity as well as the relationship between vegetable *Amaranthus* species. An average of 634 base pairs for each accession were generated which includes ITS1, 5.8S and ITS 2. With the combined analysis of *A. tricolor* and *A. blitum*, the sequence alignment showed 8 parsimonious informative sites which are the key sites that differentiate these two species. The ITS1 and ITS2 shared 4 sites each of the parsimonious sites. The neighbor joining tree constructed based on the Juke-Cantor substitution model showed a clear-cut grouping of *A. blitum* and *A. tricolor* accessions. The known taxonomic variety described under *A. tricolor* and *A. blitum* based on habit may not appropriate character for diagnostic, however, the variation showed in the DNA barcode led to the scope of further studies in this vegetable *Amaranthus* complex.

Keywords: Bar coding, ITS region, Leafy vegetables

Technical Session-III:

In situ/on-farm, *ex-situ* Conservation and Access and Benefit Sharing

TSIII-OP-01

Ex-situ conservation of wild *Allium* genetic resources at ICAR-NBPGR, Bhowali field genebank

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Allium is one of the largest genera in the family Amaryllidaceae with approximately 800 species worldwide. Out of which, 45-50 species have been naturally distributed in the Indian Himalayas at the high altitude regions including cold desert and humid alpine regions 3000m above mean sea level. At high altitude of the Himalayas local populace collect bulbs, leaves as well as flowers from forest/meadows and uses them as food seasoning spice, green vegetable, culinary herbs and medicine. During the last decade explored north western Himalaya including Uttarakhand, Himachal Pradesh, Jammu & Kashmir and Ladakh and collected 62 accessions of 15 different wild *Allium* species and conserved *ex situ* in field gene bank at ICAR-NBPGR Regional station Bhowali. For the collection of wild *Allium,* we explored Niti valley, Darma valley, Byas valley, Nelang, Saryu valley, Bhuyandar valley, Gangotri, Tungnath and Pindar valley of Uttarakhand while Peer Panjal (Reasi and Udhampur), Bani-Kathua and Kishanganga valley of Jammu & Kashmir. During the exploration economically important species namely *Allium victorialis*, *A. stracheyi, A. wallichii, A. humile* were collected from the humid alpine zone of Uttarakhand while *A. negianum, A. carolinianum* and *A. perzwaskianum* from cold arid zone of Uttarakhand. Whereas, *A. consanguianum* and *A. roylei* were collected from the Peer Panjal area and *A. farctum*, *A. chitralicum* from Kishanganga valley of Jammu & Kashmir province. Herein from Ladakh collected *A. przewalskianum, A. schoenoprasum, A. barszczewskii* and *A. tuberosum*. For the conservation, ICAR-NBPGR followed three different methods seed gene bank, *in vitro* gene bank or Cryo-gene bank and field gene bank. In the case of seed gene banks, *Allium* seeds are orthodox but show short seed viability so need adequate conservation techniques whereas medium to long-term *In vitro* conservation needs proper strategies and protocol for conservation. At Bhowali station live material of 62 wild *Allium* germplasm from western Himalaya are conserved in the field genebank and supplied for the research to various indenters in the country.

Keywords: Ex situ conservation, *Allium*, Genetic resources, Field gene bank

TSIII-OP-02

Conservation of wheat and barley genetic resources of North-Western Himalayas in the National Genebank

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Genebanks are the repositories of unique genetic resources and they conserve novel sources of genetic diversity that contribute significantly to crop improvement. Cereals form the staple diet for almost the entire global population and constitute more than 50% of the world-wide crop production. The North-Western Himalayan belt comprising Himachal Pradesh, Uttarakhand, Jammu & Kashmir and Ladakh UT, is one of the richest diversity hotspots of our country and is also the most vulnerable to habitat loss due to the extremely fragile ecosystem. Hence, ex-situ conservation of the genetic resources of this agro-ecological zone is of high priority. The National Genebank of India, located at ICAR-National Bureau of Plant Genetic Resources is the second largest genebank in the world and it conserves ex- situ collections of all crops representing diverse ecologies. The genebank currently has 4791 accessions of wheat and barley genetic resources from the north-western Himalayan states, which includes a total of 18 species. 345 accessions of crop wild relatives, mainly *Elymus* spp., are conserved in this group. Amongst them, the unique accessions of wild triticeae (Elymus & Leymus) from Ladakh and *Aegilops tauschii* collected by NBPGR explorers from the cold desert of Jammu & Kashmir are novel sources of resistance against drought and pests. The collection also has landraces/farmers' varieties that were grown locally in specific ecological niches for centuries and hence are a gold mine for resilience genes. Safed Mundri, Lal Mundri, Naphal, Mundiya, Safed Misri, Jhusia, Dhaulia, Gerua, Satti and Munda Gehun are some of the prominent ones conserved in NGB. Barley diversity is also well represented and wild accessions of *Hordeum vulgare* ssp *himalayense* have been collected and conserved from J&K. Some 400 unique barley landraces including naked barley are part of the *ex-situ* collection.

Keywords: Conservation, Genetic resources, North-Western Himalayas, National genebank

TSIII-OP-03

Conservation and characterization of Protected Farmer's Varieties of apricots in cold arid regions for future breeding programmes in Kargil (UT-Ladakh)

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Kargil is always known for its quality apricots and rich genetic bio-diversity existing in the region. The available genetic biodiversity has been documented by various researchers, but very little work has been done on the conservation of these elite germplasm within or outside the region. Due to one insect menace of Codling moth, there was a complete ban on the export of fresh fruits from Ladakh and farmers were compelled to dry their fresh produce apricots before exporting it out of Ladakh to have some monetary benefits otherwise which was going to be waste as the processing capacity of the farmer or region was not up to the mark. The suitable drying type known to the farmers to date was Halman and farmers converted their orchards to Halman in the recent past so that the available variability in their farms could be put to some income generation. This practice in the region was causing serious extinction of elite germplasm diversity. The present task was undertaken by the MARES, Kargil to conserve thirty varieties of farmers which were identified and registered by the PPV&FRA, New Delhi in collaboration with CITH, Srinagar. These varieties were characterized as per the DUS guidelines and are being conserved at MAR&ES, Kargil farm. The author conducted the survey of the area and collected the scion wood of these thirty varieties, collected the seeds and grafted these varieties at MARES farm. The grafted accessions are ready for field transplantation. These varieties have some peculiar characters and on account of this, these varieties have been registered as elite among the existing varieties. Some of these varieties have better resistance against erratic weather, pests and diseases and better TSS & yield potential. Efforts are also being made to identify drying types and short-statured canopy spread accessions. The dwarfing types can be utilized in the concept of high-density planting as there is no dwarfing rootstock available in Apricots. The conservation of these accessions in the form of reference blocks will be of great importance in future breeding programmes.

Keywords: Conservation, Characterization, Protected farmer's varieties, Apricot, Cold arid region

TSIII-OP-04

In vitro regeneration and freezing behaviour for cryopreservation in walnut winter buds

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Walnut is a temperate nut crop of the world. *In vitro* protocol was standardized using dormant buds as explant in *Juglans regia.* Explants were cultured on Murashige and Skoog (MS) and DKW medium supplemented with different concentrations/combination(s) of phytohormones. BAP (0.5 mg l^{-1}) showed a very good response in shoot initiation as well as shoot induction and took less time for bud sprouting. Maximum shoot induction (80%) and earliest bud sprouting (17 days) were observed for dormant buds in DKW medium supplemented with 0.5 mg l^{-1} BAP followed by 1.0 mg l^{-1} BAP and 0.1 mg l^{-1} TDZ. In the MS medium, the highest shoot induction (50%) was found in BAP (0.5 mg l^{-1}) and TDZ (0.1 mg l^{-1}). Minimum shoot induction (10%) was observed for dormant buds in MS medium supplemented with 1.0 mg l^{-1} TDZ. BAP showed higher shoot induction with DKW as well as MS medium. MS basal medium showed the lowest shoot induction and took the longest duration. Cultures showed very poor response for rooting in all combinations of PGRs. Rooting is a great problem for the walnut cultures. It needs further experimentation for improvement of the protocol. The protocol developed would be of great use for mass propagation of walnuts and also support *in vitro* conservation. The freezing behaviour of the walnut dormant bud was examined using scanning electron microscopy (SEM) and light microscopy. All living cells in bud tissues showed distinct shrinkage without intracellular ice formation as a result of slow cooling (5°C/day) of dormant buds to -30°C through SEM. However, the re-crystallization of these slowly cooled tissue cells after LN and then re-warming to -10°C confirmed that some of the cells in the apical meristem lost freezable water with slow cooling to -30°C, indicating adaptation of these cells by deep super cooling. Deep supercooling could not occur in dormant bud primordia if xylem vessels formed a continuous conduit connecting the dormant bud primordia with the remainder of the plant. If xylem continuity was established, ice could propagate via the vascular system and nucleate the water. It is concluded that no extracellular ice crystals accumulated in such tissues containing deep supercooling.

Keywords: In vitro regeneration, Freezing behavior, Cryopreservation Walnut, Winter buds

TSIII-OP-05

Advanced methods of conservation of plant biodiversity

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Plant biodiversity is a term used to describe the variety and variability of plant species, both within a specific ecosystem or on a global scale. It encompasses the different types of plants, such as trees, shrubs, herbs, grasses, and more, and the genetic diversity within these species. It offers a variety of essential raw materials and helps to spread new genetic knowledge that is beneficial for breeding programmes, creating more productive crops and plants that are quite resilient to biological and environmental challenges. Mountain habitats are focal points for plant conservation initiatives because they include a significant proportion of endemic species in addition to a high level of total plant variety as communities alternate along altitudinal and climatic gradients. In-situ and ex-situ are the two basic categories into which many conservation techniques can be grouped. Ex situ (off-site) conservation involves keeping genetic resources outside the natural ecosystem in which they exist, whereas in situ (on-site) conservation keeps genetic resources inside the ecosystem in which they are found. Maintaining and managing protected areas, as well as taking activities that are aimed at the species and population level, are all part of the complicated and varied process of conserving plant species in situ. The presence and persistence of species in protected areas as a gauge of conservation have received the majority of attention to date. Ex-situ conservation is a method of protecting all levels of biological diversity outside their natural habitats using various techniques such as botanical gardens, sanctuaries and genebanks. Limitations of ex-situ conservation include keeping organisms in artificial habitats, loss of genetic diversity, inbreeding depression, adaptation in

captivity, and accumulation of deleterious alleles. Hence, there is a need for new advanced methods of conservation of plant biodiversity.

Keywords: Conservation, Plant biodiversity, Genebanks

Technical Session-IV:

Plant Biodiversity and Local Food Systems

TSIV-OP-01

Evaluation of potato germplasm in early crop season

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Potato (*Solanum tuberosum* L.) is the most consumable vegetable crop among the vegetables and the third most important non-cereal crop after wheat and rice. It belongs to the family Solanaceae with chromosome number 2n=48. It is utilized throughout the year in India in different ways and due to its great utility, the potato is known as the "King of Vegetables". In the present investigation, fifty potato germplasm accessions including 13 varieties were evaluated for tuber yield and yield components at 75 days in early crop season at ICAR-Central Potato Research Institute, Regional Station, Modipuram, Meerut during 2022. The observations were recorded on germination (%), plant vigour, foliage maturity, marketable tuber no./plant, total tuber no./plant, marketable tuber yield (g/plant), total tuber yield (g/plant), hopper burn infection (%), mite infection (%) and tuber traits. Significant differences were recorded among the genotypes for tuber yield and tuber attributes like plant vigour (1-5 scale), foliage maturity (1-5 scale), tuber colour, tuber shape, eye depth and flash colour. Germination (%) ranged from 53-100% and 42 genotypes had 100% germination. The very good plant vigour was found in CP3085, K. Surya, K. Mohan, K. Arun and K. Lima. The results on foliage maturity reflected CP1648 and CP3288 to be early maturing. The total tuber yield (g/plant) ranged from 26-267g/plant and high total tuber yield was recorded in K. Lima (267g) followed by K. Arun (255g), K. Ganga (241g), K. Mohan (214g), K. Garima (212g), K. Lalit (208g), K. Lalima(174g) K. Sindhuri (155g), K. Pukhraj (152g) and K. Neelkanth (149g). The marketable tuber yield (g/plant) ranged from 11-257g/plant and high marketable tuber yield was found in K. Lima (257g) followed by K. Arun (233g), K. Ganga (217g), K. Mohan (198g), K. Garima (195g), K. Lalit (170g), K. Lalima (152g), K. Sindhuri (136g), K. Neelkanth (129g) and K. Pukhraj (128g). The total tubers/plants ranged from 3-11 and the highest tubers/plants were recorded in K. Sindhuri, CP3353 (11), CP3385, K. Lalit, CP1648, K.Lalima (9)CP3469 (8), K. Ganga (7), K. Sindhuri, K. Neelkanth and K. Lima. The marketable tuber/plant ranged from 1-5 and the highest marketable tubers/plant was recorded in K. Lalit, K. Lalima, K. Lima, K. Sindhuri, K. Ganga (5), K. Garima, K. Mohan, K. Neelkanth, CP3469, CP3421, K. Pukhraj (4). The incidence of hopper burn ranged from 0-100% and only potato variety K. Garima was found highly tolerant with 0% hopper burn incidence, however genotypes namely CP1471, CP16930, CP1648, CP3085, CP3353, CP3385, CP3437, CP3438, CP3464, CP3469, K. Surya, K. Mohan, K. Lima, K. Lalima, K. Ganga and K. Arun with 20% hopper burn were also found tolerant. All 50 genotypes were found highly tolerant with 0% mite damage incidence. On an overall basis, only K. Garima was found promising genotype in terms of germination, total tuber yield, total tuber number, nil hopper burn and mite damage

Keywords: Evaluation, Potato germplasm, Early crop season

TSIV-OP-02

Reviving grasspea (*Lathyrus sativus* L.) - a potential green leafy vegetable source for the Himalayan regions

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Grasspea (*Lathyrus sativus* L.) is a cool season legume with a high nutritional profile in its seed and leaves as it can be used as food (pulse and green leafy vegetable) and for fodder purposes. However, its cultivation has waned due to the presence of β-ODAP, a neurotoxin responsible for causing lower-limb paralysis. Yet, it remains unclear whether β-ODAP is the sole contributor to the condition known as lathyrism. The present study was defined and accomplished to characterize the grasspea germplasm for its biochemical traits including β-ODAP of leaf to trace out the shreds of evidence to bring back this golden legume "grasspea" into Indian agriculture. The experiment was conducted at Pusa research farm, ICAR- NBPGR, New Delhi during the two consecutive years of rabi season (2019-20 and 2020-21) with 168 accessions in augmented block design. The leaf samples are collected at the pre-flowering stage followed by drying, and powdering. The powdered samples were selected through clustering after NIR scanning and were further used for biochemical analysis such as protein, sugar, TDF, phenol, amino acids and ODAP estimation. The results showed that high nutritional composition in the leaf as follows: protein content- 33.50 % (IFLA1193); TSS content - 7.36 g/100 g (IFLA1715); total phenolic content - 0.36 g/100g (IC349809); TDF content - 31.05 % (BANG198). Amino acid profiling of leaves showed that sarcosine accounts for the highest (14.6 g/100g protein) followed by cysteine (7.85 g/100g protein), glutamic acid (6.82 g/100g protein) and the lowest observed is valine (0.3 g/100g protein); β-ODAP estimation revealed that it ranged from 0.03 to 0.29mg/100g [IFLA1193 (0.03); IC470982 (0.04); IC18879 (0.25); IFLA479 (0.29)]. These findings highlight the potential for harnessing the nutritional benefits of grasspea leaves while addressing concerns associated with β-ODAP.

Keywords: Potential green leafy vegetable, Himalayan region, Nutritional benefits

TSIV-OP-03

Understanding genetic variability for morphological and nutritional traits in the linseed germplasm collection at the National Genebank of India

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The Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources (ICAR-NBPGR) conserves one of the largest base collections of *Linum* with around 2,800 germplasm accessions at the National Genebank, of which 2,576 are the unique accessions belonging to cultivated linseed (*Linum usitatissimum* L.). These accessions were characterized for 10 qualitative and 26 quantitative traits at two locations ICAR-NBPGR, New Delhi for four consecutive years (2018-19 to 2021-22) and NBPGR, Regional station-Akola for two years (2020-21 and 2021-22). The resultant multi-environment data was analyzed as per Augmented Randomized Block Design and used to assess the nature and magnitude of prevalent diversity. Wide range of variation was observed for key traits of economic importance such as plant height (15.69-107.67 cm), technical plant height (6.90-81.22 cm), number of primary branches (1-14), seed yield/plant (0.16-25 g), thousand seed weight (1.1-11.7 g), chlorophyll content (211-418.37 mg/m^2), days to maturity (114-166 days), oil content (30.14-45.96%), α-linolenic acid content (25.4-65.88%), seed and capsule morphometrical traits. Promising accessions were identified for various traits for use in linseed breeding. In addition, a multipurpose core collection comprising 259 linseed accessions was developed maximizing the diversity as well as representativeness of the entire collection. The trait-specific germplasm and core collection are expected to cater to the needs of linseed breeders and germplasm curators and thus pave the way for expedited access to genetically diverse material for trait introgression.

Keywords: Genetic variability, Morphological and nutritional traits, Linseed germplasm, National genebank

TSIV-OP-04

Agricultural biodiversity: Participatory knowledge and autonomous learning for rural food systems

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Global endogenous development-based food self-reliance social movements are emerging. The diffused yet networked food sovereignty movement faces several interrelated science, commerce, and mainstream politics issues. It emphasises the need to modify knowledge and ways of knowing to rejuvenate local food systems. There is a need to critically examine agricultural biodiversity and agro-ecosystem functioning throughout time and space and discuss its ecological and economic effects on rural living. Wild and domesticated plant and animal diversity is needed for complex existence. The food sovereignty movement must aggressively promote autonomous and participatory knowledge to develop ecologically literate, socially just, and context-relevant information. This requires a fundamental transformation from top-down, corporate-controlled research to one that empowers farmers, indigenous peoples, food workers, consumers and citizens to develop social and ecological knowledge. The method seeks to democratise research, encourage diverse co-inquiry, extend horizontal networks for autonomous learning and action, and boost oversight transparency. This includes 1) direct citizen participation in research agendas, regulations, and policies; 2) new professional values and participatory methodologies; 3) a learning process approach to knowledge production and validation; and 4) local food system policies that provide material security and democratic deliberation. Action research in many bio-cultural contexts provides practical examples and case studies. One must understand how money, gender, age, and ecological circumstances affect agricultural biodiversity production, herding, fishing, collecting, usage, and marketing to determine their economic value. Agricultural biodiversity improves the environment and facilitates low- and high-input-output production. Evidence regarding soil organic matter decomposition, nutrient cycling, pollination, insect control, yield functions, soil and water conservation, climate and water cycle action, biodiversity conservation, and landscape structure influence is synthesised. Besides food and livelihood security, agricultural biodiversity supports eco-tourism, local food systems, and rural economies.

Keywords: Agricultural biodiversity, Participatory knowledge, Rural food systems

Abstracts of POSTERS

Technical Session-I:

Status and Management of Plant Biodiversity of North-West Himalayas (NWH)

TSI-PP-01

Plant biodiversity: importance, management and status in North-Western Himalayas

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Biodiversity is crucial for life necessities like food, shelter, water, clean air and medicine. The Himalayas, the youngest and most dynamic mountain range, is known for its high biodiversity due to its diverse topography, climate and altitude. The Indian North West Himalayan (NWH) Region houses approximately half of all flowering plant species in India, with 30% being indigenous. These ecosystem services provide the foundation for human survival. Under NWH, Kashmir, known for its diverse vascular plant species, is a hub of Himalayan biodiversity. Uttarakhand, India's "herbal state," boasts over 5,000 species, with one-third of them therapeutic. Himachal Pradesh, is a state with diverse agroclimatic zones, green forests, snow-capped mountains, and diverse population, rich biological resources, captivating horticultural orchards and a culturally diversified population. Climate change and increasing human demands are threatening the sustainable availability of biotic resources in the Himalayan biozones. Recent studies show that high-elevation, temperature-sensitive plant species are moving up at a high species- and site-specific rate. Urbanization and the anticipated rise in global temperature in the twenty-first century may cause habitat fragmentation, potentially threatening biodiversity, including indigenous plant species and ancestors of cultivated and commercial plants. Alien species with a competitive advantage over native ones invade more quickly due to changes in the climate. Remarkable efforts have been made lately to preserve species in their natural habitat by creating protected zones at various elevations in the Himalayan region. Unfortunately, there is currently a dearth of species-specific ecological research and long-term ecological monitoring, which are fundamentally needed to comprehend the relative susceptibility of species to environmental changes in the Himalayan area. For the Himalayan area to develop suitable biodiversity management policies, such long-term empirical research is necessary. To do this, accurately dated plant growth rings must be used to determine the chronology of species dynamics in response to environmental changes. This ought to offer pertinent insight into the precise chronology of species dynamics in reaction to alterations in their surroundings.

Keywords: Plant biodiversity, North-Western Himalayan region, Current status, Management

TSI-PP-02

Genetic resources of wild edibles in the high altitude of Kumaon region of Uttarakhand

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The India Himalayan region is rich in unique and remarkable biodiversity. The north-western Himalayan region is particularly rich in genetic resources of wild edible of several wild temperate fruit crops and other wild economical species *viz. Malus*, *Pyrus*, *Prunus*, *Sorbus*, *Ribes*, *Rubus*, *Viburnum*, *Fragaria*, *Allium*, *Berberis*, etc. Uttarakhand is a state in northern India and the Kumaon division is the part which situated in the west-central section of the Himalayas which is part of the Siwalik range in the south and part of the great Himalayas in the north with unique climatic and topographic conditions which supports rich agro-biodiversity. The Bhotia tribes of bordering districts of the Kumaon region have been traditionally foraging wild edibles from forests or

meadows which have been substantially contributing to their house hold economies. For the collection of wild edibles and records of ethnobotanical information surveyed high altitude area of Kumaun region of Uttarakhand including Byas valley, Darma valley, Johar valley (Milam) from Pithoragarh and Saryu valley & Pindar Valley from Bageshwar. A total of 52 species of wild edible plants belonging to 31 genera were collected from explored areas and conserved in field genebank or Cryo/seed genebank. The study was based on ethnobotanical uses of wild edible plants, diversity, distribution, threat status and potential of domestication or utilized. Wild edible fruits play a significant role in human dietary and nutritional requirement such as minerals and vitamins as well as livelihood needs, so it is more valuable for forest dwellers and high altitude remote area villagers. Among the collections, 35 species of wild edibles were found to be facing threats from their habitat due to anthropogenic activity and excessive harvesting.

Keywords: Wild edible, Western Himalaya, Genetic resource, Ethnobotanical, Domestication

TSI-PP-03

Therapeutic and aromatic plant resources of Himachal Pradesh: A review

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Medicinal or therapeutic plants synthesize several phytochemicals such as phenols, flavonoids, alkaloids, peptides, and tannins which are useful in defence mechanisms and protection against insects, fungi, and diseases. As one of the top repositories of medicinal herbs, the state of Himachal Pradesh in the Himalayas is one of the major sources of raw materials for the global market. Himachal Pradesh is said to be the home of medicinal and aromatic herbs as its diverse topography and climatic conditions make it suitable for the cultivation of such crops. The flora of Himachal Pradesh consists of 1600 plant species. Out of which, about 260 plant species are attributed to medicinal plants, and about 100 species are aromatic. Moreover, the inhabitants of hilly regions of the Indian Himalayas largely depend on these plants for curing various diseases and few people depend upon the cultivation of medicinal plants for their livelihood too. Medicinal plants have been widely used as folk medicine in non-industrialized societies, as they are readily available and cheaper than modern medicine. But due to our incline towards western culture, the indigenous knowledge and traditional practices of medicinal herbs are vanishing fast which makes it evident for us to realise the worth and importance of our traditional herbs.

Key words: Medicinal plants, Phytochemicals, Traditional knowledge

TSI-PP-04

Edible flowers: A blooming culinary trend

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In a world where culinary enthusiasts seek evermore tantalizing and flavoursome dishes, the aesthetics and nutritional content of food have gained paramount significance. Edible flowers have emerged as a charming addition to certain dishes, enhancing their allure and visual appeal. This age-old practice of incorporating edible blooms into meals for their nutritional and sensory attributes has seen a remarkable resurgence globally. Edible flowers have become a prevailing culinary trend in many nations, driving a substantial surge in their consumption. Recent research endeavours have shed light on the diverse array of phytochemicals, antioxidants, bioactive compounds, and nutraceutical components concealed within these edible blossoms. And provides a succinct synthesis of the current body of knowledge concerning the utilization of edible flowers, emphasizing their nutritional and sensory value. Furthermore, it examines the most commonly encountered species of edible flowers in contemporary culinary practices.

Keywords: Edible flowers, Food, Phytochemicals, Nutritive value, Ornamental plants

TSI-PP-05

Alien plant species invasion in Himachal Pradesh: present and future scenario

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Plant invasion is a huge threat to native plant diversity along with climate change in the 21st century throughout the world. It is considered as the second highest threat to global biodiversity after the habitat loss. The loss due to invasive plant species is huge. A recent study has shown that Indian economy has faced a loss of Rs. 8.3 trillion in the last 6 decades. Himachal Pradesh is one of the hilly States of India and has a rich diversity of floral due to variations in climatic conditions from sub-tropical, temperate to alpine regions. However, due to rapid industrialization and anthropogenic activities several alien plant species have invaded here in the last century which poses a threat to its native species and dependent fauna. In the last two decades, there are number of studies have been conducted on alien plant species invasion in Himachal Pradesh and their impact on the structure, dynamics and composition of native plant species (Kohli et al., 2004, 2006; Dogra et al., 2009; Dogra et al., 2011) such as *Lantana camara* L. (Verbenaceae), *Parthenium hysterophorus* L. (Asteraceae), *Ageratum conyzoides* L., *A. houstonianum* Mill. (Asteraceae), *Ageratina adenophora* (Spreng.) R. M. King & H. Rob. (Asteraceae). These species have invaded in a wide range of habitats and further expanding their range in different ecosystems. Jaryan et al. (2013) have reported a total of 497 alien plant species from Himachal Pradesh along with their purpose of introduction and have concluded that the State flora of Himachal Pradesh comprises around 14% alien plant species. The present study was undertaken to look into the present and future scenario of alien plant invasion in Himachal Pradesh and to document their ecological status. We collected data on alien plant species through primary sources (floristic survey and herbarium records) as well as secondary sources (published literature). We documented a total of 758 alien plant species belonging to 469 genera from 102 families of plants. This indicates an increase of 261 alien plant species in Himachal Pradesh in the last 10 years (Jaryan et al., 2013). Further, our study will also provide a database on the present ecological status and future scenarios of some newly invaded alien plant species [*Tecoma stans* (L.) Juss. Ex Kunth (Dogra et al., 2019); *Solidago canadensis* L. (Asteraceae) (Dogra et al., 2020); *Bidens pilosa* L. (Asteraceae); *Fagopyrum esculentum* Monech (Polygonaceae); *Verbena* sp. (Verbenaceae)] in Himachal Pradesh.

Keywords: Alien plant, Invasion, Diversity, Threat

TSI-PP-06

Impact of climate change on the temporal and spatial distribution of crop wild relatives (CWRs) of *Vigna* spp. in India using Bioclim model

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Global warming and climate change refer to the long-term increase in the Earth's average temperature over the past century and the resulting consequences it brings. The various consequences of climate change are anticipated to affect biodiversity across all levels, ranging from individual organisms to entire ecological regions. Prediction of the projected geographical distribution of a species is crucial for several conservation and protection goals. The present study was focused on predicting the distribution of Crop Wild Relatives of *Vigna* spp. in India, using occurrence data of *Vigna* spp., BioClim model and environmental variables. The Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources (ICAR-NBPGR) collected 928 germplasm accessions of various taxa of the wild *Vigna* genus through collaborative explorations undertaken from 1976 to 2021. Out of 34 wild taxa, 19 taxa are conserved in the Indian National Genebank (INGB). The current distribution pattern of the wild *Vigna* taxa is mapped with the help of the BioClim model interfaced with DIVA-GIS software and the 19 bioclimatic variables were interpolated. Maximum predicted areas were observed for Odisha (55.0%) followed by Andhra Pradesh (28 %), Chhattisgarh (14.5%) and Telangana (2.5%), out of the total high suitable area estimated in India. Habitat suitability maps were generated for the years 2050 and 2080 using different climate scenarios. These species and the predicted suitable areas need to be given top priority for focused investigation and germplasm collecting. This study outlines the future emphasis on investigations to be made for the collection of the germplasm of wild *Vigna* species.

Keywords: Biodiversity; BioClim modelling; Habitat suitability mapping; Wild *Vigna* species

TSI-PP-07

Assessment of morphological variability in *Cyclanthera pedata* (L.) Schrad, an underutilized vegetable found in the wet temperate zone of Himachal Pradesh

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Cyclanthera pedata (L.) Schradis an herbaceous plant of the Cucurbitaceae family native to the Andean territories of South America. In India, it is known as Pahadi Karela or Ram Karela and is mainly found in natural habitats of hilly states like Himachal Pradesh, Uttarakhand, West Bengal, Sikkim and other North Eastern states growing in small farms/ home gardens with little agronomic management. From a nutritional point of view, *C. pedata*, has interesting nutritional properties for human health, among which are: anti-inflammatory, hypoglycemic effect and reduction of cholesterol levels. These three properties are currently important worldwide, due to the increase in diseases associated with unhealthy lifestyles, among them. In view to assess the plant biodiversity of this underutilized vegetable crop in Tehsil Thunag, district Mandi, HP, a survey was planned in September 2023. Four villages (Mayadhar, Mughan, Joodh and Thunag Bazar) were selected which are situated approximately at an altitude of 1,900 m msl, where a survey was done to locate the plants of *C. pedata* and data about morphological variability among plants and fruits were recorded. During the survey, the plants of *C. pedata* were located and tagged. It is observed that the plant population was very small, found in kitchen garden as well as the backyard of the house of rural people. Vigorous vine growth was seen near partially shaded areas as well as near well-fertile soil. Fruits varied from spun and spineless, pale green to dark green and ovoid to spindle-shaped in different villages and among the village's plant populations. Average fruit size varied from 5.5 to 9.7 cm. Further, phytochemical and nutritional analysis will provide insight into the promotion and popularization of this underutilized vegetable as an alternative source of food, nutrition and health security among rural people of Himachal Pradesh.

Key words: Pahadi karela, Morphological variability, Underutilized vegetable

TSI-PP-08

Evaluation of maize genotypes under Subhash Palekar natural farming in lower hills of Himachal Pradesh

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Maize is a widely cultivated cereal grain, serving as a staple food crop in various regions. Its versatility allows it to be used for human and animal food, biofuels, and industrial products. Excessive use of chemical fertilizers and pesticides can lead to environmental degradation and health risks. Natural farming methods, such as Subhash Palekar's approach, prioritize soil health, biodiversity, and sustainability, resulting in healthier crops and reduced environmental impact. Subhash Palekar's natural farming method is based on the principles of zero-budget farming, which means that farmers do not need to spend money on costly inputs such as fertilizers and pesticides. Instead, it focuses on restoring the health of the soil through the use of natural techniques like cow-based farming, intercropping and mulching. This method is beneficial for the environment as it promotes biodiversity, reduces the use of chemicals and minimizes the carbon footprint of agriculture. Selecting the right maize varieties is crucial for natural farming practices. By choosing maize varieties that are well-adapted to the local climate and require minimal external inputs, farmers can improve the sustainability of their farming practices while increasing their yields. Natural farming also emphasis on conservation and promotion of local varieties. To assess and identify the maize genotypes that can be successfully grown in Subhash Palekar natural farming, twelve maize composites were evaluated in a randomized block design using three replications during the kharif season of 2022 at Palampur. Each plot comprised four lines of 3 m. The crop was raised in a 7.2 m2 plot with a spacing of 60 cm × 20 cm and following standard practices of Subhash Palekar natural farming

conditions. The data was collected for different characters viz. days to 50% tasseling, days to 50% silking, days to 75% maturity, plant height, cob height, kernel rows per cob, kernels per row, ear length, ear circumference, grain yield per plant, shelling (%), 100-grain weight and harvest index (%). After recording the observations from each genotype and replication, their mean values were used for the statistical analysis. The analysis of variance (ANOVA) demonstrated significant differences between the mean sum of squares of the twelve genotypes of maize. The grain yield per plant ranged from 45 to 146.94 g with a mean value of 114.54 g. The varieties having grain yield per plant higher than the average are L-315, L-316, L-317, L-318, Girija, Bajaura Makka and Sainj local. The highest grain yield per plant was shown by L-317 (146.94 g) followed by L-318 (143.61 g). The number of kernel rows per cob ranged from 10 (Jwalapur local) to 15 (L-316) with a mean value of 13. The number of kernels per row ranged from 24 (Bajaura Popcorn) to 36 (Jwalapur local) with a mean value of 30. The shelling (%) ranged from 69.08 (Sainj local) to 82.02% (VL-78) with a mean value of 77.32%. These maize composites having high grain yield and desirable characters can either be grown in natural farming or can be further improved to be more suitable for production under Subhash Palekar natural farming.

Keywords: Maize genotype, Natural farming, Subhash Palekar natural farming

TSI-PP-09

Detection strategies for checking unauthorized GMOs in fruit and vegetable crops of North-Western Himalayan Region: a precautionary approach

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The cultivation of temperate fruit crops plays a vital role in the global agricultural industry, providing a significant source of nutrition and economic revenue. Temperate fruits and vegetables refer to those adapted to the temperate zone climates including that of the North-Western Himalayas (NWH). Some of the examples in the NWH Region include apple, plum, pear, peach, grapes, strawberry, potato, tomato, cauliflower, and capsicum. The advent of genetically modified (GM) crops has revolutionized agriculture through increased yields, tolerance to biotic and abiotic stresses and nutritional enhancement. However, the regulation of such crops has prompted the need for robust and efficient detection methods in India as only *Bt* cotton has been approved. As per the Food Safety and Standards Authority of India (FSSAI), every consignment of 24 specified food crops, including apple, plum, potato and tomato need to be accompanied by non-GMO certification, with a tolerance level of 1% for inadvertent presence of GMOs in imported food crops. Given the stringent regulation of GM fruit and vegetable crops in the country, following extensive global trade, GM detection strategies for tracking unauthorized genetically modified organisms (GMOs) in fruit and vegetable crops of the NWH Region are being presented herein. GMO matrix of GM events of apple, plum, potato, and tomato was developed for screening of common targets present in these crops. The identified screening targets were *CaMV 35S* promoter (P-35S), *nos* terminator (*T-nos*), *nptII* marker gene and *cp4-epsps* gene. These elements were targeted for the development/validation of GM diagnostics with multiplexing in PCR/ real-time PCR/loop-mediated isothermal amplification (LAMP). These diagnostics could be employed for checking unauthorized GMOs in seeds, fruits and food products of these crops in the NWH region. This study can contribute to ensuring the transparency of the food supply chain, thereby supporting biodiversity preservation and sustainable agriculture, particularly in the context of temperate fruit and vegetable crop production and the broader agricultural landscape.

Key words: GMOs, Fruit and vegetables, North-Western Himalayan Region

TSII-PP-10

Characterization of elite germplasm of North Western Himalayas using DUS traits

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The current study was carried out at the CSKHPKV Rice and Wheat Research Centre, Malan during the *kharif* season of 2022. The experimental material for this investigation included 40 elite rice genotypes, including red rice, white rice and aromatic rice along with three checks *viz.,* HPR-2880, Kasturi and HPR-2720. DUS testing of forty germplasm lines of rice was done for 62 morphological characteristics according to the National DUS test guidelines on rice. The 62 morphological characteristics comprised 44 visually assessed characteristics and 18 measurable characteristics. The dendrogram was generated using the UPGMA clustering method through the NTSYSPC 2.02 version in which genotypes were grouped into diverse clusters based on 62 DUS descriptors. The genotypes were grouped into nine clusters at a genetic similarity coefficient of 0.80. Cluster 1 comprised of maximum number of genotypes i.e., 27 followed by clusters 2, 6,7, 8, and 9 having 2 genotypes and clusters 3, 4 and 5 having only 1 genotype. The maximum contribution toward diversity was by decorticated grain shape, decorticated grain colour, leaf pubescence of leaf blade, spikelet density of pubescence of lemma, leaf sheath intensity of anthocyanin colour and lemma and palea colour. The lowest value for the Shannon index was found for leaf auricles. Out of 62 characters, three were found monomorphic which are leaf ligule, male sterility and endosperm presence of amylose. The genotypes *viz*., *Purple, Bongal Dhan, Byada-3, Byada – 4, Byada Basmati* and *Parmal Byada -1* were found to possess long slender grains (basmati types) and *Lakhamandal, Bhagolta Local* and *Parmal Byada – 2* were found with extra-long grains which can be further used in the future breeding programme for developing rice varieties with superior grain characters. Genotypes *Acchoo, Deval, Deval Kullu, Karad, Gosha Dhan, Gharsai* and *Chohartu* were red-grained genotypes and can be used for developing red rice varieties. *Nirmand Choharu, Gosha Dhan, Karad 21-4, Gharsai, Chattar -2 Parmal, Acchoo, Bongal Dhan, Local Jhemka, Chattar Parmal -1, Local Lal Dhan, Lakhamandal, Bhagolta Local* and *Byada -3* were found to be in the category of aromatic rice while *Acchoo* was the only red rice that falls under aromatic rice category.

Keywords: Characterization, DUS traits, Aromatic rice, Red rice, Genetic similarity coefficient

TSII-PP-11

Trait discovery and genomics in plants of North-Western Himalayan

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Medicinal plants of the North-Western Himalayan region are known for their valuable secondary metabolites that are unique to this dynamic geo-climatic region. These medicinal herbs have been used for their therapeutic properties since ancient times. However, the illicit and unorganized trade in these medicinal plants, along with the rise in pharmaceutical demand over the past 20 years, has exacerbated the rate of over-exploitation in a non-scientific way. In addition, climate change and anthropogenic activities also affected their natural habitat and drove most of these endemic plant species to critically endangered foresee the peril of mass extinction from this eco-region. Hence there is an urgent need to develop alternative sustainable approaches and policies to utilize this natural bioresource ensuring simultaneous conservation. In the lack of genomic information, the development of sequencing-based transcriptome research has made a substantial contribution to our understanding of the background of key metabolic pathways and associated genes/enzymes of valuable medicinal herbs. The use of comparative transcriptomics in conjunction with biochemical techniques in North-Western Himalayan medicinal plants has resulted in significant advances in the identification of the molecular players involved in the production of secondary metabolic pathways over the last decade. Collectively, successful adoption of these approaches can certainly ensure the sustainable utilization of Himalayan bioresource by reducing the pressure on the wild population of these critically endangered medicinal herbs. To better understand the genes and their metabolism of high-value, endangered North-Western Himalayan medicinal herbs, this information is subsequently useful by researchers globally to develop strategies for producing pharmaceutically important compounds, scaling them up for long-term use, and making progress in omics-based conservation genetics.

Key words: Medicinal plants, Metabolic pathways, NGS; North-Western Himalayas, Secondary metabolites, Transcriptome

TSII-PP-12

DUS Characterization of Japanese Plum (*Prunus salicina* Lindl.) germplasm at NBPGR, Shimla

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An investigation entitled ‘‘DUS Characterization of Japanese Plum (*Prunus salicina* Lindl.) germplasm at NBPGR, Shimla” was executed in the field gene bank of NBPGR, Regional Station Phagli, Shimla (Himachal Pradesh) during the year 2021-2022. The experimental material consisted of 14 germplasm accessions *viz.,* EC-382826, EC-393740, EC-552696, EC-513684, Frontier, IC-555314, IC-555355, Kala Amritsari, EC-538999, IC-558067, Methley, Red Beaut, Shiro and EC-552693 which were laid out in randomized complete block design with three replications each. The observations were diarized to characterize and evaluate Japanese plum germplasm for growth, floral and fruit characters during analysis. The results revealed that the maximum tree height and girth were diarized in Kala Amritsari (4.45 m and 52.37 cm), respectively. While the spread was docketed maximum in Shiro. EC-393740 inscribed the maximum leaf blade length and width. The date of full bloom was noted earliest in Red Beaut. The maximum pollen viability with acetocarmine solution and Erythrosine B test was recorded in EC-382826 (98.97%) and IC-558067 (71.46%), subsequently. *In vitro* pollen germination was catalogued maximum in EC-382826 (81.69 %) and Frontier (90.53%), respectively. Fruit weight was obtained maximum in Red Beaut (65.18 g). Maximum fruit drop was chronicled in EC-552693 (46.49%) and unrivalled fruit retention was documented in Shiro (67.92 %). The pulp-to-stone ratio was documented maximum in Red Beaut. Total soluble solids were logged maximum in Frontier (15.20 °B) whilst, the maximum titratable acidity was documented in Shiro (1.56%). The maximum total sugars, reducing sugars and non-reducing sugars were recorded in Frontier (8.20%), Frontier (6.62%) and EC-538999 (1.96%), correspondingly. The investigation specified that the germplasms studied do possess one or more horticulturally desirable characteristics and thus can be used to broaden the genetic base from the pre-existing cultivars.

Key words: DUS, Characterization, Germplasm, Desirable traits

TSII-PP-13

Characterization and evaluation of sweet cherry (*Prunus avium* L.) germplasm under the North-West Himalayan region

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The present study, entitled “Characterization and evaluation of sweet cherry (*Prunus avium* L.) germplasm under the North-West Himalayan region” was carried out in the experimental block of the Regional Horticulture Research and Training Station, Mashobra, Shimla, that falls under the wet temperate zone of Himachal Pradesh, during the years 2019 and 2020. Twenty sweet cherry varieties, *viz.*, Bing, Black Heart, Bradbourne Black, Durone Nero - II, Durone Nero - III, Early Rivers, Lambert, Lapins, Merton Glory, Noir De Guben, Rainier, Red Heart, Roundel Heart, Sam, Seneca, Stella, Sunburst, Triumph Domini, Van and Vega were used in the present study. Tree height ranged from 3.62 m (Bradbourne Black) to 4.92 m (Lambert). The longest flowering duration (13 days) was recorded for Bing, Black Heart, Bradbourne Black, Merton Glory, Stella, and Sunburst, while the shortest (8 days) was seen in Lambert. The number of days from full bloom to harvest varied from 42 days (Seneca) to 74 days (Lambert). Maximum fruit weight (8.63 g) was observed in Bradbourne Black and the minimum (weighing 3.21g) in Triumph Domini. Maximum fruit length and width (23.44 mm and 24.48 mm) were recorded in Bradbourne Black, whereas the minimum fruit length (16.92 mm) was in Noir De Guben and the minimum width (15.97 mm) was in Triumph Domini. Fruit firmness varied from 2.16 kg/cm^2 (Rainier) to 1.36 kg/cm^2 (Bradbourne Black). TSS content was highest (21.53 °B) in Sam and lowest (15.43 °B) in Lambert. The highest fruit yield (80.53 kg/tree) was observed in Stella, while the lowest yield (51.47 kg/tree) was recorded in Lapins. From the preliminary results of the present study, it can be concluded that some of the studied varieties exhibited horticulturally desirable characteristics like large fruit weight, high TSS, early maturity, dark red skin colour, etc. However, it is essential to emphasise the need for further research to yield more robust results, along with the imperative task of conserving germplasm for future investigations.

Key Words: Characterization, Diversity, Germplasm, Sweet Cheery

TSII-PP-14

Molecular characterization and identification of insect pollinators of *Punica granatum* L. from Western Himalaya, India

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Wild pomegranate (*Punica granatum* L.) is one of the most important medicinal wild fruit crops and it is highly pollinated by wild insect pollinators. So, the study analysed various pollinating insects of *Punica granatum* L. by using molecular method and a total of 24 species of flower visitors were collected from *Punica granatum* from different areas of Himachal Pradesh. Using the mtDNA marker, the cytochrome oxidase subunit sequence I (COI), about 17 pollinator insect species were characterized and identified based on the COI sequence. BLAST analysis showed 98 to 100% similarity with the existing genebank sequences. Nucleotide composition revealed the average AT content was significantly higher by 72.56% than the GC content of 27.47%. Phylogenetic analysis of 17 different species of insect pollinators of *Punica granatum* revealed the close phylogenetic relation between hymenopteran insect species in one clade, whereas another clade showed the relationship between Lepidoptera, Coleopteran and Diptera. The study concludes that *molecular identification using species identification markers in the mitochondrial region of COI* plays a critical role in the study of genetic diversity, genetic relatedness and phylogenetic analysis at the species level.

Keywords: Cytochrome oxidase subunit I, Insect pollinators, mtDNA, *Punica granatum*

TSII-PP-15

Genetic characterization and mutant analysis of chrysanthemum genotypes using SSR markers

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Chrysanthemum (*Dendranthema grandifora* Tzvelev), a widely cultivated cultivar, is one of the most economically significant decorative plants globally, captivating the interest of both horticulturists and botanists. SSR markers were used to characterize the 36 chrysanthemum genotypes, twenty-one newly evolved genotypes and fifteen standard cultivars at the molecular level. Out of the 35 SSRs initially tested, a total of 113 alleles were identified, with an average of 4.34 alleles per locus. The characterized genotypes exhibited an average polymorphism of 90.53%, demonstrating an average of 1.03 monomorphic and 3.31 polymorphic bands. The Jaccard coefficient revealed a range of similarity values from 0.41 to 0.80, illustrating substantial diversity among the genotypes. Population structure analysis, conducted with K values ranging from 1 to 10, indicated the presence of three subpopulations, aligning closely with the clustering result. The dendrogram separated the newly evolved chrysanthemum genotypes from the others by using NTSYS software. UHFSCr-114 and UHFSCr-122 were also found to be more diversified than the other chrysanthemum genotypes according to the DARwin-based neighbour joining analysis. In addition, our previous studies have also highlighted the diverse phenotypic traits exhibited by these two recently evolved genotypes. Therefore, the present investigation has uncovered notable genetic variation among the studied genotypes, providing molecular evidence of the mutant behaviour of the recently developed chrysanthemum genotypes. The SSR markers have facilitated the precise genetic identification of these newly evolved genotypes and cultivars, revealing their genetic homogeneity, thereby supporting marker-assisted breeding and protecting plant breeder rights for specific varieties and cultivars.

Keywords: Chrysanthemum, Genetic diversity, Molecular characterization, Mutants, SSR markers

TSII-PP-16

Evaluation of red rice (*Oryza sativa* L.) germplasm of Himachal Pradesh using agro morphological markers

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The present investigation was undertaken to identify and characterize the red rice genotypes by assessing the nature of variation and extent of genetic diversity and their direct and indirect effects to identify promising red rice genotypes. The experimental material comprising 43 genotypes including two checks was evaluated in Randomized Block Design during *Kharif* 2021 with three replications. Total eighteen agro-morphological and quality characters were studied including days to 50 per cent flowering, days to 75 per cent maturity, plant height (cm), flag leaf length (cm), flag leaf width (cm), total tillers per plant, effective tillers per plant, spikelets per panicle, 1000-seed weight (g), biological yield per plant (g), harvest index (%), grain yield per plant (g), seed coat colour, grain length [L] (mm), grain breadth [B] (mm), L: B ratio, lodging susceptibility (%) and awns. The mean performance of the genotypes revealed that only one genotype viz., *Desidhan* was superior to the best check HPR-2795 for grain yield per plant. Based upon the overall performance of genotypes Desi Dhan HPR-2913 and Sukara red were found to be superior for most of the traits *viz.,* days to 75 per cent maturity, flag leaf length, total tillers per plant, effective tillers per plant and grain yield and hence can be used in hybridization programme. Genetic diversity studies using Mahalanobis D^2-analysis were conducted for 43 genotypes, which grouped these genotypes into four clusters indicating the presence of considerable genetic diversity among all the genotypes. Maximum genotypes were placed in cluster II which included 19 genotypes (*Ramjuwain*, *Karad*, IC-12164, *Begmi*, *Bathidhan*, HPR-2906, Varundhan, *Hatiali*, *Naggardhan*, *Nailina*, *Matali*, *Dodadhan*, HPR-2908, HPR-2914, Gocha, New Chaina-21, Old Chaina-21, Karad 21-2 and Jattu) followed by cluster I consisting 17 (IC-12180, Kaluna, Chohartu, Kalaina, Acchoo, HPR-2800, Roda Dhan, Deval, Bhrigudhan, Kalijhini, HPR-2902, HPR-2904, HPR-2905, Karad 21-1, Karad 21-3, Karad 21-4 and HPR-2720) genotypes, cluster IV containing 4 genotypes (Kalijhini-2, HPR-2913, Phulpatas-21 and HPR-2795) and cluster III containing 3 genotypes (Sukara, Desidhan and Sukara red). The intra-cluster distance was maximum in cluster II (4.57) and minimum in cluster III (4.23), whereas, the highest inter-cluster distance (5.66) was recorded between cluster III (Sukara, Desidhan and Sukara red) and cluster IV (Kalijhini-2, HPR-2913, Phulpatas-21 and HPR-2795). Hence, it can be concluded that the genotypes belonging to these clusters are genetically diverse. Among four clusters, cluster III showed the highest cluster mean values for most of the traits suggesting that genotypes falling in cluster III (Sukara, Desidhan and Sukara red) can be selected directly based on these traits and be used in the hybridization program. Principal component analysis revealed that the first principal component (PC1) was observed to be the highest contributing (relative contribution %) to the total variation, which was mainly through the biological yield per plant, grain length, effective tillers per plant and total tillers per plant.

Keywords: Genetic diversity, Analysis of variance, PCV, GCV, Correlation, Path coefficient analysis, Mahalanobis D^2-statistics, Principal component analysis

TSII-PP-17

Resistance to stripe rust in elite wheat germplasm from the Northern Western Himalayan zone of India

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Major biotic constraints in wheat production are wheat rusts caused by *Puccinia* species. Among the three rusts i.e. (stem rust = *Puccinia graminis* f. sp *tritici*, leaf rust = *P. recondita* f. sp. *tritici* and stripe rust = *P. striiformis* f. sp *tritici*); stripe rust is the major problem in north hills of India. Sixty-six diverse genotypes were studied for (APR) adult plant resistance including five resistant mutants of HD 2967 (TYRM1, TYRM2, TYRM3, TYRM4, TYRM5) from Bhaba Atomic Research Centre, Mumbai and were evaluated under field and controlled conditions. TYRM2 and TYRM4 were found to be highly resistant to yellow rust at both seedling and adult plant stages. Genotypes HPW 368, HS 562 and TRYM1 were found to be moderately resistant under field conditions. These lines have been suggested for use in breeding programs, and some are currently undergoing network trials for their direct release. TYRM 2 mutant showed near immune response in multi-location trails. These findings are expected to contribute towards wheat improvement programs that aim to enhance resistance to stripe rust.

Keywords: Wheat, Rust, Resistant, APR

TSII-PP-18

Transcriptome study for identification of key genes involved in flowering time regulation in linseed (*Linum usitatissimum* L.)

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Linseed (*Linum usitatissimum*) is an annual crop of economic importance owing to its food, nutraceutical, and industrial applications. Flowering time is one of the crucial traits in linseed. Early flowering is desirable in linseed as it helps avoid crucial biotic and abiotic stress. Although QTLs/QTNs have been reported through association studies in linseed, more light is certainly required to identify the transcription regulatory network involved in flowering time regulation. Here, we performed transcriptome sequencing of reproductive tissues, floral bud at two developmental stages (bud 1 & bud 2), flower, and two vegetative tissues (leaf and stem) in two early flowering linseed accessions, IC0523807 and IC0525939. A total of 47.4 GB of filtered data was obtained from 20 datasets, resulting in 43,484 transcripts. Differential expression analysis between vegetative tissues vs reproductive tissues in different combinations revealed a total of 14,244 differentially expressed genes (8159 upregulated and 6085 downregulated), with 40 GO and 161 KEGG enriched terms. Several DEGs were involved in auxin, cytokinin, gibberellic acid, and abscisic acid signal transduction, sucrose, and starch synthesis pathways. From the 234 known genes associated with flowering in other plants, 174 genes were detected in any of the three comparisons (Bud1 vs vegetative tissue, bud 2 vs vegetative tissues, and flower vs vegetative tissues). Further, from the 79 putative candidate genes identified in earlier association studies in linseed, 56 candidate genes were among the DEGs common to bud1, bud2, and flower. Overall, based on previously identified QTLs/QTNs, candidate genes and DEGs identified in the present study, 2 genes, flowering locus T (*LusFT, Lus10013532*) and a flowering repressor Apetalla-2 (AP2) like transcription factor SCHLAFMUTZE (SMZ) (*LusSMZ, Lus10039650*) showed to be promising candidate genes. This study provides a detailed insight into the transcription network associated with flowering time regulation in linseed.

Keywords: Flaxseed, *Linum usitatissimum*, Flowering time, Early flowering, Transcriptome, Candidate gene

TSII-PP-19

Estimation of genetic parameters for morphological and quality traits in Pea (*Pisum sativum* L.)

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Pea (*Pisum sativum* L., 2n=2x=14) is a most important annual cool season crop grown on a commercial scale throughout the world and is consumed as a fresh succulent vegetable or in processed form. Pea is highly nutritive containing a high amount of digestible protein and other health-building substances like carbohydrates, fibres, vitamin A, vitamin C, minerals such as calcium, magnesium and antioxidant compounds. Twenty-eight genotypes of pea for eight horticultural traits were evaluated during *Rabi* season 2021-22 in Randomized Complete Block Design with three replications to determine the extent of variability, heritability, genetic advance, correlation and path coefficient analysis. The analysis of variance revealed substantial differences among all the genotypes concerning the characters studied. The genotypes Pusa Pragati, LC-P-1 and LC-P-2 outperformed the check genotype Punjab-89 for various horticultural traits. The estimates of the phenotypic coefficient of variation and genotypic coefficient of variation were high for plant height and pod weight reflecting the presence of high genetic variability among all the genotypes for these traits. High heritability along with high genetic advance was recorded in days to 50% flowering, pod length, pod weight, plant height and number of pods per plant. Correlation studies revealed that pod yield was positively and significantly correlated with pod length, pod weight, number of pods per plant, shelling percentage and total soluble solids. The path coefficient analysis indicated that pod length had the greatest positive direct effect on pod yield followed by pod weight, plant height, number of pods per plant, total soluble solids, days to 50% flowering and shelling percentage. Therefore, selection based on these traits may be rewarded for improving yield.

Keywords: Genotype, Variability, Quality traits, Heritability, Genetic advance

TSII-PP-20

Deciphering resistance to frog eye leaf spot in soybean germplasm under Mid-Himalayan region

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Soybean [*Glycine max* (L.) Merril] is a unique grain legume globally known for its dual purpose use as pulse and oil seed containing 38–44% protein and 18–22% oil. The seed protein content of soybean is higher than the non-vegetarian diet and therefore, it is also known as poor man's meat. This crop is affected by many pathogens but frogeye leaf spot caused by *Cercospora sojina* Hara is one of the major diseases occurring in epidemic form in the sub-humid hill agro-ecological zone of Himachal Pradesh causing considerable yield losses. Deployment of genetic resistance to the prevalent races of the pathogen through the identification of genotypes from diverse germplasm lines and its incorporation in a high-yielding variety is the most economically sound strategy to manage the disease. Keeping the above in view, 322 germplasm lines were grown in a randomized block design with two replications at the experimental farm of the Department of Genetics and Plant Breeding, CSK HPKV Palampur, during *Kharif* 2022. The lines were sown in two rows per replication having a length of two meters and spacing of 45cm × 10cm. These germplasm lines were screened under natural field conditions for frog eye leaf spot reaction based on a 0-9 scale given by Stone house (1994). Among all 322 genotypes, only 17 genotypes *viz*., IC 15089, EC 241756, JS 97-52, AMS-MB-5-18, BR 15, JS 20-69, AGS 205, JS 79-82, MACS 58, CAT 1149, DS 321, TGX 803-99E, TGX 573-209-23, VLS-59, EC 550828, JSM 245 and NRC 2007-1-3 showed the resistant reaction at both early and later plant stages under natural field conditions. These genotypes can be further tested for resistance by artificially inoculating with pathogens. The genotypes found as resistance at both natural and artificial conditions can be used in future soybean improvement programmes to introgress the resistance in high-yielding soybean varieties.

Keywords: Frogeye leaf spot, Resistance, Soybean, Germplasm

TSII-PP-21

Exploring the genetic diversity and population structure of *Bacopa monnieri* (L) using random amplified (RAPD and ISSR) and gene-targeted (SCoT and CBDP) markers

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Bacopa monnieri (L.), commonly referred to as Brahmi is a perennial trailing herb belonging to the Scrophulariaceae family. It is primarily distributed in wet, damp, and marshy regions across India, Australia, Europe, Africa, and America. This herb has a rich history in Ayurvedic medicine due to its therapeutic attributes. The utilization and conservation of this plant as garnered worldwide interest because of its medicinal value. Brahmi has also been the subject of comprehensive research, primarily focusing on its chemical components, particularly bacosides, which serve as the active agents responsible for enhancing memory. In this study, arbitrarily amplified (RAPD and ISSR) and gene-targeted (SCoT and CBDP)markers were used to study the genetic diversity and population structure of thirty *Bacopa monnerri* L. accessions. Polymorphic information content (PIC) was calculated using POPGENE 1.32 with the highest PIC value given by CBDP markers (0.345) followed by SCoT (0.343), RAPD (0.342) and ISSRs (0.312). The highest gene diversity was observed with SCoT markers (0.295) followed by RAPD (0.290), CBDP (0.283) and ISSRs (0.221). Neighbor joining tree was constructed using DARwin 6.0.10which divided the *Bacopa monnieri* accessions broadly into three groups with all the four marker systems. Population structure-based analysis with RAPD and CBDP markers clustered the *Bacopa monnieri* accessions into two populations while SCoT markers clustered the accessions into three populations, and ISSR markers clustered the accessions into four populations. STRUCTURE based AMOVA showed the highest variance within the population with RAPD markers (69%) followed by CBDP (67%), SCoT (47%) and ISSRs (34%). The findings suggest that all four marker systems are valuable tools for assessing the genetic relationships among various *B. monnieri* accessions originating from diverse regions in India. This

underscores the importance of understanding genetic diversity among various *B. monnieri* accessions, which is crucial for conservation efforts and breeding programs.

Keywords: RAPD, ISSR, SCoT, CBDP, Genetic diversity, *Bacopa monnieri*

TSII-PP-22

Screening of diverse *Brassica* germplasm for white rust resistance under northern-Himalayan conditions

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Brassica juncea contributes more than 80% to the total rapeseed-mustard production in the country and is an important component in the oilseed sector. There are various diseases reported in rapeseed-mustard but white rust is one of the most important disease which is caused by Albugo candida. The resistant accessions coupled with agronomic superiority may be useful genetic resources for the improvement of Indian mustard. The experimental material comprising 37 diverse strains/varieties of *Brassica juncea*, *Brassica napus*, and *Brassica rapa* (Toria) were grown during the rabi season of 2019-2020 in Randomized Block Design with 3 replications. Each treatment was sown in 3 rows of 5m length and inter and intra row spacing was 45cm and 15cm respectively. To screen Brassica plants right from seedling stage to maturity against white rust disease caused by the pathogen Albugo candida, the actual photograph based on a 0-9 rating scale was conceptualized. In case of *B. juncea*, RSPR-01 and JD-6 genotypes showed moderate resistance while as NRCHB-101, RSPR-03, RSPR-69, SKJM-5, RH-0923, RH-1209, Giriraj, RB-50, JM-12-6 and Kranti were susceptible to white rust to severity score ranging from 26-50%. In the case of *B. napus* genotypes of CNH-11-2, GSH- 1699, GSC-101, GSC-6, GSC-21, EC552608, RSPN-25, DGS-1, RSPN-29 and JGS-12-3 were found resistant to white rust with diseases severity score ranging from less than 5% to 10%. Severity scores of genotypes of RSPN-29, AKGS-1 and HNS-1102 was above 10% and hence were moderately resistant. In B. rapa (Toria) genotypes of Tapeshwari, Bhawani, PT-2012-5, RSPT-6, RSPT-2 TH-1401 and PT-303 were moderately resistant to white rust with severity score ranging from less than 11% to 25% under both environments. While as genotypes PTC-2010-2, BAUT-09, KBS-3 and RMT-10-9 were susceptible to white rust with severity score ranging from less than 26% to 50%. Screening of these genotypes against the disease will give us information about the quality of resistance genes which in turn can be utilized for breeding resistant cultivars, analysis of components of resistance and will also help determine the nature of resistance in varieties. The lines developed from experiments with diverse genotypes can be used

Keywords: Brassica, Germplasm, White rust

TSII-PP-23

Comparative studies on diversity in Safflower germplasm with SSR and SNP markers

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Carthamus tinctorius L., commonly known as “safflower”, is a member of the Asteraceae family and is an oil seed crop grown primarily for its nutritionally desirable high percentage of unsaturated fatty acids. Information about the genetic diversity of plant genetic resources (PGRs) provides useful alleles or genomic regions associated with the development and improvement of crops. From amongst various molecular markers, SSRs and SNP are often selected for genetic studies, such as for genetic diversity, population structure and the development of core collections. Simple sequence repeats (SSRs) are considered ideal genetic markers for assessment of diversity in germplasm collections due to their desirable properties viz abundant, locus-specific, co-dominant, multi-allelic, high throughput genotyping. Currently, single nucleotide polymorphism (SNP)

markers are the markers of choice for genetic diversity studies, genome-wide association mapping, genomic selection, phylogenetic relationships and population evolutionary studies. In this study, a total of 184 accessions of safflower from various geographical locations collected from the Indian National Gene Bank were analyzed for diversity and population structure using 18 SSR and 1460 SNP markers. All SSR markers showed polymorphism above 94% with a mean PIC of 0.95 whereas; SNP markers generated a mean PIC of 0.37. Mean gene diversity with SSR markers showed 0.96 whereas SNP markers generated a mean gene diversity of 0.49. Genetic relatedness among the accessions was studied; Population structure was tested using k values from 1 to 10. Ln(PD) derived Δk was plotted to determine the number of populations. In the case of SSR Δk was maximum at K=3 as SNP Δk was maximum at K=2. Principal coordinates analysis with SSR markers showed the genotypes didn't fall into any pattern of grouping but were rather distributed across the whole spectrum whereas; in the case of SNP the genotypes were grouped into two broad groups across two axes suggesting SNP markers are more efficient for diversity analysis.

Keywords: Diversity, Germplasm, Safflower, SSR

TSII-PP-24

Physio-chemical characterization of tendu fruit (*Diospyros melanoxylon* Roxb) and selection of plus trees from Majhgawan forest of Madhya Pradesh

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Tendu fruit (*Diospyros melanoxylon* Roxb.), an underutilized seasonal fruit of India, is a rich source of many medicinal and nutritional properties. Tendu fruit is one of the important forest fruits found in Madhya Pradesh. The plant is well known for its leaves which are known as Bidipatta and is used for making Bidi in tribal areas of India. The present work emphasises upon physio-chemical characterization of tendu fruit and the selection of plus trees from the Majhgawan forest areas of Madhya Pradesh. This survey was conducted to identify the plus trees based on fruit quality and morphological characters.. The physio-chemical characters were considered using samples from 9 trees representing different populations distributed in the Majhgawan forest of the district of Satna. The maximum fruit weight (26.87 g), fruit length (32.48 mm), fruit breadth (34.82 mm), fruit circum. (12.27 cm), no. of seeds/fruit (6.13), seed length (22.76 mm), seed breadth (12.62 mm), seed weight (1.73 mm), pulp weight (11.98 g), peel weight (7.96 g), pulp per cent (56.66 %), specific gravity (1.27), fruit volume (24.47 cc), TSS (17.05), acidity (0.81 %) and fruit colour (dusty yellow) were noted with BUAT Tendu – 6 followed by BUAT Tendu - 8. Minimum fruit weight (16.57 g), fruit length (27.14 mm), fruit breadth (29.01 mm), fruit circum. (10.37 cm), no. of seeds/fruit (4.10), seed length (20.25 mm), seed breadth (11.29 mm), seed weight (1.20 g), pulp weight (7.96 g), peel weight (6.06 g), pulp per cent (44.63 %), specific gravity (0.81), fruit volume (19.72 cc), TSS (15.67), acidity (1.21 %) and fruit colour (dark yellow) were recorded with BUAT Tendu - 7. Selections BUAT Tendu – 6 and BUAT Tendu– 8 were found most promising based on physico–chemical attributes and tree morphological characters.

Keywords: Physio-chemical, Tendu fruit, Bidipatti and tribal

TSII-PP-25

Molecular characterization and identification of insect pollinators of *Valenriana jatamansi* Jones from Shimla Hills, Western Himalaya

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Valeriana jatamansi Jones a perennial medicinal herb belongs to the family Caprifoliaceae and is highly pollinated by wild insect pollinators. It is on the verge of extinction due to over-exploitation. In the present investigation various pollinating insects of *Valeriana jatamansi* were examined by using molecular method and a total of 51 species of flower visitors were collected and reported on *Valeriana jatamansi* in Tara Devi (1,927 m), Dhalli (2,155 m), Chaura Maidan (2,100 m), Fagu (2,576 m), Matiyana (2,419 m), Kufri (2,609 m), Kharapather (2,703 m) and Kupper (2,850 m), localities Shimla Hills, Western Himalaya. Out of these 29 species of insect pollinators were molecularly characterized and identified based on COI sequence by using mtDNA marker. During BLAST analysis 98 to 100% similarity was observed with the existing Genbank sequences. Nucleotide composition showed that average AT content was significantly higher by 69.8% than the

GC content of 30.0%, which proved that all the sequences were AT-biased. Phylogenetic analysis of 29 different species of insect pollinators of *Valeriana jatamansi* revealed two clades, one shows phylogenetic relationship between 28 species which belong to four orders Diptera, Hymenoptera, Hemiptera and Lepidoptera and the other shows one species which belong to order Coleoptera.

Keywords: Molecular characterization, Insect pollinators, Western Himalaya

TSII-PP-26

Recent advances in plant breeding methods for self and cross-pollinated crops

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The plant breeding methods as an evolving technology considering the increasing level of knowledge for underlying mechanisms and control of the process of generating and selecting superior plant types. So, three main eras of plant breeding can be identified: (i) based on the selection of observed variants, disregarding their origin (ii) generation and selection of expanded variation by controlled mating (iii) monitoring the inheritance of within-genome variation and selection of specific recombinants. (iv) creation and introduction of novel variation into genomes through genetic engineering. Plant breeders use a variety of methods and techniques to develop pure lines, open-pollinated populations, hybrids and clones. For improving self-pollinated species tend to focus on improving individual plants and cross-pollinated species tend to focus on improving a population of plants. Here, the focus of the breeder is on improving populations instead of selecting superior individual plants. So modern methods have revolutionized the process of plant breeding with acceleration and accuracy, which are continuously empowering plant breeders around the world. The new breeding method involves marker-assisted selection, mutation breeding, speed breeding, genomic selection, doubled haploid breeding reverse breeding etc. These are the new emerging approaches due to which various problems of conventional breeding avoid and enhance the selection criteria of phenotypes with the selection of genes, either indirectly or directly and it provides opportunities to increase genetic gain of complex traits per unit time and cost. Genomic selection and high throughput phenotyping together will change the entire paradigm of plant breeding as well as lead to the effective increase in genetic gain for complex traits.

Keywords: Breeding methods, Self and cross-pollinated, Phenotyping

TSIII-PP-27

Traditional uses and conservation of *Fritillaria roylei* Hook. a critically endangered Himalayan medicinal plant: an overview

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The ecosystems found in the Himalayan region have a wide variety of plants and animals, including valuable species of medicinal and aromatic plants (MAPs). Among them *Fritillaria roylei* Hook. commonly known as Kakoli, Jungli lehsun belongs to the Liliacece family; a perennial plant known for its medicinal value worldwide and is at risk of becoming endangered. It is typically found in the sub-alpine to alpine areas of the Himalayas, primarily growing on open and sunny slopes. *F. roylei* has been reported in Jammu & Kashmir, Uttarakhand, Himachal Pradesh, within the altitudinal range of 2400-4000 m above sea level. It grows well in light sandy or medium loam-drained acidic soil. The open sunny areas with moderate slopes and rich humus are the habitats preferred by this species. It has been traditionally used by local communities in various ways i.e. dry powder, paste etc. The bulb of this species has been widely used for the treatment of bronchitis asthma, burns, health tonics and stomach troubles. It is a significant component of Ashtavarga (a set of eight medicinal herbs),

Chyavanprash, and other Ayurvedic formulations in the Indian medical system. The roots are used for healing wounds, and corns in Ayurvedic and Unani medicine. *Fritillaria* are utilized worldwide as medication and food; normally roasted bulbs of this species are utilized as food by Native Americans (Orhan et al. 2009). The bulbs of Fritillaria rolyei are utilized as a decoction or in dried form to cure bronchitis, cough, tumours, asthma, hemoptysis and insufficiency of milk (Perry 1980; Kang et al. 2002). Bulbs can be utilized in entire or in powdered form as remedies for clearing the lungs from mucus and cooling heat (Bensky et al. 2004; Li et al. 2006a, 2009) It has been utilized for the treatment of prolonged hypotension, sensory system, defective breathing and incitement of the heart muscle (Erika and Rebecca 2005)as well as treating swelling underneath the skin, for example, scrofulous swellings and breast nodules (Da-Cheng et al. 2013). However, due to high demand, the species as gained significant market value worldwide leading to unsustainable collection practices and a decline in its wild populations. This communication highlights concerns about the rapid decline of the *F. roylei* population in Himachal Pradesh, Uttarakhand, Jammu and Kashmir and by making suitable conservation strategies along with sustainable utilization are earnestly undertaken. Given its medicinal importance, it is crucial to prioritize the conservation of *F. roylei* through various methods. These include identifying areas for the conservation of medicinal plants, both in their natural habitats (in-situ conservation) and through propagation and multiplication outside their natural habitats (ex situ conservation). It is also important to strengthen biodiversity management committees, raise awareness among key stakeholders, and promote sustainable harvesting practices to ensure the long-term survival of *F. roylei*.

Keywords: Conservation, Endangered, Medicinal plant, Traditional knowledge

TSIII-PP-27

Analysis of genetic diversity in grain amaranth (*Amaranthus* sp.)

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The current study was carried out at the Integrated Research Farm, Department of Organic Agriculture and Natural farming, CSKHPKV Palampur during *Kharif* 2023. The experimental material for this investigation included 37amaranth genotypes procured from NBPGR Regional Station, Shimla along with three checks *viz.,* Annapurna, Durga and PRA-3. Data was recorded for various agro-morphological and biochemical traits *viz.,* days to 50% flowering, days to 80% maturity, plant height, number of spikelets per plant, inflorescence length, grain yield per plant and protein content. The standard procedure of Panse and Sukhatme (1985) was used for the analysis of variance which revealed a significant amount of variation among the genotypes at a 5% level of significance. The parameters of variability were evaluated as per the standard procedure of Burton and De Vane (1953). Genetic diversity analysis was done using Mahalanobis D^2 statistic. Days to 50% flowering ranged from 46.00-63.00 days, days to 80% maturity from 117.00-131.00 days, plant height from 117.17 to 177.97 cm, number of spikelets per plant from 19.78-57.07 inflorescence length from 25.08-54.42 cm, grain yield per plant from 6.90-28.16 g and protein content from 11.73-16.80%. High PCV and GCV were observed for traits *viz.,* grain yield per plant and number of spikelets per plant. Heritability in a broad sense was high for all the studied traits except days to 80% maturity. Whereas, genetic advance was high for grain yield. The genotypes were grouped into eight diverse clusters using D^2 analysis and clusters II and VII had the highest inter-cluster distance thus, they can be used for hybridization. Based on *per se* performance genotypes *viz.,* EC-169627 and EC-169628 had the highest grain yield per plant however, genotypes *viz.,* EC-170305 and EC-169629 had the highest protein content. Thus, these genotypes can be directly used in varietal development programs.

Keywords: Diversity, Variability, D^2 analysis, PCV, GCV, Heritability, Genetic advance

Technical Session-III:

In situ/on-farm, *ex-situ* Conservation and Access and Benefit Sharing

TSII-PP-29

Validation of the droplet vitrification protocol for cryo-conservation of in vitro grown Grand Naine banana (*Musa* spp.) shoot apices

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Banana provides an essential food source for more than 400 million people in the developing countries of the tropics and the sub-tropics. Bananas are the second largest fruit crop in cultivation and the fourth most important crop after rice, wheat and maize in the developing world concerning the value of production. Banana being an essential staple fruit crop with varied economic values has been facing a crucial concern in cryo-conservation *via* droplet vitrification method. Given this, shoot apices were excised from commercial cultivar Grand Naine and were subjected to droplet vitrification at varied loading and PVS 2 dehydration time intervals. Then these vitrified explants were kept in liquid nitrogen for a week. Successively, rapid thawing was adopted and the toxic effect of the PVS2 solution was removed by using an unloading solution to accelerate its survival and regeneration. Post-thaw survival and regrowth were assessed by vitrified explant inoculated in the recovery medium. After 3 to 4 weeks, the highest survival and regeneration rate of the cultures revealed that T 3 (Loading solution 20 min + Plant Vitrification Solution 2 at 60 min) and T 6 (Loading solution 30 min + Plant Vitrification Solution 2 at 60 min) treatment combinations incubated at 0°C were desirable than PVS 2 treatment incubated at 25°C. Hence, these two treatment combinations could be effectively utilized for the cryo-conservation of Grand Naine banana shoot apices in future for long-term conservation.

Keywords: Cryo-conservation, Droplet vitrification, Banana meristem, Loading solution, PVS 2 Solution

TSIII-PP-30

Sustaining wild edible fruit treasures: Ex-situ conservation of *Artocarpus lacucha* Buch.-Ham.

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Artocarpus lacucha Buch.-Ham, commonly referred to as Monkey jack, is a relatively underexplored fruit crop primarily indigenous to Southeast Asia. In the North-Western Himalayan region, it holds a special status as one of the region's wild edible treasures, cherished for its rich nutritional profile and contributions to the human diet, due to its robust antioxidant properties. A remarkable challenge in the conservation of this indigenous fruit crop arises from the recalcitrant nature of its seeds. Conventional wisdom advises keeping seeds in the fruit until just before planting, but without proper cold storage, their viability diminishes within a week. To surmount these obstacles and ensure a consistent supply of plants for plantation purposes, as well as the preservation of noble genetic variations, the establishment of *in vitro* conservation protocols becomes a matter of paramount importance. This technique plays a significant role in the ex-situ conservation of the *Lacucha* species. Experimental endeavours conducted with *A. lacucha* from the In Vitro Gene Bank (IVGB) at ICAR-NBPGR, New Delhi have revealed the efficacy of specific hormone concentrations in promoting shoot multiplication. In these experiments, shoot tips carrying 3 to 4 leaf primordia were isolated and cultivated in media featuring varying concentrations of BAP (0.2-1.5 mg/l). Notably, higher hormone concentrations, particularly 1mg/l BAP, have demonstrated promising results in terms of enhancing shoot numbers and node production. These protocols serve as a means of rapidly multiplying Monkey jack plants, thus guaranteeing a reliable and uniform source of plant material. However, for *in vitro* conservation, BAP was not required. It was found that on basal MS medium, shoots of *A. lacucha* could be conserved for up to 3 months without subculture. These strategic initiatives are significant in safeguarding and propagating this underutilized fruit crop and upholding its nutritional and economic significance.

Keywords: Wild edible fruit, Ex-situ conservation, Conservation protocols

TSIII-PP-31

Influence of plant growth regulators on flowering and yield of strawberry (*Fragaria* × *ananassa*) cv. Camarosa

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The present study entitled, "Influence of plant growth regulators on flowering and yield of strawberry (*Fragaria × ananassa*) cv. Camarosa" was carried out at Horticultural Research & Training Station and Krishi Vigyan Kendra, Solan at Kandaghat during the year 2021-2022. The experiment was laid out in Randomized Block Design (RBD) with three replications having ten treatments of different plant growth regulators viz., T1: 5 ppm NAA, T2: 10 ppm NAA, T3: 15 ppm NAA, T4: 25 ppm GA3, T5: 50 ppm GA3, T6: 75 ppm GA3, T7: 5 ppm BA, T8: 10 ppm BA, T9: 15 ppm BA and T10: Control. The observations were recorded based on flowering and yield parameters. Among different plant growth regulators plants treated with GA3 at 75 ppm concentration took minimum days for initiation (96.67 days) of flowering and prolonged duration (117.75 days) of flowering with the maximum number of flowers (29.33), fruit set (89.44 %), number of fruits (26.23) and yield (388.03 g/plant) were recorded. Therefore, it can be concluded that GA3 treatment at 75 ppm renounced the best results and can be used for further analysis.

Keywords: Strawberry, Plant growth regulators, Growth, Yield, Fruit quality

TSIII-PP-32

Factors affecting *in vitro* propagation of an endangered medicinal herb *Trillium govanianum* (Himalayan Trillium): useful insights towards conservation practices

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About 70-80% of people worldwide depend on traditional and herbal medicines to meet their primary healthcare needs. Therefore, the global demand for herbal medicines is growing day by day. In the Himalyan region, *Trillium govanianum* Wall. ex D. Don (Himalayan Trillium, Nag chhatri), is one such medicinal herb known for its multiple therapeutic values. In natural conditions, it is propagated through seeds and rhizomes. It takes about 4-6 years to grow from initial material to maturity due to weak seedlings and vegetative propagation is also very low due to its geophyte nature. The declining plant population as well as dependency and disruptive means of wild collection has put *T. govanianum* under the category of endangered Himalyan plant species. In recent decades, biotechnological approaches including plant cell, tissue and organ culture techniques offer an alternative method for propagation and active ingredient production in medicinal plants. For *in vitro* propagation, plant material was procured from the natural habitat and different parts *viz.,* seeds, roots, rhizomes, stems and leaves were used as explants for in *vitro* regeneration. Micropropagation is a complicated process and comprises of five stages, in which each stage having specific requirements and problems. During *in vitro* propagation, each stage of micropropagation was influenced by numerous factors like explants, age of explant, photoperiod, MS salt concentration, sterilant, endophytic contamination, chlorosis, sucrose contents, plant growth regulators & additives, chilling treatment, pulse treatment and bio hardening agents etc. Therefore, it was inferred that the present study would be helpful towards the evaluation of factors affecting *in vitro* culture propagation of an endangered medicinal herb *Trillium govanianum.*

Key words: *In vitro*, Endangered, Explants, Factor, Medicinal herb, Micropropagation, Himalayan Trillium

Technical Session-IV:

Plant Biodiversity and Local Food Systems

TSIV-PP-33

Expanding kiwifruit cultivation to higher hill regions of the North-West Himalayas through wild kiwi selections (*Actinidia callosa* var. *strigillosa* C. F. Liang)

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Kiwifruit (*Actinidia* spp.) is celebrated globally for its delectable taste and exceptional nutritional benefits. Its centre of origin spans across East Asia to the eastern Indian subcontinent; however, domestication has been carried out in New Zealand over the past century. In the early 1960s, kiwifruits (*A. deliciosa*) were introduced in the Indian Himalayas. Although female cultivars like Hayward and Allison are widely grown in the mid-hill regions, their cultivation is limited between 300 and 2000 m above mean sea level (MSL). The higher hills (>2000 m above MSL) of the Himalayan regions face challenges due to existing cultivars' limited adaptability, resulting in reduced yields compared to global standards. *A. callosa* and *A. strigosa* are two underutilised wild kiwi species native to northeastern India. *A. callosa* shows promise as a cold-resistant rootstock, offering new possibilities for creating cold-resistant kiwifruit varieties through selective breeding. A comprehensive survey and selection encompassing morphological, biochemical, and sensory evaluations of fruit samples from 81 healthy and bearing female wild kiwi vines in the North Sikkim district of Sikkim during the period 2021-2023, has generated six promising selections of wild kiwi (*Actinidia callosa* var. *strigillosa*). These six selected wild kiwi genotypes viz. viz. SKNLA-11, SKNBC-01, SKNBC-02, SKNLC-02, SKNLC-07, and SKNZM-02 demonstrated exceptional performance across multiple horticulturally significant traits for their commercialization. Integrating these selected genotypes into breeding programmes could expand kiwifruit cultivation in the higher Himalayan hills (2000–3000 m above MSL). Cold-hardy kiwifruit cultivar development is possible by incorporating these well-suited native species into breeding programs. This expansion will not only enhance employment prospects for mountain communities but also make a significant contribution to fruit diversification and boost the local economy as well.

Key words: Cold-hardy, Genotypes, Selections, Sensory evaluation**,** Wild kiwi, Northeast

TSIV-PP-33

Plant Diversity and Edible Macro-Fungiin Food Systems of Tribal Communities in Baspa Valley, Kinnaur (Himachal Pradesh)

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Baspa valley of Kinnaur district in Himachal Pradesh is well known for its pristine landscapes and unique biodiversity. Within this picturesque setting, local communities have for long relied on the rich biological diversity for their sustenance. The present study was undertaken for Rakchham and Chitkul villages, nestled in the upper catchments of the Baspa valley of Kinnaur in the Western Himalayas. Primary objectives focused on obtaining information on wild edible plants and some macro-fungi, cataloguing and describing them as fruits, potherbs and vegetables, consumed raw or cooked, and understanding the traditional knowledge and practices associated with them. This study documented 53 plant *taxa*, (including some wild edible macro-fungi), representing 44 genera distributed among 28 families. The documented plant *taxa* hold multifaceted roles, a source of supplementary food, serving as wild edibles, vegetables, and essential ingredients in local cuisines, and even contributing to the production of traditional alcoholic beverages. Some plants, besides being used as fruits and vegetables, are also used as herbal teas (dried petals of *Rhododendron anthopogon, Thymus serpyllum*, bark of *Betula utilis* and *Taxus contorta*) and condiments (*Angelica glauca, Carum carvi, Elwendia persica, Hippophae* spps., *Heracleum candicans* and *Mentha longifolia*). The study involved field surveys, interviews with local inhabitants, open-ended questionnaires, plant collections, and proper identification of plant species. The results highlight a wide range of species, including herbs, shrubs, trees, and macro-fungi, playing a

vital role in their local dietary regimen, highlighting the role of plant diversity in strengthening local food systems. Recognizing the nutritional and cultural value of these biological resources is essential for promoting food security, preserving cultural heritage, and conserving the diverse flora of this region. This research not only contributes to the academic understanding of biodiversity but also emphasizes the need for sustainable practices, raises awareness about the importance of these wild resources, and plans for their further conservation.

Keywords: Biodiversity, Traditional knowledge, Tribal communities, Wild edible plants, Macro-fungi

TSIV-PP-35

Momordica balasamina: an underutilized species plays imperative role in nutritional and economical upliftment in north western plains of India

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Momordica balasmina commonly known as Balsam apple or *Jhaad karela* is predominantly a monoecious annual of Cucurbitaceae family. It is acknowledged as a gifted species owing to its pharmacological potential. The leaves and fruits of the Balsam apple are consumed as fresh vegetables and rich reservoirs of phytonutrients like potassium, calcium, magnesium, sodium, phosphorus, manganese, zinc and iron. In economically weaker communities, this species is being promoted as a protein supplement in dominantly cereal-based diets. Despite its nutritional enrichment, this species remains largely underutilized and negligible in the country. However, a village, Gholian Khurd in district Moga of Punjab is leading as an example in extricating economic benefits from this species. The crop grown on approximately 70 acres by 25 farming families of the village has also led to considerable improvement in the germplasm and production technology of the Balsam apple over the years. Farmers are earning a minimum net profit of 1.2 lakhs per acre and the retail price remains Rs 90-150/kg in the local market. The high profits earned by the farmers of this village created a ripple effect in the neighbouring villages which led to the further adoption of *jhaad karela* in the district.

Keywords: Underutilized species, Nutritional, Economical, Phytonutrients

TSIV-PP-36

Evaluation of common bean genotypes for yield and related traits in zone IV of Himachal Pradesh

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Common bean (*Phaseolus vulgaris* L.), locally known as rajmash is a major commercial crop in the north-western Himalayan region of India. The present investigation was carried out at Mountain Agricultural Research and Extension Centre, Sangla, District Kinnaur representing zone IV of Himachal Pradesh. A total of 48 genotypes of common beans including two checks Baspa & Jawala (released varieties) were evaluated for yield and its related traits in randomised block design with three replications. Sufficient genetic variability was observed for seed yield and its component traits suggesting the scope of selection for these traits. High heritability coupled with high genetic advance was observed for 100-seed weight, seed yield per plant and biological yield per plant. Seed yield per plant was significantly positively correlated with all characters studied except days to flowering. Path analysis revealed a high and positive direct effect on seed yield per plant by biological yield per plant followed by harvest index. The highest indirect effect on seed yield per plant was observed through biological yield per plant followed by branches per plant, plant height and harvest index. Biological yield per plant followed by branches per plant were observed to be the best selection indices for increasing seed yield per plant.

Keywords: Common bean, Genotype, Genetic variability, Traits

TSIV-PP-37

Characterization of basmati rice genotypes of North Western Himalayas

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An experiment was conducted with 36 rice genotypes at Rice and Wheat Research Station, Malan during the *kharif 2022* season and evaluated yield contributing characters using D^2 analysis to study the diversity pattern among the genotypes were grouped into 8 clusters, of which cluster VII and cluster VIII (42.92) followed by cluster VI and cluster VIII (39.80) and cluster V and cluster VIII (35.02) and cluster V and cluster VIII observed inter-cluster distance. Hence the genotypes in cluster VII, cluster VI and cluster V had wider diversity than genotypes in cluster VIII and these lines may be utilized in further breeding programmes for the exploitation of hybrid vigour. The intra-cluster distance was maximum in cluster I (18.31) followed by cluster II (12.62) indicating hybridization involving genotypes within the same clusters may result in good cross combinations. The traits viz., spikelets per panicle, 1000-grain weight, plant height and days to 75% maturity contributed 66.84% towards total divergence. Therefore, these characters may be given importance during the hybridization programme.

Keywords: Genetic diversity, Yield contributing characters, Rice, Cluster

TSIV-PP-38

Analysis of genetic diversity in grain amaranth (*Amaranthus* sp.)

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The current study was carried out at the Integrated Research Farm, Department of Organic Agriculture and Natural farming, CSKHPKV Palampur during Kharif 2023. The experimental material for this investigation included 37 amaranth genotypes procured from NBPGR Regional Station, Shimla along with three checks viz., Annapurna, Durga and PRA-3. Data was recorded for various agro-morphological and biochemical traits viz., days to 50% flowering, days to 80% maturity, plant height, number of spikelets per plant, inflorescence length, grain yield per plant and protein content. The standard procedure of Panse and Sukhatme (1985) was used for the analysis of variance which revealed a significant amount of variation among the genotypes at a 5% level of significance. The parameters of variability were evaluated as per the standard procedure of Burton and De Vane (1953). Genetic diversity analysis was done using Mahalanobis D2 statistic. Days to 50% flowering ranged from 46.00-63.00 days, days to 80% maturity from 117.00-131.00 days, plant height from 117.17 to 177.97 cm, and number of spikelets per plant from 19.78-57.07. inflorescence length from 25.08-54.42 cm, grain yield per plant from 6.90-28.16 g and protein content from 11.73-16.80%. High PCV and GCV were observed for traits viz., grain yield per plant and number of spikelets per plant. Heritability in a broad sense was high for all the studied traits except days to 80% maturity. Whereas, genetic advance was high for grain yield. The genotypes were grouped into eight diverse clusters using D2 analysis and clusters II and VII had the highest inter-cluster distance thus, they can be used for hybridization. Based on per se performance genotypes viz., EC-169627 and EC-169628 had the highest grain yield per plant however, genotypes viz., EC-170305 and EC-169629 had the highest protein content. Thus, these genotypes can be directly used in varietal development programs.

Keywords: Diversity, variability, D^2 analysis, PCV, GCV, heritability, genetic advance.

TSIV-PP-39

Comparative evaluation of phytochemical and antioxidant properties of *Rauwolfia serpentina* and *Picrorhiza kurroa* wild plant species

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This study sought to evaluate two endangered plant species in the western Himalayas, specifically *Rauwolfia serpentina and Picrorhiza kurroa*. The objectives encompassed an analysis of their phytochemical and antioxidant compositions using a variety of qualitative and quantitative techniques. In the quantitative analysis, the aqueous extracts exhibited a total phenolic content ranging from 22±0.19 to 92±0.23 mg/g, while the acetone extracts ranged from 102±0.42 to 181±0.21 mg/g. The total flavonoid content in the aqueous extracts varied from 7.2±0.003 mg/g to 51±0.21 mg/g RU, and in the case of acetone extracts, it ranged between 12.6±0.34 to

65±0.31 mg/g RU. Antioxidant activity was assessed through DPPH and nitric oxide radical scavenging, as well as FRAP assay methods. In the DPPH assay, the IC50 value for aqueous extracts of phenolic content was 68.1 µg/ml, and for acetone extracts, it was 56.8 µg/ml. In the nitric oxide radical scavenging assay, the best IC50 value for aqueous extracts of phenolic content was 53.7 µg/ml, and for acetone extracts, it was 50.1 µg/ml. The highest FRAP value was observed in acetone extracts of phenolic compounds (0.536±0.045), while the lowest was found in aqueous extracts (0.147±0.001). The TLC study showed the presence of secondary metabolites such as total phenols, alkaloids, flavonoids, saponins, steroids, etc. that were present in the acetone and aqueous leaf extracts of field-grown and wild varieties of *Rauwolfia serpentina* and *Picrorhiza kurroa.* This study provides a comprehensive overview of the phytochemical profile and antioxidant activity of *Rauwolfia serpentina* and *Picrorhiza kurroa*, contributing valuable insights for potential medicinal applications.

Keywords: *Rauwolfia serpentina, Picrorhiza kurroa*, Phenolic compound, DPPH, FRAP, IC50

TSIV-PP-40

A comparative analysis of biosolvents for efficient extraction of polyphenolic phytochemicals from diverse citrus peel varieties in the Western Himalayan Region

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Citrus peel, a prominent byproduct of citrus fruit, serves as a substantial source of fruit waste. This study investigates the potential of citrus peels as a source of antioxidants and antimicrobial agents for food preservation. The study also focuses on optimizing different solvents for extraction to enhance the yield of bioactive compounds. The purpose of this study was to optimize the solvent used in the soxhlet extraction method. Various citrus peel varieties, including *Citrus aurantifolia* (Key lime), *C. pseudolimon* (Hill Lemon), and *C. maxima* (Pomelo), were subjected to extraction using three distinct solvents: Dichloromethane, n-hexane, and methanol. This optimization process was based on evaluating parameters such as total phenolic content, total flavonoid content, DPPH (2,2-diphenyl-1-picrylhydrazyl) radical scavenging activity, and antibacterial activity using the agar well diffusion method. The study revealed that methanol is the most efficient solvent for extracting phytochemicals from citrus peels of different species. Key Lime peels, when extracted with methanol, yielded the highest concentration of phenols, flavonoids, and showed enhanced antioxidant activity. However, methanolic extracts from all three species exhibited significant antibacterial properties against food-borne pathogens such as *V. cholerae*, *S. boydii*, *E. faecalis*, *B. cereus*, *P. aeruginosa*, and *E. coli* using the agar well diffusion method. Key Lime peel extract showed the most substantial inhibitory effect, followed by Hill lemon and Pomelo, suggesting their potential as natural antimicrobial agents. The present study concludes that among the different solvents tried methanolic solvent was found best for the extraction of bioactive compounds from *C. aurantifolia*, *C. pseudolimon* and *C maxima*. The methanolic extract from different citrus species also showed antimicrobial activity against the various tested microorganisms and can be used as a potential antimicrobial agent in edible packaging to extend the shelf life of perishable agricultural produce.

Keywords: Citrus peel, Polyphenolic phytochemicals, Biosolvents, Extraction

TSIV-PP-41

Food security in India

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Eat healthy and live healthy" is one of the essential needs for long life. today's world has been adapted to a system of consumption of foods which has several adverse effects on health. Fast foods include momos, chips, sandwiches, hamburgers, choumin, cold drinks, French fries, chicken nuggets, pizza or chocolate although so many fast food restaurants offer slower foods like chilly mashed potatoes or salads. From the study, certain types of factors were identified that influence the students to eat fast food. It was observed that above 80% of students prefer fast food for taste, while 7 % of students prefer fast food for convenience and fast service. So it is clear that the ingredients of fast food give great taste, and flavour and are easy to prepare and ready to consume within no time influencing students to eat them. The opinion would be attributed to the fact that most of the teenagers today do not like spending more time on eating and are always in a hurry.

Keywords: Food security, Fast food, Adverse effect

TSIV-PP-42

Studies on diversity, distribution and relative abundance of insect pollinators on *Bergenia ciliata* (Haw.) Sternb. and *Vinca major* (Linneaus) in Shimla Hills, Himalaya

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Medicinal plants are highly valuable and most of them depend on insect pollinators for their reproduction. Therefore, it is important to study the insect pollinators for the conservation of medicinal plants in the Himalayan regions. The present study on diversity and distribution reveals a total of 29 insect pollinators collected on two medicinal plants i.e. *Bergenia ciliata* (Haw.) Sternb. and *Vinca major* L. in different localities of Shimla Hills, Himalayas. Of these 29 insect pollinator species, 8 species have been collected on Bergenia ciliata (Haw.) Sternb. belongs to 3 orders i.e. Coleoptera, Hymenoptera and Diptera.Whereas 24 species have been recorded and collected on Vinca major (L.) under four orders i.e. Coleoptera, Hymenoptera, Lepidoptera and Diptera. Besides diversity & distribution, the study has also been conducted on the relative abundance of insect pollinators on these two medicinal plants. During this study period, it has been observed that dipterans were the most abundant insect pollinators of *Bergenia ciliata* (Haw.) Sternb. in all the four localities i.e. Dhalli (80%), Kufri (63.41%), IGMC (60.86%) and Fagu (64%), whereas lepidopterans were the most abundant insect pollinators of Vinca major (Linnaeus) at Dhalli (60.76%), Summerhill (58.46%), Chauda Maidan (58.95%), IGMC (57.42%), Kasumpti (63.20%) and Chotta Shimla (63.06%).

Keywords: Diversity, Distribution, Relative abundance, Insect pollinators conservation

TSIV-PP-43

Pharmaceutical and microbial potential of *Acorus calamus* Linn.: An endangered highly valued medicinal plant species

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India has a very rich plant biodiversity, abundant of which are medicinally useful. Plant biodiversity is disappearing at an alarming rate due to over-exploitation environment unfriendly harvesting loss of growth habitat and unmonitored trade of medicinal plants. Therefore, as a matter of urgency, there is a critical need for the management of traditional medicinal plant resources. Acorus calamus is a perennial medicinal herb with creeping rhizomes and identified as an endangered species of medicinal plant. The active phytoconstituents such as sesquiterpenes, phenyl propanoids, and monoterpenes, as well as xanthone glycosides, flavones, lignans, steroids obtained from the plant, have been proven to show various pharmacological activities such as larvicidal, antibacterial, mutagenic insecticidal, cytotoxic, hepatoprotective, anticonvulsant, neuroleptic, smooth muscle relaxant and smooth muscle stimulant activity. The present study focuses on the pharmaceutical and microbial potential of Acorus calamus. The antimicrobial activity of the plant extract against various pathogenic strains was evaluated by using the agar well diffusion method. In the present investigation, we observed that the methanol rhizome extract of *Acorus calamus* showed 27 peaks in the chromatogram from GC-MS analysis. A total of 10 compounds were identified as 4, 22-Stigmastadiene-3-one (1.83%), β – Asarone (18.71 %), 9, 12-Octadecadienoic acid, methyl ester, (E,E)- (14.26 %) etc. These identified phytoconstituents were responsible for various biological activities. The maximum antibacterial potential of Methanolic (rhizome) extract was observed against Staphylococcus aureus (19.5 mm) whereas methanolic (Leaves) extract was highly effective against Staphylococcus aureus (16 mm) which was more effective than positive control Ciproflaxin (11mm and 6.6mm respectively). Our results revealed that methanolic crude rhizome and leaves extract of the *Acorus calamus* contain medicinally important bioactive compounds and it justifies their use in traditional medicines for the treatment of various diseases.

Keywords: Acorus calamus, Phytochemical, Glycosides, *Staphylococcus aureus*, GC-MS, β – Asarone

Technical Session-V:

Enterpreneurship and Value Chains: Role of Youth and Women

TSV-PP-44

Promoting Entrepreneurial Skills among the Youths of the Indian Himalayan Region

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The word entrepreneurship has been derived from the French word 'entrependre' which means 'to undertake' or 'how to do something'. Entrepreneurs are the persons who can see and evaluate business opportunities, gather the necessary resources, exploit opportunities to take advantage of them and initiate appropriate action to ensure success. Entrepreneurship development is a process involving three phases at the community level namely the stimulatory phase, the support phase and the sustaining phase. The first phase involves initial entrepreneurial pursuits like drivers of motivation and information seeking to establish enterprise, second phase involves activities such as infrastructure facility, resources, credit and skill development, while the last phase pertains to sustaining and developing enterprise through technological advancement, diversification, discovering new products, value addition etc. However, the requisite skills are very important for entrepreneurship not only to establish but also to sustain the enterprise in the long run because it is estimated that only about 5 per cent of the total workforce in India has undergone formal skill training. Hence, the government is making concerted efforts to provide essential skills required to run an enterprise which may become not only a source of income but also a solution for solving the problems of our educated and uneducated unemployed youths. Though there are a lot of challenges like difficult terrain, lack of infrastructure, limited market, shortage of skilled trainers, lack of access to training for vulnerable and marginalized groups etc. a lot of schemes/ programmes such as as Pradhan Mantri Kaushal Vikas Yojana, Udaan, Deen Dayal Upadhyaya Grameen Kaushalya Yojana, Startup India, Northeast Industrial and Investment Policy, Pradhan Mantri Yuva Udyami Vikas Abhiyan etc. have been initiated by the government for promoting entrepreneurship among our youths which may certainly enabling them to job providers rather than job seekers.

Keywords: Entrepreneurship, Skill development, Difficult terrain, Startup India, Job providers marginalized groups, Diversification, Technological advancement.

TSV-PP-45

Empowering Women Entrepreneurship in India

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The development of a nation to a great extent depends upon the quality of its human resources. Innovative, honest, sincere, hardworking, and creative people lead the country in the right direction. Dr Shiv Khera, a well-known thinker has rightly stated that winners do not do different things, but they do things differently, which very well applies to entrepreneurs. For long female entrepreneurship has been overlooked forgetting that women entrepreneurship can also play a significant role in the economic growth and poverty reduction in our country. However, it has been observed that social customs/traditions compel the woman to stay at their home, doing household work, and caring for children and elderly members. Various countries have different entrepreneurial ecosystems in terms of their respective culture, economy, finance, institutions, infrastructures, policies, politics and programs which influence the ability of women entrepreneurs to enter the global market. Self-determination, self-esteem, hope for recognition, career goals etc. are the main elements which motivate the woman to undertake entrepreneurship, while poor economic conditions, unemployment in the family, family responsibilities and divorce are the factors which may diversely affect the woman's entrepreneurial activities.

But it should be remembered that a society in which woman cannot realize their full potential loses significant potential for Innovations, economic growth, and job creation. Lack of professional education, problems collaborating with male workers, economic life, skill problems, negligence by financial institutions, lack of self-confidence, lack of family support/encouragement etc. are major problems of women entrepreneurs in India. However, women entrepreneurs need to be given assurance, freedom, and mobility to come out of their irrationalities. There are some challenges like problems with finance arrangements, lack of professional education, infrastructure, lack of skills, lack of self-confidence, problems in family support and gender equality etc faced by women entrepreneurs. Our government has taken several initiatives like Rashtriya Mahila Kosh, Prime Minister Rosary Yojana (PMRY), Working Woman's Forum, Indira Mahila Yojana, India Priyadarshani Yojana, Integrated Rural Development Programme (IRDP), Training of rural youths for self-employment, Trade and Village Industries Commission, Woman's Development Corporation Scheme(WDCS), Mahila Samiti Yojana etc. which can prove to be a boon for empowering woman entrepreneurship in the country.

Keywords: Women entrepreneurship, Economic condition, Unemployment

TSV-PP-46

Impact of tourism on plant biomass and carbon stock in North-West Himalayas

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Studies in environmental science, ecology, and travel management have turned their attention to the effects of tourist disturbance on the environment. The purpose of the current research, conducted between the years 2021 and 2023, was to examine the influence of tourism on plant biomass and carbon stock along the tourist trail of Hatu in the Shimla district of Himachal Pradesh. We compared plant biomass and carbon at three elevations and five distance points from the trail, where the intensities of tourist disturbance were distinct. Three elevation and five distance points from the trail were used to categorise the study area: E_1=2700 m, E_2=2900 m, and E_3=3100 m; 0-10 m, 10-20 m, 20-30 m, 30-40 m and undisturbed region. Results revealed that tree biomass and carbon stock increased significantly with increasing distance from the trail. Thus, current tourist activities have a significant negative impact on the ecological environment on the Hatu religious trail. Furthermore, human disturbances can cause reductions in biomass and vegetation height, changes in species composition, formation of informal trails and an increase in weeds and plant pathogens in the vegetation. Hatu Peak is located in Hatu beat of Kotgarh Forest Division, Shimla, Himachal Pradesh. It is a famous tourist site for its scenic beauty and at the top of a peak is a small wooden temple (Hatu temple). Most of the tourists visit this temple every year due to religious beliefs. The present study was carried out during 2021-2023 in Shimla district of Himachal Pradesh situated between 31°14'37" N to 31°14'45" North latitude and 77°27'20" E to 77°30'38" East longitude. The study area was divided into three altitudes *viz*., E_1 - 2700 m, E_2 - 2900 m and E_3 - 3100 m and five distance points *viz*., 0-10 m, 10-20 m, 20-30 m, 30-40 m and undisturbed. In the present study, tree biomass increased significantly with increasing distances from the trail. This indicated that tourist disturbance significantly altered the biomass of trees within 20 m of the trail but imposed a low impact in farther areas. Hence, the negative impact of tourism on the tree biomass in Hatu Peak seemed to have resulted from the vulnerability of trees to the direct impact of tourist behaviour. The maximum value (146.39 Mg ha^{-1}) for total biomass was recorded at an undisturbed distance from the tourist trail and the minimum value (77.42 Mg ha^{-1}) was observed at a 0-10 m distance from the trail. The lower biomass near the trail was attributed to the high intensity of disturbance and trampling of vegetation resulting in the compaction of soil. The lower biomass in DS may be the result of lower density of trees and it may also be associated with disturbance activities like tree felling and removing for timber, firewood collection, lopping, grazing, and selective logging.

Keywords: Tourism, Plant biomass, Carbon stock, Protected natural areas

TSV-PP-47

Development of wheat flour cookies fortified with carrot pomace and beetroot

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The purpose of the study was to investigate the effects of using whole wheat flour and carrot or beet pomace powder in the creation of high-fiber cookies on the physico-chemical and sensory properties of the cookies. The convective dehydration and vacuum drying processes were used to create the carrot pomace powder (CPP) and beet pomace powder (BPP). To establish the level of significance of variation in observations induced by changes in the cookies formulations, all the data collected were statistically analysed. In comparison to control biscuits, the carrot pomace and beetroot pomace enriched cookies had higher levels of ash, crude fibre, and moisture content, but lower levels of carbohydrate, protein, calorific value, and pH. In terms of physico-chemical and sensory qualities, the product was judged to be more acceptable after fibre fortification. Cookies packed in an LDPE pouch showed a significant decrease in colour and appearance followed by PET jar as compared to the other two packaging materials. A pronounced change in the colour was observed in cookies with beetroot pomace powder. However, cookies packaged in a metalized pouch showed the least changes in colour and appearance. The Crispness of the control and oat cookies decreased in all packaging materials as compared to fibre-rich cookies with pomace powders. The texture and crispness of cookies with beetroot pomace powder showed the least changes as compared to other cookies. Cookies with pomace powders showed fewer flavour changes in LDPE as compared to wheat flour and control cookies. The flavour score was highest in cookies with beetroot pomace powder. A pronounced effect on the overall acceptability of the cookies was found in LDPE pouches and it was observed that the overall acceptability of the cookies stored in LDPE significantly decreased with time. Cookies with pomace powders maintained better overall acceptability as compared to control and wheat flour cookies. The results obtained suggested that all three pomace powders are good sources of dietary fibre and thus can be used for fibre enrichment in cookies as well as in other food products.

Keywords: Wheat flour, Cookies, Fortified, Carrot pomace

TSV-PP-48

Creating and evaluating an active xanthan gum nano-emulsion coating infused with betel leaf extract for enhancing fresh produce shelf life

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In this study, a novel approach to enhance food quality and preserve fresh produce is explored through the development of an active xanthan gum (XG) based coating. However, it is worth noting that XG-based coatings alone do not possess inherent antimicrobial properties against common food-borne pathogens. To address this limitation, the researchers devised an innovative active coating by incorporating betel leaf extract (BLE) into XG emulsions. The study involved a thorough characterization of the BLE extract, assessing key properties including total phenolic content, total flavonoid content, and antioxidant capacity. Importantly, the BLE extract exhibited remarkable fungicidal and antibacterial properties, enhancing its potential for food preservation. The investigation further delved into the influence of varying concentrations of xanthan gum (XG) (0.1% to 0.5%), Tween 80 (1% and 3%), and BLE (1% to 5%) on the performance of the active coating based on XG emulsions loaded with BLE extract. The results of this research revealed that the active coating demonstrated significant antimicrobial effectiveness against a spectrum of bacterial and fungal food-borne pathogens, including *B. cereus, L. monocytogenes, E. coli, S. aureus,* and *P. aeruginosa*, as well as fungal cultures like *C. albicans, A. brasiliensis, R. stolonifier* and *F. oxysporum*. Furthermore, the study encompassed an examination of the shelf-life of tomatoes treated with the active coating. Various quality parameters of the tomatoes were scrutinized, such as weight loss, total soluble solids (TSS), pH, texture profile, total phenolic content (TPC), sensory attributes, and the enumeration of bacterial, mould, and yeast populations. The results demonstrated that tomatoes coated with the active formulation and stored at 4°C for 27 days remained free from spoilage or off-flavours. Consequently, this research underscores the significant potential of the developed active coating, which incorporates betel leaf extract into a xanthan gum emulsion, to substantially extend the shelf life of fresh produce.

Keywords: Active xanthan gum, Nano-emulsion coating, Leaf extract, Shelf life

TSV-PP-49

Transforming food waste into versatile and high-performance edible packaging using starch nanoparticles

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The growing interest in sustainable and edible biopolymer packaging arises from concerns about the environmental impact and health risks associated with traditional non-biodegradable plastics. Food waste contributes significantly to resource, economic, and social challenges, underscoring the urgency to enhance global sustainability and food security. To address these issues, we repurpose fruit seed waste into high-value, high-performance nano starch-based edible packaging materials. Utilizing starch nanoparticles derived from mango kernel waste, we made edible films by integrating these nanoparticles into native starch. Our study examines the impact of varying SNP concentrations (0-10%) on the mechanical, barrier, water solubility, and biodegradability properties of the nano starch-based films. Results demonstrate that the film with 5% SNP concentration exhibits optimal performance and biodegradability (within 3 weeks). These versatile edible films have potential applications as anti-fog food wraps and bags for safeguarding and storing a range of food items, including fresh produce, dairy products, meat, burgers, and spices, at room and frozen temperatures. Notably, the nano starch packaging bags effectively extend the shelf life of raspberries when compared to low-density polyethylene bags. Moreover, the film can serve as a quick-dissolving packaging solution in hot water. In sum, the conversion of food waste into nano starch film highlights its superior performance and diverse utility as an eco-friendly alternative for food preservation and storage.

Keywords: Food waste, Edible packaging, Starch nanoparticles

TSV-PP-50

Study on the Development of a Novel Biological Consortium for the Efficient Treatment of Wastewater

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Moringa oleifera is a tropical plant which is found in the Himalayas of North-Western India and is widely used as a vegetable, functional food, and medicinal plant with high nutritional composition. The properties of this tree include: antioxidant properties, antitumor activity, antidiabetic activity, anticancer activity, analgesic activity, anti-inflammatory activity, antiasthmatic activity, antifungal and antibacterial activities, and acts as a natural coagulant for wastewater treatment. The coagulant properties of this plant are used for the treatment of various water quality parameters such as turbidity, alkalinity, total dissolved solids and hardness. Our study is aimed at the optimization of various parameters for the treatment of sewage wastewater and industrial wastewater using *M. oleifera* and its consortiums. In this study, the untreated sewage water samples and effluent samples were collected from Dr Reddy's Laboratories and were initially analysed for parameters such as pH, chemical oxygen demand (COD), total dissolved solids and total suspended solids with different grades of seeds of the *M. oleifera* at different concentrations at various time intervals. The results showed that the 500mg/L to 1g/L concentration of the coarse seeds reduced COD up to 15% to 20% and it also effectively reduced the amounts of total dissolved solids and total suspended solids in sewage wastewater whereas in effluent wastewater the COD was decreased up to 20% to 25% after treatment. Further, the parameters to be checked are biological oxygen demand, amount of phosphates, nitrates, chlorides, sulphates, heavy metals and the microbiological examination of the samples. Our results suggest that the plant *M. oleifera* can be used further in consortiums for effectively reducing COD and other parameters.

Keywords: Himalayas, Moringa, Wastewater

TSV-PP-51

Role of fermented organic manure in fruit cultivation and sustenance of soil health

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Continuous indiscriminate use of chemical fertilizers not only leads to deteriorated reduction production of fruit crops, soil physico-chemical and biological characteristics and the accumulation of heavy metals which in turn affect fruit nutrients, and above all also creates environmental pollution. Modern fruit cultivation across the world uses bulky organic manure, biological agents and PGPRs/ biofertilizers along with chemical inputs among the organic inputs. Bulky organic manure (FYM/Compost), balanced use of concentrated organic manure and Fermented Organic Manure (FOM) are being used to sustain productivity and soil health. These inputs help in improving soil structure, increasing soil aeration, water holding capacity, cation exchange capacity, and buffering capacity of soil diversity of soil microbes. In the recent past, FOM is a byproduct of operational/compressed biogas plants that are being used as these contain high contents of essential nutrient elements and useful microbes in the cultivation of fruit crops alone or with a combination of chemical fertilizers. Based on the research carried out in different parts of the world, the present investigations are being carried out at Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh on apple crops.

Keywords: Bulky organic manures, Fruit crops, Soil characteristics, Fermentation

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