Mission: Shaping the future of crop improvement and seed innovation in Nepal

First National Convention on Genetics, Plant Breeding and Seed Science

(Plant Breeding Convention)
Venue: NTNC Auditorium Hall, Khumaltar, Lalitpur, Nepal
Date: 6-8 Magh 2082 BS (20-22 Jan 2026), Tuesday to Thursday

Programs and Abstracts

Organizers

Plant Breeding and Genetics Society of Nepal (PBaGSoN: https://plantbreeding.org.np/)

National Agricultural Research Institute (NARI, NARC: https://narc.gov.np/)

Co-organizers

Local Initiatives for Biodiversity, Research and Development (LI-BIRD: https://libird.org/)

Oxfam in Nepal https://nepal.oxfam.org/

National Agri. Genetic Resources Center (Genebank: https://genebank.narc.gov.np/)

National Trust for Nature Conservation (NTNC) https://www.ntnc.org.np/

Supporters

Karma and Sons Traders, https://karmagroups.com/

Nepal Agricultural Federation (NAF), http://naf.org.np/

Seed Entrepreneurs Association of Nepal (SEAN), https://nepalseedassociation.org.np/

Society of Agricultural Scientists Nepal (SAS-Nepal), https://sasnepal.org.np/

Muktinath Seed Bank LTD, https://muktinathseedbank.com.np/

Media Partner कृषि सञ्जाल https://krishisanjal.com/

Mission: Shaping the future of crop improvement and seed innovation in Nepal

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Citation

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Mission: Shaping the future of crop improvement and seed innovation in Nepal

First National Convention on Genetics, Plant Breeding and Seed Science

Plant Breeding Convention

Venue: NTNC Auditorium Hall, Khumaltar, Kathmandu, Nepal
Date: 6-8 Magh 2082 BS (20-22 Jan 2026), Tuesday to Thursday

Programs and Abstracts

Technical and publication team

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Special contribution from Jiban Shrestha, Promise Shrestha and Bal Krishna Joshi to prepare this book

Acknowledgements

We feel proud and honored to have received invaluable support and guidance from all individuals and institutions who contributed to the successful organization of the First National Convention on Genetics, Plant Breeding and Seed Science in Nepal. This landmark event would not have been possible without the collective commitment, cooperation, and enthusiasm of many stakeholders. We sincerely acknowledge all the organizers, co-organizers, and supporters whose vision, dedication, and tireless efforts laid the foundation for this convention. Our heartfelt gratitude goes to the keynote speakers and invited speakers for sharing their expertise, insights, and inspiration, which greatly enriched the scientific discourse of the convention. We extend our deep appreciation to the support team and all committees and sub-committees for their meticulous planning, coordination, and execution of various activities. We are equally grateful to the researchers, students, professors, and agriculturists whose active participation and scholarly contributions would make the convention vibrant and meaningful.

We acknowledge with thanks the private companies for their support and collaboration, as well as the farmers and innovators whose practical knowledge and innovations continue to bridge science with real-world agricultural challenges. Our sincere appreciation also goes to NARC, MoALD, DoA, and various professional societies for their institutional support and guidance. Special thanks are due to the PBaGSoN Executive Committee and its members for their leadership, commitment, and unwavering efforts in making this convention a reality. Together, all contributors demonstrated a shared dedication to advancing genetics, agrobiodiversity, plant breeding, seed science, agri-biotechnology, and agri-biostatistics, with the common goal of securing food and nutrition, improving health, strengthening agri-business, and protecting the environment. We are deeply grateful to everyone who played a role in this collective endeavor.

Contents

INTRODUCTION

Nepal, with its rich agrobiodiversity and diverse agro-ecological zones, has significant potential for agricultural advancements through the application of genetics, plant breeding, seed science, plant biotechnology and agriculture biometrics. However, the agricultural sector faces several challenges, including low productivity, limited access to improved seeds, and the need for sustainable practices that can adapt to climate change. Globally, advances in genetics, plant breeding and biotechnology have played a crucial role in enhancing food, nutrition, health, business and environment security and livelihoods. In agriculture and forestry, disciplines such as genetics, plant breeding, seed science, agrobiodiversity, biotechnology-ag, and biometrics-ag are key to improving food, nutrition, health, business, and environmental outcomes. Despite these global advancements, Nepal has not fully advanced in these fields, with research and development efforts being sparse and scattered.

To address these challenges, it is essential to bring together experts for collaborative brainstorming and innovation. Institutions like the Nepal Agricultural Research Council (NARC), Seed Quality Control Centre (SQCC), Department of Agriculture (DoA), academia, private companies, international and national non-governmental organizations (I/NGOs) and professional societies need to work together to advance these fields. While NARC, SQCC and other key institutions have made efforts in plant breeding, genetics, and seed science, significant gaps remain in knowledge, technology development and adoption, and policy implementation.

There is a growing recognition of the need to integrate modern biotechnology, biometrics, and innovative tools into traditional breeding and seed systems. This integration is vital for improving crop yields, conserving agrobiodiversity, and ensuring food security in the face of population growth and environmental challenges. Strengthening public-private partnerships and aligning with global advancements in these fields are also critical for realizing Nepal’s full agricultural potential.

In response to these needs, the First National Convention on Genetics, Plant Breeding, and Seed Science (Plant Breeding Convention) is going to be organized to bring together experts, researchers, policymakers, and stakeholders from across Nepal and beyond. The convention aims to facilitate knowledge sharing, address existing gaps, and chart a collaborative path forward for the sustainable development of Nepal’s agricultural sector. By focusing on key disciplines such as genetics, plant breeding, agrobiodiversity, seed science, biotechnology-ag, and biometrics-ag, the convention seeks to promote innovation, strengthen capacities, and develop actionable strategies that will contribute to the nation’s agricultural growth and food/nutrition/ health/ business and environment security.

OBJECTIVE

- **Share and Disseminate Knowledge**: To present and discuss the latest advancements, research findings, and existing gaps in the fields of Genetics, Plant Breeding, Agrobiodiversity, Seed Science, Biotechnology (ag), and Biometrics (ag).

- **Foster Collaboration and Networking:** To bring together professionals, experts, and stakeholders to foster networking, collaboration, and partnerships that can lead to future projects, research, or initiatives.
- **Enhance Public-Private Partnerships**: To create a framework and mechanisms for effective public-private partnerships in the areas of GAS-3B, encouraging joint efforts in research, development, and application.
- **Policy and Practice Development**: To discuss and develop policies, guidelines, and best practices that can guide future actions in the respective field or industry.
- **Addressing Challenges and Opportunities**: To identify and discuss current challenges, gaps, and opportunities in the field, and to explore potential solutions and strategies.
- **Promoting Innovation and Excellence**: To demonstrate cutting-edge technologies, innovations, and exemplary work, encouraging high standards and innovation within the industry or field.
- **Identify Future Directions**: To generate group recommendations and establish clear future directions for research, policy, and practice in the GAS-3B disciplines.
- **Document and Disseminate Outcomes**: To compile and disseminate the proceedings of the convention, including keynote speeches, thematic papers, general papers, posters, and recommendations, ensuring broad access to the knowledge shared.

Themes

GAS-3B: Genetics, Agrobiodiversity, Seed Science, Breeding, Biotechnology-ag & Biostatistics-ag

The convention will focus on six key disciplines within the broader sectors of Agriculture, Forestry, and Policy: Genetics, Agrobiodiversity, Plant Breeding, Biotechnology-ag and Biometrics-ag and Seed Science. These disciplines will be examined through the lens of both practical application and policy development, with the goal of advancing research, fostering innovation, and creating sustainable practices in these critical areas. Followings are the themes in the Convention.

I. Genetics and its Implication in Agriculture
II. Agrobiodiversity Conservation and Utilization for Resilient Agriculture
III. Plant Breeding for Food, Nutrition, Health, Business and Environment Security
IV. Agricultural Biotechnology for Smarter and More Efficient Crop Production
V. Agricultural Biostatistics and Data Science for advancing research and decision-making in the Agricultural Sciences
VI. Innovation and Good Practices in Seed Science and Technology
VII. Policy and IPR in Agriculture and Plant Breeding

Program

First National Convention on Genetics, Plant Breeding and Seed Science (Plant Breeding Convention)

Venue: NTNC Auditorium Hall, Khumaltar, Lalitpur, Nepal
Date: 6-8 Magh 2082 BS (20-22 Feb 2026), Tuesday to Thursday

Day I (6 Magh 2082BS, 20 Jan 2026)

Opening session

Chairperson: Dr Krishna Prasad Timsina; ED, NARC
Convenor: Dr Krishna Hari Ghimire
Rapporteurs: Khem Raj Pant and Jharana Upadhyaya

Time	Activity	Facilitator/ speaker
9.15 am	Registration and networking	Dr Pallavi Singh, Simran Khadka, Pratikshya Shrestha, Anjali Bajracharya, Mandira Chitrakar, Volunteers
	Poster registration and display	Jiban Shrestha, Promise Shrestha, Rita Gurung, Volunteers
	Exhibition registration and management	Dr Kalika Prasad Upadhyay, Dr Mukunda Bhattarai, Dr Sunita Sanjyal, Dr Ujjawal KS Kushwaha
10.30 am	• Chief Guest: Hon'ble Minister, Dr Madan Prasad Pariyar, MoALD • Special Guest: Dr Rajendra Prasad Mishra, Secretary, MoALD • Special Guest: Dr Naresh Subedi; Member Secretary, NTNC • Expert Guest: Bimal Kumar Baniya	
	National anthem (with script display)	Surendra Shrestha, Volunteers
10.35 am	Welcome and objectives	Binesh Man Sakha; Director, NARI
	Inauguration (lamp in Kalash)	Chief Guest
10.40 am	**Key note speech**: Innovating for Tomorrow: Integrating Genetics, Biotechnology, and Biostatistics to Advance Agrobiodiversity, Plant Breeding and Seed Science	Shiva Bahadur Nepali Pradhan; Former ED, NARC and Former DG, DoA
11.00 am	Awards distribution (1. Top-cited Researcher Award, 2. Golden Seed Award, 3. Plant Breeding Excellence Award)	Dr Hari Kumar Shrestha; Chair, Award Committee
11.15 am	Organizers' perspectives and what next	Dr Bal Krishna Joshi; President, PBaGSoN
11.20 am	Remarks: Expert Guest	Bimal Kumar Baniya; Former Director, NARC

11.25 am	Remarks: Special guest	Dr Naresh Subedi; Member Secretary, NTNC
11.30 am	Remarks: Special guest	Dr Rajendra Prasad Mishra; Secretary, MoALD
11.35 am	Remarks: Chief Guest	Hon'ble Minister, Dr Madan Prasad Pariyar
11.40 am	Closing with remarks	Dr Krishna Prasad Timsina; ED, NARC
11.45 am	Photo session and coffee break	All
12.00 pm	Poster session and stall visit	All

Scientific session I: Genetics and its Implication in Nepalese Agriculture

Chairperson: Uma Shankar Shah; Sr. Scientist, NARC Technical lead: Dr Damodar Poudyal
Rapporteurs: Amrit Prasad Poudel and Keshab Raj Pokhrel

Time	**Paper**	**Presenter**
12.30-12:50 pm	**Invited paper I**: Advances in Genetics and Plant Breeding Technologies: Global Perspectives and Implications for Nepal	Prof Dr Madhav Prasad Pandey; Prof, AFU
12:50-1:00 pm	Molecular Diversity Assessment of Nepalese Fine and Aromatic Rice Landraces using SSR markers	Dev Nidhi Tiwari; Director, DoAR
1:00-1:10 pm	SSR marker-based genetic diversity assessment of Nepalese wild rice accessions	Pradip Thapa; Tech Officer, Genebank
1:10-1:20 pm	Genome-wide association mapping of resistance to pre-harvest sprouting in winter wheat	Pratikshya Shrestha; Tech Officer, ARS, Jumla
1:20-1:30 pm	Computational Identification and Characterization of Candidate Catalase Genes in Proso Millet (Panicum miliaceum L.) Using TSA Datasets	Abhisek Chaudhary; Banaras Hindu University
1:30-1:40 pm	Screening of Drought-Tolerant Rice Genotypes Using SSR Markers	Biswash Raj Bastola; NRRP
1:40-2:00 pm	**Discussion (Q&A and suggestions/ issues)**	Technical lead
2:00-2:10 pm	**Session remarks, recommendations, and closing**	Chairperson/ session team
2:10-2:40 pm	**Lunch break, poster and stall visit**	All

Scientific session II: Agrobiodiversity Conservation and Utilization for Resilient Agriculture

Chairperson: Shiva Sundar Shrestha; President, NAF Technical Lead: Bharat Bhandari
Rapporteurs: Pradip Thapa and Ramesh Acharya

Time	Paper	Presenter
2.40-3:00 pm	**Invited paper II**: Agrobiodiversity for Climate-Resilient, Nutrition-Sensitive, and Sovereign Agri-Food Systems	Dr Pratap Shrestha; Program Specialist, SSPGR
3:00-3:10 pm	Soil biodiversity in agrobiodiversity – A mycorrhizal case study from Tarai, Manang, and Mount Everest region	Dr Roshan Babu Ojha; Soil St, NAERC
3:10-3:20 pm	Phenological variation and Yield performance of Nepalese Rice Landraces in Madhesh Province, Nepal	Nawaraj Yadav; CNRM
3:20-3:30 pm	Reflection of Agrobiodiversity in Nepalese folk songs	Dr Kalika Prasad Upadhyay; Chief, NATIC
3:30-3:40 pm	Genetic diversity analysis in fiber-related traits of different tossa jute (Corchorus olitorius L.) germplasm	Sujan Karki; JRP, NARC
3:40-3:50 pm	Genetic Diversity Assessment of Nepalese Chilli Landraces by Agro-Morphological Characterization	Dr Mukunda Bhattarai; Tech Officer, Genebank
3:50-4:00 pm	Performance of elite local germplasms of barley at HRS Dailekh	Jeet Narayan Chaudhary; Chief, HRS, NARC
4:10-4:30 pm	**Discussion (Q&A and suggestions/ issues)**	Technical lead
4:30-4:40 pm	**Session remarks, recommendations and closing**	Chairperson/ session team
4:40-5:30 pm	Tea/coffee break, Exhibition and Posters Observation	All

Day II (7 Magh 2082BS, 21 Jan 2026)

Scientific session III: Plant Breeding for Food, Nutrition, Health, Business and Environment Security

Chairperson: Bimal Kumar Baniya; Former Director, NARC Technical lead: Dr Nabin Bhusal/ Dr Dilraj Yadav
Rapporteurs: Bishnu Prasad Kandel and Md Ekram Hussain

Time	Paper	Presenter
9:30-9:50 am	**Invited paper III**: Plant Breeding: History, Achievements, Contributions, Challenges, and Future for Resilient Agriculture	Dr Rajendra Darai, Director, DoAR
9:50-10:00 am	Wheat Breeding in Nepal: Achievements, Emerging Challenges, and Future Prospects	Khem Raj Pant; NWRP

10:00-10:10 am	Examination of Promising Genotypes of Rajma (Phaseolus vulgaris L.) for Variety Release	Dr Anil Pokhrel; Coordinator, GLRP
10:10-10:20 am	Hybrid breeding and varietal development of chili pepper in Nepal	Dr Amar Bahadur Pun Magar; Senior St, NHRC
10:20-10:30 am	Diversity rich plant breeding methods for resilient agriculture	Dr Bal Krishna Joshi; Chief, Genebank
10:30-10:50 am	**Discussion (Q&A and suggestions/ issues)**	Technical lead
10:50-11:10 am	**Tea/ coffee break, Poster and Stall visit**	All

11:10-11:20 am	Genetic Analysis and Performance Evaluation of Diverse Carrot (Daucus carota L.) Genotypes	Avishek Thakur; IAAS
11:20-11:30 am	Assessment of Genetic Variability and Milling Quality of Rice Landraces (Oryza Sativa L.) of Nepal	Prashansa Pandey; AFU
11:30-11:40 am	Performance and Adaptability of Foxtail Millet Genotypes in Mid and High Hills of Nepal	Bishnu Bushal; LI-BIRD
11:40-11:50 am	Evaluation of Grain Quality Traits of Nepalese Rice Landraces	Prajita Devkota; AFU
11:50-12:00 pm	Evaluation of Grain Quality and Cooking Characteristics of Nepalese Rice (Oryza sativa L.) Landraces	Saurabh Joshi; AFU
12:00-12:20 pm	**Discussion (Q&A and suggestions/ issues)**	Technical lead
12:20-12:30 pm	**Session remarks, recommendations and closing**	Chairperson/ session team
12:30-1:30 pm	**Panel discussion** Topic: **Next-Gen Breeding: Integrating Genomics, AI, Speed Breeding and High-Throughput Phenotyping for Climate-Resilient and Nutraceutical-Rich Crops** Panelists: ● Dr Hari Bahadur KC, Joint Secretary, MoALD ● Dr Bhanu Bhakta Pokhrel, Director, NARC ● Dr Puspa Poudel, Assist Dean, IAAS ● Bharat Bhandari, ED, LI-BIRD ● Durga Adhikary, Vice Chairperson, SEAN Q&A cum discussion	Moderator: Resham Babu Amgai; Chief, NABC Rapporteur: Dr Sumitra Pantha and Mahesh Subedi
1:30-2:00 pm	**Lunch break, poster and stall visit**	All

Scientific session IV: Agricultural Biotechnology for Smarter and More Efficient Crop Production

Chairperson: Dr Tek Prasad Gotane; Director, NARC Technical lead: Dr Bal Kumari Oliya
Rapporteurs: Suman Ghimire and Pukar Bashyal

Time	**Paper**	**Presenter**
2.00-2:20 pm	**Invited paper IV**: Agricultural Biotechnology: History, Achievements, Contributions, Challenges, and Future for Smart Agriculture	Dr Shanta Karki; Chief, CAL
2:20-2:30 pm	Assessment of Induced Mutagenesis as a Tool of Genetic Variance on Seedling Quality Traits in The Local Rice Landrace	Ramesh Acharya; St, NPGRC
2:30-2:40 pm	Optimization of In Vitro Callogenesis and Plant Regeneration in Elite Sugarcane Genotype SRPJ2016 Coll#02	Dr Dil Raj Yadav; Coordinator, NSRP
2:40-3:00 pm	**Discussion (Q&A and suggestions/ issues)**	Technical lead
3:00-3:10 pm	**Session remarks, recommendations and closing**	Chairperson/ session team
3:10-3:30 pm	Tea/ coffee break, poster and stall visit	All

Scientific session V: Agricultural Biostatistics and Data Science for advancing research and decision-making in the Agricultural Sciences

Chairperson: Dr Kishor Chandra Dhahal; Dean, IAAS Technical lead: Dr Roshan Babu Ojha
Rapporteurs: Dinesh Ghimire and Sony Bhattarai

Time	**Paper**	**Presenter**
3:30-3:50 pm	**Invited paper V**: Agricultural Biostatistics in Nepal: History, Current Strengths and Weaknesses, Challenges for the Future, and Strategies for its Efficient Use for Advancement in Agri. Research and Crop Productivity in the Country.	Bharat Adhikari; Former Senior St, NARC
3:50-4:00 pm	Experimental Research Design, Sample Survey, and Statistical Analysis Practice in Agricultural Research in Nepal	Nabaraj Poudel; St, NASRI
4:00-4:10 pm	An Insight into Applied Research and Agricultural Statistics	Dr Kishor Chandra Dahal; Dean, IAAS
4:10-4:20 pm	A least used stability analysis tools by Plant breeder for varietal recommendation-GGE Biplots	Dr Umesh Kumar Acharya; Chief, NCCRC
4:20-4:30 pm	Genotype × Environment Interaction of medium grain rice genotypes using additive main effect and	Dr Nabin Bhusal; Ass. Prof., AFU

	multiplicative interaction (AMMI) across different environments of Nepal	
4:30-4:40 pm	Yield Performance and Stability of Soybean Genotypes across Multiple Environments in Western Nepal Using BLUP and GGE Analysis	Padam Prasad Poudel; St, GLRP
4:40-4:50 pm	UAV-Based Remote Sensing for Data-Driven Crop Improvement in Plant Breeding	Dinesh Ghimire; PhD Candidate, Cornell Univ.
4:50-5:10 pm	**Discussion (Q&A and suggestions/ issues)**	Technical lead
5:10-5:20 pm	**Session remarks, recommendations and closing**	Chairperson/ session team

Day III (8 Magh 2082BS, 22 Jan 2026)

Scientific session VI: Innovation and Good Practices in Seed Science and Technology

Chairperson: Benu Prasad Prasain; Chief, SQCC Technical lead: Dr Suchit Shrestha
Rapporteurs: Anoj Adhikari and Dr Sabina Manandhar

Time	**Paper**	**Presenter**
9:30-9:50 am	**Invited paper VI**: Seed Science and Technology: History, Achievements, Contributions, Challenges, and Future for Agriculture	Dr Hari Kumar Shrestha; Member, NSB
9:50-10:00 am	Key Findings and Policy Implications from Rapid Rice Seed Stock Survey at Seed Producer Organizations	Dr Narayan Prasad Khanal; CIMMYT
10:00-10:10 am	Agriculture in Vedic Civilization: A Perspective on Seed Conservation and Promotion	Basu Dev Kaphle; Chief, APTRC
10:10-10:20 am	Review of Seed Research work carried out by Nepal Agricultural Research Council during the National Seed Vision time frame	Dr Tara Bahadur Ghimire; Former Principal St, NARC
10:20-10:40 am	**Discussion (Q&A and suggestions/ issues)**	Technical lead
10:40-10:50 am	**Session remarks, recommendations and closing**	Chairperson/ session team
10:50-11:00 am	**Tea/ coffee break, poster and stall visit**	All

Scientific session VII: Policy, IPR and farmer's right in Agriculture and Group Discussion

Chairperson: Dr Ram Krishna Shrestha; Joint Secretary, MoALD Technical lead: Dr Rama Paudel
Rapporteurs: Deependra Dhakal and Padam Prasad Paudel

Time	Paper	Presenter
11:00-11:20 am	**Invited paper VII**: Policy, IPR and FR dimension and gaps in Genetics, Agrobiodiversity, Plant Breeding, Ag-Biotechnology, Ag-Biostatistics and Seed Science	Dr Devendra Gauchan; ICIMOD and President, NAES
11:20-11:30 am	Public-Private Community Partnership for Seed Sector Transformation in Nepal	Anoj Adhikari; Head, MSBL
11:30-11:40 am	कृषिजन्य भौगोलिक संकेतः पहिचानसहितको ग्रामिण विकासको माध्यम	Bimal Baral; Secretary, OCMCM
11:40-11:50 pm	Promotion of Climate Resilient Crop Varieties and Technologies in the Gandaki River Basin of Nepal	Prem Neupane; NTNC
11:50-12:10 pm	**Discussion (Q&A and suggestions/ issues)**	Technical lead
12:10-12:20 pm	**Session remarks, recommendations and closing**	Chairperson/ session team

Closing session

Chairperson: Prakash Kumar Sanjel; DG, DoA Convenor: Simran Khadka Chhetri
Rapporteurs: Dr Pallavi Singh and Dr Ujjwal Kumar Singh Kushwaha

Time	Activity	Facilitator/ speaker
12:20 pm	Reports/ Recommendations/ Declaration/ Issues (Genetics, Agrobiodiversity, Plant Breeding, Agricultural Biotechnology, Agricultural Biostatistics, Seed Science and Policy)	All technical leads
12.35 pm	Award distribution: 1. Best Oral Presentation and Research Paper Award for a student, 2. Best Poster Award for a student Token of appreciation: 1. LI-BIRD, 2. Oxfam, 3. NTNC, 4. Genebank, 5. Karma Group, 6. Muktinath Seed Bank, 7. NARC, 8. Volunteers-8	
12.45 pm	Remarks from participation	
12.50 pm	Issues, concerns and lesson learn	
1.00 pm	Remarks from guest	
1.10 pm	Convention closing remark and future strategy	Chairperson
1.30 pm	Snacks, stall visit, poster observation and networking	All

2nd General Assembly (GA) of PBaGSoN

From 2 pm onwards, 8 Magh 2082BS

For further details

Dr Binesh Man Sakha, Mbl: 9851086919
Dr Bal Krishna Joshi, Mbl: 9863020222
Ms Simran Khadka Chhetri, Mbl: 9845964894
Dr Ujjawal KS Kushwaha, Mbl: 9844033976
Email: pbagson19@gmail.com

Invited speakers, team for scientific sessions and panelists

Key note and invited speakers

SN	Tentative title	Speaker	Email	Session and date
1.	Innovating for Tomorrow: Integrating Genetics, Biotechnology, and Biostatistics to Advance Agrobiodiversity, Plant Breeding and Seed Science	Shiva Bahadur Nepali Pradhan	shivabnepalipradhan@gmail.com	I. Opening session, 20 Jan
2.	Genetics: History, Achievements, Contributions, Challenges, and Future in Agriculture	Prof Dr Madhav Prasad Pandey	mppandey.pb@gmail.com	II. Genetics and its Implication in Nepalese Agriculture, 20 Jan
3.	Agrobiodiversity Conservation and Utilization: History, Achievements, Contributions, Challenges, and Future for Sustainable Agriculture	Dr Pratap Shrestha	pratap.shrestha@libird.org	III. Agrobiodiversity Conservation and Utilization for Resilient Agriculture, 20 Jan
4.	Plant Breeding: History, Achievements, Contributions, Challenges, and Future for Smart Agriculture	Dr Rajendra Darai	rajendra5042@yahoo.co.uk	IV. Plant Breeding for Food, Nutrition, Health, Business and Environment Security, 21 Jan
5.	Agricultural Biotechnology: History, Achievements, Contributions, Challenges, and Future for Smart Agriculture	Dr Shanta Karki	shantakyoto@gmail.com	V. Agricultural Biotechnology for Smarter and More Efficient Crop Production, 21 Jan
6.	Agricultural Biostatistics: History, Achievements, Contributions, Challenges, and Future for Shaping the Agriculture	Bharat Raj Adhikari	biostatistix@gmail.com	VI. Agricultural Biostatistics and Data Science for advancing research and decision-making in the Agricultural Sciences, 21 Jan
7.	Seed Science and Technology: History, Achievements, Contributions, Challenges, and Future for Agriculture	Dr Hari Kumar Shrestha	harikumar.hk@gmail.com	VII. Innovation and Good Practices in Seed Science and Technology, Jan 21
8.	Policy, IPR and FR dimension and gaps in Genetics, Agrobiodiversity, Plant Breeding, Ag-Biotechnology, Ag-Biostatistics and Seed Science	Dr Devendra Gauchan	dgauchan11@gmail.com	VIII. Policy, IPR and farmer's right in Agriculture, 22 Jan

Scientific session team

Chair, technical lead, rapporteurs for each session

SN	Session	Name	Email	Office	Tel
1	**Opening session**				
	Chair	Dr Krishna Prasad Timsina	krishnatimsina2000@gmail.com	NARC	
	Convenor	Dr Krishna Hari Ghimire	ghimirekh@gmail.com	NPBGRC	
	Rapporteur	Khem Raj Pant	pantkhemraj07@gmail.com	NWRP	
		Jharana Upadhyaya	jharanaup@gmail.com	DoAR	
	Registration team	Dr Pallavi Singh, Simran Khadka, Pratikshya Shrestha, Anjali Bajracharya, Mandira Chitrakar, Volunteers	pallaviid.singh@gmail.com itsmepratikshya83@gmail.com simrankhadka0@gmail.com, bajracharyaanjali7@gmail.com chitrakarmandira28@gmail.com	NRRP, NARI, ARS, Genebank	
	Poster registration team	Jiban Shrestha, Promise Shrestha, Rita Gurung, Volunteers	jibshrestha@gmail.com rgurung@libird.org sthapromise0584@gmail.com	NPBGRC, LI-BIRD, Genebank	
	Exhibitions team	Dr Kalika Prasad Upadhyay, Dr Mukunda Bhattarai, Dr Sunita Sanjyal, Dr Ujjawal Kushwaha, volunteers		NATIC, Genebank, NPBGRC	
2	**Scientific session I: Genetics and its Implication in Nepalese Agriculture**				
	Chair	Uma Shankar Shah	ushah_gene@yahoo.com	PBaGSoN	
	Technical lead	Dr Damodar Poudyal	damodarpoudyal@gmail.com	SEAN	
	Rapporteur	Amrit Prasad Poudel	psdamrit@gmail.com	NRRP	
		Keshab Raj Pokhrel	pokhrel.keshab2010@gmail.com	NWRP	
3	**Scientific session II: Agrobiodiversity Conservation and Utilization for Resilient Agriculture**				
	Chair	Shiva Sundar Shrestha	shivastha1951@gmail.com	NAF	
	Technical lead	Bharat Bhandari	bbhandari@libird.org	LI-BIRD	
	Rapporteur	Pradip Thapa	pradip.thapa876@gmail.com	Genebank	
		Ramesh Acharya	rameshacharya.narc@gmail.com	NPBGRC	
4	**Scientific session III: Plant Breeding for Food, Nutrition, Health, Business and Environment Security**				
	Chair	Bimal Kumar Baniya	baniyabk@gmail.com	PBaGSoN	
	Technical lead	Dr Nabin Bhusal/ Dr Dilraj Yadav	nbhusal@afu.edu.np/ ydv.dilraj@gmail.com	AFU/ SRP	
	Rapporteur	Bishnu Prasad Kandel	bkandel33@gmail.com	IAAS	
		Md Ekram Hussain	ekram.hussain12@gmail.com	MAU	

SN	Session	Name	Email	Office	Tel
5	**Scientific session IV: Agricultural Biotechnology for Smarter and More Efficient Crop Production**				
	Chair	Dr Tek Gotame	gotame@gmail.com	NARC	
	Technical lead	Dr Bal Kumari Oliya	balkumarioliya1@gmail.com	PBaGSoN	
	Rapporteur	Suman Ghimire	suman.ghimire@foa.edu.np	AFU	
		Pukar Bashyal	pukarbashyal@gmail.com	PBaGSoN	
6	**Scientific session V: Agricultural Biostatistics and Data Science for advancing research and decision-making in the Agricultural Sciences**				
	Chair	Dr Kishor Chand Dhahal	dahalkcc@gmail.com	IAAS	
	Technical lead	Dr Roshan Babu Ojha	rbojha21@gmail.com	NAERC	
	Rapporteur	Dinesh Ghimire	dg663@cornell.edu	USA	
		Sony Bhattarai	sonybhattarai01@gmail.com	AFU	
7	**Scientific session VI: Innovation and Good Practices in Seed Science and Technology**				
	Chair	Benu Prasad Prasain	benuprasai200@gmail.com	SQCC	
	Technical lead	Dr Suchit Shrestha	suchit.shrestha@gmail.com	Karma Group	
	Rapporteur	Bishnu Bhusal	mrbishnubhusal@gmail.com	LI-BIRD	
		Dr Sabina Manandhar	sabina.mdhr20@gmail.com	Sarba Shrestha Seeds	
8	**Scientific session VII: Policy, IPR and farmer's right in Agriculture and Group Discussion**				
	Chair	Dr Ram Krishna Shrestha	rksathi05@gmail.com	MoALD	
	Technical lead	Dr Rama Paudel	paudelrama@gmail.com	IAAS	
	Rapporteur	Deependra Dhakal	ddhakal@afu.edu.np	AFU	
		Padam Prasad Paudel	pp44poudel@gmail.com	GLRP	
9	**Closing session**				
	Chair	Prakash Kumar Sanjel	sanjel55@gmail.com	DG, DoA	
	Convenor	Simran Khadka Chhetri	simrankhadka0@gmail.com	NARI	
	Rapporteur	Dr Pallavi Singh	pallaviid.singh@gmail.com	PBaGSoN	
		Dr Ujjwal Kumar Singh Kushwaha	kushujjwal@gmail.com	PBaGSoN	

Expected roles

- All sessions are expected to complete within given time. Start session on time
- Technical lead should design respective sessions (in their own innovative style) making more scientific and effective and keeping all engaging
- All issues, suggestions, recommendations, questions-answer along with session team views should be compiled and shared. These will be presented during closing session and compile as convention recommendations
- Better to copy all ppt in advance
- Manage projector, laptop and slide show along with pointer
- Discussion may be at the end of all paper presentation in each session
- Floor should be given time for specific questions and issues
- Control, manage all participations
- Make sessions very informative and interesting
- Arrange chair in front for sessions team and all presenters of this specific session during discussion
- Mobilize volunteers
- Cut off background (during asking questions, talk, speech…)

Panel Discussion

Topic: **Next-Gen Breeding: Integrating Genomics, AI, Speed Breeding and High-Throughput Phenotyping for Climate-Resilient and Nutraceutical-Rich Crops**

Role	Name	Email	Office	Tel
Moderator	Resham Babu Amgai	reshamamgain@yahoo.com	NARC	
Panelist 1	Dr Hari Bahadur KC	kchari2002@gmail.com	Joint Secretary, MoALD	
Panelist 2	Dr Bhanu Bhakta Pokhrel	bhanu.pokharel@gmail.com	Director, NARC	
Panelist 3	Dr Puspa Raj Poudel	poudelpuspa@gmail.com	Assistant Dean, IAAS	
Panelist 4	Bharat Bhandari	bbhandari@libird.org	ED, LI-BIRD	
Panelist 5	Durga Adhikari	ssscseed@gmail.com	Vice Chairperson, SEAN	
Rapporteur	Dr Sumitra Pantha and Mahesh Subedi	sumi_400@yahoo.com m.subedig@gmail.com	NPBGRC	

To make convention scientific and effective, lets follows these (plant breeding convention, 20-22 Jan 2026)

1. सम्बोधन नगर्ने (पहिलो उदघोषकले मात्र गर्ने)
2. मंचमा अशान गर्न गरि कार्यक्रम नगर्ने (सिधै आसनमा लगेर राख्ने)
3. अगाडी मंचमा एक दम थोरै अतिथिलाइ मात्र राखेर जति सक्तो कम भाषण गर्ने
4. सिधै कार्यक्रम गर्ने
5. समय सिमा भित्र नै सक्नु पर्ने, न सके त्यही नै रोक्नु पर्ने, एक जनाले समयको जानकारी गराउने (technical lead), समयलाई कुर्ने न कि अथिति/ सहभागीलाइ
6. उदघाटन (पानसमा दियो) and national anthem को बेला script screen मा देखाउने
7. खाता/ गुच्छा दिने कार्य नगर्ने
8. सबैलाई पुरा समय बस्ने गराउने, wifi को सुबिधा दिने
9. प्रश्न छोटो र सिधै राख्ने, धेरै भूमिका न बादी (बोल्दा, भाषण गर्दा, प्रश्न गर्दा)
10. सबै सहभागीलाई engage गराई राख्ने, make interactive
11. सबै सुझाव, issue, प्रश्न संकलन गर्ने, प्रश्नहरु लेखेर पनि दिन सकिने
12. कार्यक्रम/ सूचना ठाउँ ठाउमा टास्ने, समयमा नै सबैलाई सबै थोकको जानकारी गराउने
13. Volunteer लाइ orientation गरि परिचालन गर्ने
14. Live and photo live streaming गर्ने
15. Technical lead ले session design गर्ने
16. Chair, technical lead and rapporteur in front राख्ने
17. All presenters in front during discussion/ Q&A time
18. Screen show: panelist and topics/ banner/ session team/ invited speaker/ program/
19. Extra talent show
20. Regular email to all participants along with asking suggestions
21. Keep mobile in silent mode, make everything/space clean, respect each other
22. Prepare all ppt in advance in laptop. Minimize as much as possible the preparatory time
23. आफ्नो पालोमा पहिलानै गएर तयार हुने..

Contact

Ms. Simran Khadka: 984-5964894; Dr. Ujjawal Kushwaha: 984-4033976

Abstracts

Keynote and invited paper

Keynote paper

GPS-IP-01

Innovating Tomorrow: Integrating Genetics, Biotechnology and Biostatistics to Advance Agro biodiversity, Plant Breeding and Seed Science

Shiva Bahadur Nepali Pradhan
Corresponding author's email: shivabnepalipradhan@gmail.com

ABSTRACT

Nepal, within narrow latitude and longitude coupled with altitudes, is uniquely endowed with diverse climates in which Bio diversities built the basis of food security and nutrition security. With natural forest of mandarin in Hills of east, Citron in Hills of far west, Olive in Hills far west, Walnuts in High Mountains, Bel trees in river basins are the examples of gifts of Bio diversities. Introduction of genetics of rice, wheat, radish have given a remarkable increase in productivity. Hybrid maize, bred in Nepal, is the example in increasing productivity. Along with the introduction of genetics, improved cultural management helped further to increase in productivity. Agriculture Department's presentation during The World Food Day 2025 on current agriculture situation expressed the need to address the food security and malnutrition and anemic in health needing agriculture production, conservation of bio diversities and to address the effect of climate change with the involvement of science and technology with proper investment. The deficit in agriculture trade has to be made favorable too. Research needs proper placement of well-trained manpower. A strong link with International Research Institution is imperative. This Convention shall lead to Food Security and Nutritional Security and Favorable Trade Surplus.

Keywords: Convention, food security, climate change, biodiversity

Brief Bio

He holds M.Sc. Agri. Hort. He joined Government Service in 1958 in Gram Vikash. After 1960 transferred to Department of Agriculture as an Assistant Horticulturist. Transferred to District Agriculture Office Lalitpur. Assigned to Remote Area Development Board as Horticulturist. Later transferred to Department of Horticulture as Senior Horticulturist

- Worked as Project Manager, JADP
- Deputy Director General (Crops) DOA
- Director General Department of Agriculture
- Visitor at Reading University
- Joined FAO/UN
- Assigned to NARC as Council Member first and later ED

He helped to organize Annapuna Seed Bhandar in private sector. Was in the group to start Nepal Dairy in private sector. For the first time he initiated the cultivation of straw mushroom.

He was assigned at the beginning to establish Citrus Farm Dhankuta; Apple Farm in Marpha, Jomsom, Mustang. With Remote Area Development Board expanded the apple cultivation in Karnali Zone, Mustang, Solukhumbu and Rasuwa districts. As a consultant on High Value Commodity in APP emphasized Apple, Citrus, Vegetable cultivation – Seasonal and Off seasonal, Bee Keeping and Sericulture.

Attending Hill Land Symposium, West Virginia, USA, was instrumental in the establishment of ICIMOD. Appointed as an Advisor, Asia Agri. History Foundation, Bangalore, India. Conferred Honorary Appointment to the Research Board of Advisors, The American Biographical Institute, USA

Member:

- Life Member and former President, Nepal Agriculture Association, Kathmandu, Nepal
- Life Member and former President, Nepal Horticulture Society, Kathmandu, Nepal
- Member, International Society of Horticulture Sciences, ISHS

Book Publication: "Krishi maa Mero Baatoo", "5.25", Nepal Speaks – Conscious Social Order

"Shaping the future of crop improvement and seed innovation in Nepal"

First National Convention on Genetics, Plant Breeding and Seed Science

MEET OUR KEYNOTE SPEAKER

JOIN US

20th Jan, 2026

Khumaltar, Lalitpur, Nepal

Shiva Bahadur Nepali Pradhan

Senior Horticulturist; Serving agriculture since 1958 (more than 60 years)
Former Executive Director, NARC
Former DG, DoA

"Innovating for Tomorrow: Integrating Genetics, Biotechnology, and Biostatistics to Advance Agrobiodiversity, Plant Breeding and Seed Science"

No Registration Fee

Organized by: NARI, PBaGSoN

Co-organizers: Genebank, LI-BIRD

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Invited paper

Theme 1: Genetics and its Implication in Nepalese Agriculture
GPS-IP-02

Advances in Genetics and Plant Breeding Technologies: Global Perspectives and Implications for Nepal

Madhav Prasad Pandey

Department of Genetics & Plant Breeding, Agriculture & Forestry University, Chitwan
Corresponding author's email: mpandey@afu.edu.np

ABSTRACT

Since life first appeared on Earth, heredity has existed; however, its scientific principles were discovered only in the mid-nineteenth century through the pioneering work of Gregor Mendel. The concept of plant breeding began with the domestication of plants by humans during the Neolithic period (10,000–12,000 years ago). Advances in genetics and plant breeding have since played a pivotal role in the development of modern civilization. The discovery of genetic principles enabled plant breeders to systematically create and manipulate heritable variation, leading to substantial increases in crop productivity through the deployment of semi-dwarf, high-yielding, and input-responsive varieties. Hybrid breeding, mutation breeding, and tissue culture–based doubled haploid (DH) technology have also had a tremendous impact on the genetic improvement of crop plants. Conventional breeding, which is primarily based on phenotypic selection, is often constrained by long breeding cycles, complex trait inheritance, and strong genotype × environment interactions. The development of DNA markers in the 1980s, along with linkage mapping and quantitative trait loci (QTL) analysis, enabled breeders to dissect complex traits and better understand their underlying genetic architecture. Concurrently, advances in molecular biology and recombinant DNA technology provided new avenues for plant breeding. Marker-assisted selection (MAS) further improved selection efficiency and precision, particularly for traits with low heritability or latent expression. Subsequent breakthroughs in high-throughput genotyping and next-generation sequencing accelerated gene discovery and expanded access to genome-wide variation across crops and their wild relatives. Approaches such as genomic selection, pan-genomics, genome-wide association studies, and multi-omics integration are enabling breeders to capture both major- and minor-effect loci controlling complex traits. More recently, the development of high-throughput phenotyping platforms, speed breeding protocols, and the convergence of genomics, bioinformatics, and computational biology have ushered in a new era of smart, predictive, and data-driven plant breeding. Moreover, genome-editing technologies, most notably CRISPR/Cas systems, have provided unprecedented opportunities for precise, rapid, and targeted genetic improvement. Given Nepal's diverse agro-ecologies, smallholder-dominated farming systems, and increasing climate-related stresses, priority should be given to strengthening molecular breeding infrastructure, integrating MAS with conventional breeding, and effectively leveraging publicly available breeding resources to enhance breeding efficiency, accelerate genetic gains, and develop climate-resilient crop varieties.

Keywords: Conventional breeding, molecular breeding, speed breeding, genome editing, climate-resilient crop varieties

Brief Bio

Prof. Madhav Prasad Pandey is a Professor of Plant Breeding at the Faculty of Agriculture, Agriculture & Forestry University (AFU), Rampur, Chitwan, Nepal. He has over 25 years of experience in teaching, research, and academic leadership, with a strong focus on cereal crop improvement, particularly wheat and barley. He earned his Ph.D. in Plant Breeding from Justus Liebig University, Germany, and has held prestigious international fellowships, including a Postdoctoral Fellowship at Agriculture & Agri-Food Canada. Since 2016, Prof. Pandey has led AFU's flagship wheat improvement research program, resulting in the development of wheat varieties and genetic resource for climate-resiient wheat breeding. His research integrates conventional and molecular breeding, utilize genomics, phenotyping, and root system studies to develop climate-resilient, stress-adapted crop varieties. Prof. Pandey has received several competitive national and international grants. He has published extensively in reputable international journals and continues to contribute to strengthening plant breeding research and capacity in Nepal.

"Shaping the future of crop improvement and seed innovation in Nepal"

First National Convention on Genetics, Plant Breeding and Seed Science

Scientific Session - I

Invited Speaker

JOIN US

20th Jan, 2026

Khumaltar, Lalitpur, Nepal

Prof Dr Madhav Prasad Pandey

Agriculture and Forestry University
Rampur, Chitwan

Genetics: History, Achievements, Contributions, Challenges, and Future in Agriculture

Organized by:
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Theme 2: Agrobiodiversity Conservation and Utilization for Resilient Agriculture
GPS-IP-03

Agrobiodiversity for Climate-Resilient, Nutrition-Sensitive, and Sovereign Agri-Food Systems

Pratap Shrestha

Program Specialist, SSPGR; pratap.shrestha@libird.org

ABSTRACT

Agricultural biodiversity is foundational to the sustainable agricultural production that meets the food and nutrition, income and cultural needs of the smallholder farmers. It is basis for a resilient food system in the face of growing climate change uncertainties and risks. The rich agrobiodiversity of plants, animals and aquatic species used for food and agriculture evolved, created, conserved and used over millennia rapidly started shrinking with the advent of industrial agriculture in early nineteen century which further accelerated with the introduction of green revolution agriculture in early 1960s. The earlier efforts on conservation were limited to crop species with collection and preservation of seeds in the research centers' genebanks i.e. *ex-situ* conservation. After Vavilov's historic work in early 1990s many countries started their genebanks starting late 1950s and the *ex-situ* became main conservation strategy with the creation of 11 CGIAR genebanks which currently house 700,000 accessions of various PGRFA. Though farmers have been practicing in-situ on-farm conservation of agrobiodiversity traditionally and locally since they started farming, the recognition and need for this only started in early 1990s with the adoption of the Convention of Biological Diversity and implementation of a multi-country *in-situ* agrobiodiversity conservation project by IPGRI in 1996.

The international trend in the *ex-situ* and *in-situ* agrobiodiversity conservation is also well reflected in the context of Nepal. Though some collection missions took place before 1960, the seeding of *ex-situ* conservation started with the establishment of Plant Genetic Resources Section within the Agriculture Botany Division of NARC in 1984 which was integrated into the National Agriculture Genetic Resources Center, functioning as a national genebank in 2010. While the national genebank played role in *ex-situ* conservation and supporting formal plant breeding programs, its contribution to the *in-situ* conservation only started to show with the inception of an *in-situ* on-farm agrobiodiversity conservation project in 1996. Since then, the national gene bank has been taking a number of innovative strategies to support *in-situ* conservation. The Ministry of Agriculture and Livestock Development has institutionalized the conservation and sustainable use of agrobiodiversity with the formulation of the National Agrobiodiversity Policy and revision of a number of related laws, and adopted it in its agricultural extension programs. A number of non-government organizations are also actively supporting community-based agrobidiversity management programs. The recent drafting of the National Agroecology Roadmap of Nepal is going to add further impetus to the agrobiodiversity conservation in Nepal. Despite these efforts and successes, there is a pressing need to undertake a coherent, integrated

and long-term approach supported with assured investment in R&D to develop and sustain agrobiodiversity conservation strategies and initiatives in the country.

Brief Bio

Pratap Shrestha holds a Master's Degree in Agricultural Economics from the University of East Anglia and a PhD (Local Ecological Knowledge and Innovation) from the Bangor University, UK. He has over 35 years of working experience in designing and implementing agricultural research and development programs for smallholder farmers using a multi-disciplinary and integrated system-based approach. He has strong experience and expertise in participatory crop improvement; community-based biodiversity conservation and utilization; formal and farmer seed systems; agroecology for resilient food systems; gender and cross-cutting social issues; planning, monitoring and evaluation; farmer knowledge and innovation; and national and international policies related to governance of plant genetic resources and farmers' rights.

He has extensive experience in managing and governing large capacity national development organizations, fundraising with multiple funders, engaging with a wide range of stakeholders, and undertaking national and international consultancies. In 2014, he worked as a National Advisor helping the Government of Timor Leste draft it's National Seed Policy. He is currently working with SeedChange Canada as a Program Specialist for Seed Systems and Plant Genetic Resources. He is also serving as a member of the Crop Trust's BOLD (Biodiversity for Opportunities, Livelihoods and Development) Project Advisory Group (PAG). Dr. Shrestha is the current Chairperson of the LI-BIRD Executive Board. He has served as a member and advisor for a number of development organization, including Co-Chair of the governing body of the PROLINNOVA International Program.


"Shaping the future of crop improvement and seed innovation in Nepal"

First National Convention on Genetics, Plant Breeding and Seed Science

Scientific Session - II

Invited Speaker

JOIN US

20th Jan, 2026

Khumaltar, Lalitpur, Nepal

Dr. Pratap Shrestha

Program Specialist

Seed Systems and Plant Genetic Resources

Agrobiodiversity Conservation and Utilization: History, Achievements, Contributions, Challenges, and Future for Sustainable Agriculture

Organized by: NARI PBaGSoN

Co-organizers: Genebank LI-BIRD OXFAM

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Theme 3: Plant Breeding for Food, Nutrition, Health, Business and Environment Security
GPS-IP-04

Plant Breeding: History, Achievements, Contributions, Challenges and Future for Smart Agriculture

Rajendra Darai, PhD

Principal Scientist/ Director, DoAR, Koshi Province, Tarahara, Sunsari, Nepal
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ABSTRACT

Plant breeding, the science of modifying plant traits to enhance crop yield, quality, and resistance, has evolved from traditional selection to advanced biotechnological techniques. Its primary goal is to develop superior crop varieties that ensure global food security, adapt to climate change, and promote sustainability. Historically, early farmers practiced selective domestication, which laid the foundation for modern breeding methods such as hybridization, Mendelian genetics, and molecular biology. The Green Revolution marked a significant milestone by introducing high-yield varieties, boosting food production worldwide. Recent advances, including genetic engineering, molecular markers, and genome editing techniques like CRISPR, have revolutionized crop improvement, enabling precise and rapid development of resilient varieties. The integration of digital tools IoT, sensors, AI, and big data has further accelerated phenotyping, trait selection, and resource optimization, making plant breeding more efficient and targeted. Key achievements include high-yielding, disease-resistant, drought-tolerant, and biofortified crops addressing micronutrient deficiencies such as iron and zinc deficiency, which cause widespread health issues. Despite progress, challenges persist, including climate change impacts, loss of genetic diversity, regulatory hurdles, and societal concerns over GMOs. Future plant breeding hinges on integrating genomics, proteomics, and metabolomics, alongside precision breeding, participatory approaches, and sustainable practices. Technologies like CRISPR, speed breeding, and open-source genomic databases will facilitate the development of climate-resilient, resource-efficient crops. Collaboration among scientists, policymakers, and farmers is essential to harness these innovations responsibly. Ultimately, plant breeding will play a crucial role in transforming agriculture into a sustainable, resilient, and productive system capable of feeding a growing global population amidst environmental challenges. The future of smart agriculture relies on interdisciplinary approaches, technological advancements, and ethical practices to ensure food security and environmental health for generations to come.

Keywords: Plant Breeding, Genomics and Biotechnology, Smart Agriculture, Climate resilient crops

Brief Bio

"Shaping the future of crop improvement and seed innovation in Nepal"

First National Convention on Genetics, Plant Breeding and Seed Science

Scientific Session - III

Invited Speaker

JOIN US

21st Jan, 2026

Khumaltar, Lalitpur, Nepal

Dr. Rajendra Darai

Principal Scientist
NARC

Plant Breeding: History, Achievements, Contributions, Challenges, and Future for Smart Agriculture

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Theme 4: Agricultural Biotechnology for Smarter and More Efficient Crop Production
GPS-IP-05

Agricultural Biotechnology for Smarter and More Efficient Crop Production

Shanta Karki and Govinda Rizal

Central Agricultural Laboratory, Hariharbhawan, Lalitpur, Nepal
Corresponding author's email: shantakyoto@gmail.com

ABSTRACT

Agricultural biotechnology utilizes living organisms, biological system and processes to improve agricultural system efficiency and productivity by integrating bio-technological innovations with precision agriculture to enhance factor productivity, sustainability, and resilience. Through modern scientific tools such as genetic engineering, genome editing, molecular breeding, multi-omics, tissue culture and bioinformatics, biotechnology enables the development of crop varieties with improved yield potential, resistance to pests and diseases, tolerance to abiotic stresses which ensure stable yields even under unfavorable environments, nutrient-efficient and enhanced nutritional quality. These innovations support farming systems to be smarter by reducing dependence on synthetic inputs, optimizing resource use efficiency, and enabling crops to adapt to changing climatic conditions. In Nepal, there is very limited use of agricultural biotechnology, mostly tissue culture and molecular marker-assisted breeding have been used to produce virus free planting materials of banana, potato and development of stress tolerant rice and wheat varieties. Use of modern biotechnological tools such as genetic engineering, genome editing and transgenic technologies have not been started yet. As such a lot of potential remain untapped. As domestic and global food demand rises alongside environmental adversity and availability of cultivable land constraints, agricultural biotechnology offers sustainable solutions to ensure food security. Therefore, it is essential to integrate contemporary biotechnology into conventional agricultural system to develop smarter crop production systems through disease and pest resistance, tolerance or wider adaptability to increasing environmental uncertainness including climate change related challenges, development of biofortified varieties for improved nutrient content and targeted genomic changes to alter specific traits as required. It is high time that Nepal makes rational use of advanced agricultural biotechnology for an effective production system which will ensure sustainable increase in agricultural productivity and improve farmer's livelihoods, thereby helping to make our farming system smarter and much more efficient.

Keywords: Genetic engineering, genomics, production, sustainability, technology

Brief Bio

"Shaping the future of crop improvement and seed innovation in Nepal"

First National Convention on Genetics, Plant Breeding and Seed Science

Scientific Session - IV

Invited Speaker

JOIN US

21st Jan, 2026

Khumaltar, Lalitpur,
Nepal

Dr. Shanta Karki
Chief
Central Agricultural Laboratory

Agricultural Biotechnology: History, Achievements, Contributions, Challenges, and Future for Smart Agriculture

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Theme 5: Agricultural Biostatistics and Data Science for advancing research and decision-making in the Agricultural Sciences

GPS-IP-06

Agricultural Biostatistics in Nepal: History, Current Strengths and Weaknesses, Challenges for the Future, and Strategies for its Efficient Use for Advancement in Agriculture Research and Crop Productivity in the Country

Bharat Raj Adhikary

Corresponding author's email: biostatistix@gmail.com

ABSTRACT

Agricultural research in Nepal has been customarily using experimental designs and statistical analyses from its very infancy. The research had a modest beginning in 1954 when the aims were mainly on introduction and selection, and identification of natural constraints like diseases and insect pests on exotic crop varieties. The year 1966 ce, which saw establishment of Agronomy Experiment Farms/Stations across the nation, initiation of various Disciplinary Divisions in the center under the aegis of Department of Agriculture Education and Research (HMG/N), was the the beginning of true scientific research with a good number of graduate scientists, technical assistants, and a robust official guidebook on procedures of experimental design, field plot techniques, and statistical analyses and presentation. The year 1973 ce, the year of the beginning of National Crop Improvement Programs on major cereals and a number of cash crops, gave way not only to integrated team approach but also accelerated interest in biostatistics and presentation techniques. About the year 1985 ce, or the late 80's, availability of desktop computers and hosts of statistical software helped make more sophisticated tools available to larger number of users. Finally, post 2000 ce, use of multivariate techniques, and advanced modeling, etc have been on the rise. Throughout these advancements, the scientists have been doing the necessary analyses on their own, with possible assistance from colleagues at hand. Trainings have been organized by NARI, National Crop Programs, and various Disciplinary Divisions with interdisciplinary group of scientists having more skill on the subject. This paper also deals with various strengths and weaknesses in the growth of the area. Suggestions based on his interactions with a number of scientists actively involved in the field as well as his own observations or impressions are incorporated.

Keywords: Experimental Design, Statistical Analysis, Biostatistics, Agriculture Research.

Brief Bio

Earned B. Sc. (Agriculture and Animal Husbandry) degree with majors in Plant Breeding and Genetics from PAU, Ludhiana in 1970. Joined the services of the Dept. of Agriculture, HMG/N in 1971 as Asst. Agri. Botanist (Plant Breeder). For nearly two decades of involvement in research, he mostly worked as Rice Breeder with NRIP, Parwanipur. His interest mostly focused on screening of rice germ-plasm and several exotic breeding lines against major diseases, insect-pests, and drought stresses in interdisciplinary links with other scientists. The other area of equal interest was to him the experimental design and analyses of the data from various sources; he enjoyed helping coworkers in the work and used opportunities to lecture and organize trainings on the subject. In latter years in Agri. Botany Division, Khumaltar he worked to organize Plant Genetics Unit. During the intervening years, he earned his M.S. (Genetics) degree from Texas A&M University, College Station, Tx. in 1979. He also twice received trainings on Field Experimentation and Statistics from IRRI with direct supervision of Dr. Kwanchai A. Gomez. With his brief stay at NARSC (the initial version of NARC in the making) he made efforts to initiate a Biostatistics Unit at Khumaltar, though with no significant success.

From the early 1990's Bharat Raj Adhikary has been known as a Statistician in various NGO's, INGO'S circles. He has given lectures in India, Bhutan and Bangladesh as part of the statistics consultancies. With a number of colleges that proliferated in the early 2000's he is a Biostatistician. He has been a visiting faculty in almost every university – TU, KU, PU, AFU, SMU, etc. for several semesters in each, teaching biostatistics in agriculture, forestry, environmental science, biotechnology, medicine, etc. He also advocates use of open source/free software and is actively promoting use of R-Statistics.

"Shaping the future of crop improvement and seed innovation in Nepal"

First National Convention on Genetics, Plant Breeding and Seed Science

Scientific Session - V

Invited Speaker

JOIN US

21st Jan, 2026

Khumaltar, Lalitpur, Nepal

Bharat Raj Adhikari
Former Senior Scientist
NARC

Agricultural Biostatistics: History, Achievements, Contributions, Challenges, and Future for Shaping the Agriculture

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Theme 6: Innovation and Good Practices in Seed Science and Technology
GPS-IP-07

Seed Sector in Nepal: A Review of its History, Seed Systems, Seed Transactions, Contribution to Agriculture, Challenges and Future Directions

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ABSTRACT

As the fundamental vector of genetic potential, quality seed is one of the most pivotal inputs for crop production, directly determining yield ceilings and underpinning national food, feed, and nutrition security. Adopting quality seed can increase crop yields by 20–30%, with a gain being observed in hybrid varieties. Consequently, the advancements achieved in plant breeding and genetics are realized only when a resilient seed system ensures farmers' access to timely, affordable, and high-quality seed. Similarly, seed research is inevitable to make the domestic seed system viable and sustainable. In Nepal, however, the yield of staple crops such as rice, maize and wheat persistently trail behind that of neighbouring countries, underscoring a critical systemic gap. This article traces the evolution of Nepal's seed sector from its nascent stages pre-1950 to its contemporary structure, critically evaluating its strengths and limitations in research, seed replacement rate (SRR) and variety replacement rate (VRR), production, and distribution. The analysis affirms that an integrated, multi-stakeholder seed system—spanning public, private, and community sectors across federal, provincial, and local tiers of governance—is imperative. While institutional reforms since the 1990s, supportive policies, and growing private investment have laid a foundation for growth, progress remains insufficient to overcome entrenched challenges. A rising demand for hybrid seeds in vegetables, maize, and rice is countered by the pervasive illegal import of untested and unapproved varieties across porous borders, introducing significant biosecurity risks and potential crop failures in Nepal's diverse agroecological zones. Despite a favourable policy landscape, the slow adoption of novel seed technologies persists as a major bottleneck. This review concludes that synergistic collaboration among all seed sector stakeholders is crucial to fortifying the seed system, thereby enhancing agricultural productivity and national food and nutritional security. The lessons derived from Nepal's experience offer valuable insights for strengthening seed systems in comparable developing contexts.

Keywords: Quality seed, seed system, productivity, food security, SRR, VRR

Brief Bio

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"Shaping the future of crop improvement and seed innovation in Nepal"

First National Convention on Genetics, Plant Breeding and Seed Science

Scientific Session - VI

Invited Speaker

21st Jan, 2026

Khumaltar, Lalitpur, Nepal

Dr. Hari Kumar Shrestha
Member
National Seed Board

Seed Science and Technology: History, Achievements, Contributions, Challenges, and Future for Agriculture

Organized by: NARI PBaGSoN

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Theme 7: Policy, IPR and farmer's right in Agriculture
GPS-IP-08

Policy Gaps and Issues in IPR on Agriculture, Plant Breeding, Seed Systems and Sustainable Use of Agrobiodiversity in Nepal

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ABSTRACT

Policy on Intellectual Property Rights (IPR), plant breeding, seed systems and sustainable use and management of agrobiodiversity is crucial to promote innovation in agriculture, conserve biodiversity, and promote social equity. This paper reviews and presents existing policy provisions, gaps and challenges related to IPR, access and benefit sharing (ABS), plant breeding priorities, seed systems (formal and informal) and the conservation and sustainable use of agrobiodiversity in Nepal. The study is based on desk review, consultations with researchers and the authors' professional experiences over the past three decades. The finding revealed that Nepal lacks specific policies and laws on plant variety protection (PVP), geographical indication (GI), digital sequence information (DSI), ABS, farmers rights, plant breeding priorities (classical, agrobiotechnology, and participatory), biosafety, priority agrobiodiversity conservation (on-farm, *in situ, ex situ*). While general policies on biodiversity, biotechnology, and seed systems exist, they do not adequately address emerging issues such as modern biotechnology, protection of farmers' and breeders' rights, promotion and protection of agroecological products through GI, regulation of GMOs and DSI and use of local landraces in plant breeding including ABS issues. The paper recommends developing clear policy and legal framework along with guidelines and protocols in PVP, GI, DSI, ABS, GMO and Farmers rights to support sustainable use of local crop diversity, enhanced access and fair benefit sharing, responsible use of genetic data, and innovation in agriculture for the wellbeing of the Nepali people in a globalized economy.

Keywords: ABS, biosafety, DSI, farmers rights, GI, plant breeding, PVP and policy gaps

Brief Bio

Devendra Gauchan, PhD is an agricultural economist and policy specialist with experience and expertise in agricultural and resource economics, agrobiodiversity, agroecology and agricultural policy. He holds a PhD Degree from the University of Birmingham, United Kingdom (2000-2004) and was a post-doctoral fellow at International Rice Research Institute, Philippines (2008-2011). He is currently Agroecology Specialist at ICIMOD and serves as an Adjunct Professor of Agricultural Economics at Tribhuvan University's Institute of Agriculture and Animal Sciences, Kathmandu and Policy Lead and Senior Research Fellow in Agricultural Economics and Biodiversity at Institute of Integrated Development Studies (IIDS), Kathmandu, Nepal. He is also serving as Honorary Research Fellow of Alliance of Bioversity International and CIAT, Rome, Italy; and Advisor (Agricultural Economics and Policy), The Raffaella Foundation, USA and a Senior Thematic Expert in Natural Resource and Technology Policy at the Policy Research Institute (PRI)-a Think Tank of the Government of Nepal, Kathmandu. He is currently President of Nepal Agricultural Economics Society, Kathmandu, Nepal.

Previously, Dr. Gauchan was a Senior Scientist & Head of Socioeconomics & Agri-Research Policy Division of Nepal Agricultural Research Council (NARC), Kathmandu (2005-2015) and the National Project Manager at the Alliance of Bioversity International and International Centre for Tropical Agriculture (CIAT)-a CGIAR center based in Nepal office (2015-2022). He has 30 years' R &D experience in national and international organizations working as a researcher, project manager, visiting research fellow/professor and policy expert. He has technically contributed to the drafting of some important national policies in agriculture and food systems in Nepal specifically National Seed Vision of Nepal (2013-2025), Agrobiodiversity Policy (2014), Strategic Framework for Nature Conservation for Sustainable Development (2015-2035); Strategic Plan for Food Systems Transformation (2025-2030) and draft Agroecology Roadmap of Nepal (2025) including providing inputs on some of the important draft Bills such as Plant Variety Protection (PVP) and Farmers Rights draft Bill (2008), ABS draft Bill (2018) and Agrobiodiversity Conservation and Utilization draft Bill (2018). He is actively involved in policy research, analysis and advocacy for the resilient and sustainable transformation of agrifood systems in Nepal and South Asia with specific focus on agrobiodiversity, agroecology, agriculture value chain and seed policy. He has published and edited several research papers, policy briefs and book chapters in national and international Journals, proceedings and books.

"Shaping the future of crop improvement and seed innovation in Nepal"

First National Convention on Genetics, Plant Breeding and Seed Science

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Invited Speaker

22nd Jan, 2026

Khumaltar, Lalitpur, Nepal

Dr Devendra Gauchan

Former Senior Scientist, NARC

Policy, IPR and FR dimension and gaps in Genetics, Agrobiodiversity, Plant Breeding, Ag-Biotechnology, Ag-Biostatistics and Seed Science

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Oral Presentations

GPS- 1

Soil biodiversity in agrobiodiversity – A mycorrhizal case study from Tarai, Manang, and Mount Everest region

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ABSTRACT

Agrobiodiversity encompasses a vast array of floral and faunal diversity accounted within cultivating land use. However, soil biodiversity is overlooked while studying agrobiodiversity because of measurement complexity and limited interest. The study on soil mycorrhizal diversity in Nepal is limited. In this study, we adopted fungi metagenomics to understand the mycorrhizal diversity in East to West Tarai, Manang, and Mount Everest Zone in 2023. A total of 64 composite (30 from Tarai, 4 from Manang, and 30 from the Everest region) soil samples were collected in a cool box from 0-20 cm depth within a 30 m^2 transect, which was then stored in -80 ^{0}C for DNA extraction. Microbial DNA extraction was done using the Quiagen DNeasy PowerSoil Pro Kit and was sequenced for targeted IST2 regions. Soil DNA concentration ranges from 16.4 to 211.3 ng/µL. Altogether, 23 Ectomycorrhiza genus identified in Tarai zones, including Manang, and 41 genera in the Mount Everest region. The abundance of mycorrhiza was found to be 5000-10,000 times higher in forest soils compared to cropland soils. Dominant ectomycorrhiza genera of Tarai regions are *Ruhlandiella*, *Russula*, *Scleroderma*, and *Sebacina*; similarly, dominant genera in Manang are *Inocybe* and *Laccaria*, and Mount Everest regions are *Rusulla*, *Cortinarius*, *Suillus*, and *Laccaria*. Similarly, ectomycorrhizal abundance decreases by five times with the altitudinal gradient. These preliminary findings suggest that cultivated soil requires intensive mycorrhizal biofertilization to improve yield and soil sustainability. Further study is necessary to understand the soil physico-chemical properties linked to the mycorrhizal diversity relationship to better understand soil microbe interactions.

Keywords*:* Ectomycorrhiza, Fungi metagenomics, Mycorrhizal abundance, Soil fungi diversity

GPS-2

Diversity rich plant breeding methods for resilient agriculture

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ABSTRACT

Conventional plant breeding has substantially increased crop yields and improved resistance or tolerance to major stresses; however, it has largely focused on creating uniform, monogenotypic varieties derived from broad genetic diversity. These varieties are typically "true to type," dependent on single genes or alleles, and maintained through narrow genetic bases, making their long-term performance less sustainable under changing environments. Such uniform cultivars also require repeated seed purchase and are commonly produced outside their target production domains. To address these limitations, the Nepal Genebank, LI-BIRD and Bioversity International initiated diversity-rich plant breeding approaches beginning in 2000, aiming to generate cultivars (variety and landraces) that retain high internal genetic diversity, evolve across generations, and allow farmers to produce their own seed within local environments. This paper documents the Genebank's experiences and success cases across Nepal using a suite of methods designed to create, maximize, and utilize genetic diversity. These include diversity blocks, diversity kits, diversity fairs and participatory seed exchange, evolutionary plant breeding, cultivar mixtures, participatory landrace enhancement and conservation, household diversity trials, site-specific broad genetic-based landraces, mass selection, participatory plant breeding, nature-based wide hybridization (eg, hybrid swarms in rice near wild relatives), meiosis-based variety development, class-bulking selection, informal seed systems, and the strengthening of community seed banks. Practices that favor natural cross-pollination—such as agro-insect-friendly field environments, farmer/researcher movement within fields during flowering, and co-cultivation of cross-compatible varieties and species—further support the development of broad genetic-base cultivars. Evidence from multiple crops, including rice, buckwheat, barley, proso millet, finger millet, foxtail millet, amaranth, beans, cucumber, soybean, and broadleaf mustard across diverse districts (eg, Jumla, Humla, Lamjung, Bara, Banke, Kaski, Lalitpur, Ramechhap, Sankhuwasabha, Dolakha, Mugu, Dang, Sindhupalchowk), demonstrates that evolving, diversity-rich cultivars outperform static uniform varieties under variable climates. These successes contributed to policy revisions after 2013, allowing farmers to register broad genetic-based landraces within the formal seed system. As climate conditions continue to shift, diversity-rich and evolutionary breeding methods offer a robust pathway toward self-reliant, resilient, and sustainable agriculture, rather than true to type, and their application should be expanded to all plant genetic resources.

Keywords: Class-bulking selection, broad genetic base, evolving population, climate resilient, genetic diversity

GPS- 3

Key Findings and Policy Implications from Rapid Rice Seed Stock Survey at Seed Producer Organizations

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ABSTRACT

In Nepal, seed producer organizations (SPOs) engaged in rice include groups, cooperatives, companies operated by public and private sectors, and government farms. This paper assessed the rice seed stock maintained by 125 SPOs spreading across 27 districts covering both hills and Terai. These organizations were selected using snowball sampling methods, and data collection was done in March 2023. It was found that these organizations produced and stocked 11,518t seeds, where the share of improved seed was 85% and it was followed by foundation seed (6%), label seed (4%) and certified seed (3%), potentially constraining the rapid scaling of preferred and newly released varieties. In the total seed stock, the share of early, medium and late maturing variety was 5%, 33% and 62%, respectively. These SPOs had stocked 79 varieties of rice; however, ten rice varieties constitute about 80% of the total seed stock. These varieties include Sarju 52, Radha 4, Saba Sub 1, Sabitri, Sona Masuli, Hardinath 1, Ranjit, Sabha Masuli and Ramdhan suggesting slow variety turnover in farmers' fields. Genetic gain is limited because production is dominated by old varieties. In terms of eating quality, 20% of seeds were associated with coarse variety, 78% medium fine, and the share of fine aromatic varieties was <1%. Also, there is dominance of old varieties in improved seed production stock even if many new varieties are included under source seed production. So, policy interventions should prioritize fast-track varietal replacement, optimize foundation seed production, and develop incentive mechanisms to promote the rapid adoption of market-preferred rice varieties in Nepal.

Keywords: Rice, seed, varieties, rapid survey, Nepal

GPS-4

Genetic Analysis and Performance Evaluation of Diverse Carrot (*Daucus carota* L.) Genotypes

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ABSTRACT

Carrot is one of the important root vegetables grown in Nepal. The works on genetic analysis on carrot is limited in Nepal. A field experiment was carried out at research farm of Rampur campus, Chitwan to assess genetic variability and character association of five carrot genotypes. The research was conducted in randomized complete block design (RCBD) with five treatments replicated four times, during November, 2024 to February, 2025. The evaluated genotypes revealed considerable genetic variability for yield and yield-related traits, particularly root weight, root length to shoot length and root diameter ($P<0.05$), which exhibited high to moderate phenotypic coefficient of variation (root weight: 35.43%, yield: 32.80%, root length to shoot length: 18.82%, root diameter: 15.63 %), high to moderate genotypic coefficients of variation (root weight: 32.75%, yield: 32.05%, root length to shoot length: 16.45%, root diameter: 14.74%), high heritability (yield: 0.95, root diameter: 0.89, root weight: 0.85, root length to shoot length: 0.76) coupled with high genetic advance as a percentage of mean (yield: 64.51%, root weight: 62.36%, root length to shoot length: 29.64%, root diameter: 28.65%). SK-3 Carotte (20.38 t/ha) and Nepa Dream (19.37 t/ha) emerged as superior genotypes, recording the highest yields and favorable root attributes such as larger root diameter (3.62 cm & 3.60 cm respectively) and heavier root weight (113.09 g & 102.86 g respectively). Correlation and path analysis confirmed that root weight, root length to shoot length, root diameter and number of leaves are the primary contributors to yield, either through strong direct effects or significant indirect associations. Hence, selection strategies for carrot improvement should prioritize these root related traits. Genotypes like SK-3 Carotte and Nepa Dream can be used as potential parent materials for varietal improvement programs aiming at yield enhancement.

Keywords: Character association, Path analysis, Root attributes, Varietal screening

GPS- 5

Agriculture in Vedic Civilization: A Perspective on Seed Conservation and Promotion

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ABSTRACT

It has been universally acknowledged that the Veda is the earliest available literature of human civilization meaning to knowledge. Vedic agricultural production system works in harmony with nature, sustains the health of soils, ecosystems and people. This paper presents the agricultural wisdom expressed in different vedic literatures and its relevancy in the present context with reference to seed conservation and promotion. The importance of seed in crop production is known to human being from the very beginning of vedic civilization (युनक्त सीरा वि युगा तनुध्वं कृते योनौ वपतेह वीजम् । गिरा च श्रुष्टिः सभरा असन् नो तेदीय इत् सृण्यः पक्वमेयात् ॥ (ऋग्वेद) (Vaidik Sukta Sangraha, 2020). Vedic civilization inspires to use local knowledge and skills derived from experienced practices and passed from generation to generation on agricultural including seed management. Over thousands of years of vedic civilization, farmers have developed a variety of seed management practices that continue to exist in Nepal. Seed supply system had been maintained by farmers producing and conserving their own seeds for subsequent planting and exchanging with other farmers and relatives. In vedic civilization, human societies developed various institutional mechanisms, customs and religious beliefs to conserve, protect and promote their natural resources including seed (बीजसंरक्षणं कार्यं कृषि कर्म विशारदैः). Thus, it has a great message that the ancient people developed and invented many effective measures to safeguard our seed systems as well as to cultivate different types of crops which reflects sustainable agriculture biodiversity conservation and utilization. Due attention needs to be given to value and respect the vedic wisdom of seed conservation practices supported by further research and development.

Keywords: Vedic, Agriculture, Seed, Conservation

GPS-6

Advances in Seed Science and Technology in Nepal: Review of Nepal Agricultural Research Council Activities (2013-2025)

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ABSTRACT

Seed is the main carrier of new technology in agriculture. Quality seed play significant role in productivity enhancement and contributed about 15-25 percent yield gain. Variety development and seed research were solely mandated to Nepal Agricultural Research Council and separate focal division on seed was created in 2010. Crop commodity programs and National Seed Science Technology Research Centre accomplished large number seed related activities and generated some useful technologies during 2013-2025. This paper attempted to assemble all seed related research findings and initiative made in the past in a single paper. This review synthesize seed research and development activities carried out by the Nepal Agricultural Research Council (NARC) during 2013-2025 time frame, with the objective of highlighting major scientific advances, technological innovation and their contribution to national seed system strengthening. Advances in molecular based variety identification using DNA fingerprinting enhanced genetic purity evaluation across major crops such as rice, wheat, maize, lentil, rapeseed, and soybean. This review study demonstrate substantial progress in strengthening seed quality assurance, variety identification and seed production technologies in Nepal. These advances have contributed to improve availability of quality seed and provide a strong foundation for further research, policy formulation and sustainable development of the national seed sector.

Keywords: DNA finger printing, genetic purity, seed quality, seed research, variety identification

GPS-7

A least used stability analysis tools by Plant breeder for varietal recommendation-GGEBipolts

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ABSTRACT

While varietal recommendation in Nepal mandates stability analysis across diverse agro-ecological zones, plant breeders often underutilize a critical graphical tool: the GGE biplot. This powerful method uniquely integrates genotype (G) and genotype-by-environment (GE) interaction effects—the two components essential for cultivar evaluation—into a single, interpretable visual display. Using principal component analysis, it plots both genotypes and test environments, enabling breeders to visually identify high-yielding, stable varieties, delineate mega-environments, and recommend specific genotypes for target locations. Despite its necessity for official varietal registration submissions in Nepal, adoption remains low, primarily due to limited awareness of its application and a lack of technological proficiency in its implementation and interpretation. A significant barrier is the cost associated with specialized commercial software, such as "GGE Biplot" by Weikai Yan, which is prohibitive for many public research institutions in developing nation like Nepal. However, accessible open-source alternatives exist, particularly within the R programming environment (e.g., the ‘metan’ and ‘GGEBiplotGUI’ packages), offering free, robust analytical capabilities. This paper advocates for capacity building and the promotion of these open-source tools within Nepal's breeding programs. Enhancing the use of GGE biplot analysis will empower breeders to conduct more rigorous, data-driven stability analyses, leading to more resilient, context-specific varietal recommendations that optimize productivity and strengthen national food security.

Keywords: Biostatistics, Graphical tools, Plant breeder, Varietal registration

GPS-8

Phenological and Yield Attributes variation of Nepalese Rice Landraces in Madhesh Province, Nepal

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ABSTRACT

Madhesh province of Nepal is recognized as a rich depository of traditional crop landraces due to its diverse agro-ecological condition, long history of cultivation and farmer-led selection practices. This study aimed to assess the phenological attributes, yield attributes, and productivity of Nepalese rice landraces under field conditions in farm of CNRM Bardibas of Madhesh Province from June to November 2025. The experiment was laid in randomized complete block design (RCBD) with two replications. Thirty landraces were planted in 20 × 20cm spacing. Agronomic practices were conducted as per protocol. Phenological and yield attributes were collected at time of different growth stage. The result showed that there is variation in days of flowering from 95DAT to 120DAT and maturity from 135 DAT to 155 DAT. The yield and yield attributes were significantly varies with landraces. The panicle length was found range 19.2-27.1cm, grain per panicle (44-139) and test weight (17.9-36 g) found significantly at 5% level of significance. Harinkith gave highest yield (4.05t/ha) followed by Lajhi (3.98 t/ha) and lowest by Akshaviya (0.78 t/ha). Straw yield ranged from 10.2 t/ha (Aangaa) to 36.2 t ha^{-1} (Dewosar) producing the highest straw yield. Similarly, highest harvest index was 15.3% by Harinkith followed by Gahuma (14.0%) and lowest by Bangaliya (4.65%). In conclusion, Under the study conditions, Harinkith proved to be a promising landrace; however, additional multi-location trials and participatory evaluations are needed to confirm its adaptability and acceptability among farmers.

Keywords: Rice landraces, phenology, yield attributes, grain yield, harvest index

GPS-9

कृषिजन्य भौगोलिक संकेतः पहिचानसहितको ग्रामिण विकासको माध्यम

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ABSTRACT

कुनै खास भौगोलिक क्षेत्रमा खास गुण तथा विशेषता भएका बस्तु वा उत्पादन भूगोल विशेषको नामबाट ख्यातिप्राप्त भएमा भौगोलिक संकेतको रुपमा लिने गरिन्छ । समुदाय तहमा बसोबास गर्ने मानिसले जीवनयापनको लागि अभ्यास गरिआएका जीवनोपयोगी ज्ञान, सीप तथा कलाको माध्यमबाट बस्तु उत्पादन गर्ने प्रचलन मानव सभ्यतासँगै नेपालसहित अन्य मुलुकमा प्रचलनमा रहि आएको छ । उदाहरणका लागि नेपालमा गोर्खाको सुन्तला, सिन्धुलीको जुनार, खोकनाको तेल, धुनीबेसीको अम्बा, छैमलेको नास्पाति, मुस्ताडको स्याउ, जुम्लाको स्याउ र विदेशमा स्कच हिव्स्की, दार्जलिङ टी, सिलोन टी, पर्मिगियानो चिज, बोर्डेक्स वाइन, जमैका ब्लु माउण्टेन कफि र टकिला आदि । यस्ता बस्तु उत्पादन तथा प्रशोधनको क्रममा मानिसको बौद्धिकताको उपयोग हुनेहुँदा यस्ता वस्तु वा उत्पादनलाई बौद्दिक सम्पत्तिको विषयको रुपमा लिने गरिएको छ ।

भौगोलिक संकेत अधिकार संरक्षणको लागि सुई जेनेरीस ल, ब्यापार चिन्ह कानुन, अस्वस्थ्य प्रतिस्पर्धा विरुद्धको कानुन, उपभोक्ता हित संरक्षण गर्ने कानुन, कार्यकारी योजना जस्ता ब्यवसायिक कानुनका माध्यमबाट भौगोलिक संकेतको संरक्षण गर्ने प्रचलन रहेको छ । विश्व बौद्दिक सम्पत्ति संगठनबाट सन् २०२५ मा प्रकाशित विश्व बौद्दिक सम्पत्ति सूचक (प्रतिवेदन) अनुसार सन् २०२४ मा सदस्य राष्ट्रहरुमा ६२,३०० भौगोलिक संकेत कार्यान्वयनमा रहेका छन् । विश्वभर खासगरी मदिराजन्य (वाइन र स्पीरिट), कृषिजन्य तथा खाद्य बस्तु, हस्तकलाजन्य भौगोलिक संकेत प्रचुर मात्रामा पाइन्छन् । वाइपो सदस्य राष्ट्रमा बस्तु वा उत्पादनको प्रकृतिको आधारमा मदिराजन्य ४८.१, कृषिजन्य तथा खाद्य बस्तु ४४.८ र हस्तकलाजन्य भौगोलिक संकेतको उपस्थिति ४.२ प्रतिशत रहेको छ । सन् २०२४ मा भौगोलिक संकेतका बस्तुको उत्पादन ७९०१ अर्ब यूरो बराबर, ४९५०३२ प्रत्यक्ष रोजगारी, २०५९ अर्ब यूरो बराबरको आन्तरीक खपत, ५८४२ अर्ब यूरो बराबरको निर्यात र १२,९५,५४४ वर्ग किलोमिटर क्षेत्रफलमा विस्तार भएको हुँदा यस्को विकास अर्थतन्त्रको एउटा अभिन्न अंग बन्न पुगेको छ। नेपालमा ट्रेडमार्क सम्बन्धमा पेटेण्ट, डिजायन र ट्रेडमार्क ऐन २०२२ र कलेक्टिभ मार्कको दर्ता सम्बन्धी निर्देशिका २०६७ ले सामुहिक चिन्ह अन्तर्गत भौगोलिक संकेतजन्य बस्तुको दर्ता तथा कानुनी संरक्षण गर्ने हुनसक्ने ब्यवस्था गरेको छ ।

GPS-10

Yield Performance and Stability of Soybean Genotypes across Multiple Environments in Western Nepal Using BLUP and GGE Analysis

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ABSTRACT

Multi-environment trials were conducted to evaluate yield performance, stability, and genotype × environment interaction (GEI) of sixteen soybean genotypes in western Nepal. The experiments were carried out at Khajura, Dailekh, and Doti during the rainy season 2021, 2022, and 2023 cropping seasons using an alpha-lattice design with three replications. Grain yield data were analyzed using mixed models to obtain best linear unbiased predictions (BLUPs), along with stability parameters including harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV), and rank-based measures. Multivariate analyses were further explored using boxplot and mean performance comparisons to identify high-yielding and stable genotypes. Highly significant effects ($p < 0.01$) of genotype, location, year and their interactions confirmed the presence of substantial GEI for grain yield. Mean grain yield ranged from 1353 kg/ha for Puja to 2364 kg/ha for TGX1989-19F, with an overall mean of 1762 kg/ha. Genotypes TGX1989-19F, TGX1485-ID, CM9125, SB0095, and TGX1890-106FN consistently ranked among the top performers based on mean yield, BLUP, HMGV, and RPGV, showing zero rank difference between mean-based and BLUP-based rankings. Genotype TGX1989-19F showed the highest values of mean yield (2364 kg/ha), highest BLUP 442, more b (1.12), maximum HMGV (13.3), and RPGV (1.3), indicating superior yield potential and stability across environments. Based on overall performance and stability, TGX1989-19F and TGX1485-ID are recommended for further on-farm evaluation and potential varietal release in western Nepal.

Keywords: Soybean, multi-environment trial, BLUP, GGE biplot, yield stability

GPS-11

Wheat Breeding in Nepal: Achievements, Emerging Challenges and Future Prospects

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ABSTRACT

Wheat is the second most important cereal crop in terms of consumption in Nepal, playing a vital role in national food security, nutrition, and livelihood improvement for rural farming communities. This paper aims to synthesize the current status, major achievements, key challenges, and future perspectives of wheat breeding in Nepal. Wheat productivity in the country is increasingly constrained by erratic winter rainfall, terminal heat stress, a shortened cool growing period, and the emergence of new and aggressive races of rust diseases. In response to these challenges, the National Wheat Research Program (NWRP) has prioritized the development of high-yielding, climate-resilient wheat varieties with broad-spectrum resistance to major diseases, improved end use quality, and enhanced micronutrient content. The program is accelerating and shortening the breeding cycle through shuttle breeding by utilizing the highlands of Mustang (2,600 masl) during the off-season and Bhairahawa (112 masl) during the main season, enabling two breeding cycles per year. Previously, the national wheat breeding program focused on developing agro-ecology specific resistant varieties. However, the emergence of new aggressive Leaf rust (121R60-1) and yellow rust races (238S119, 110S119, and PstS16) has necessitated a strategic shift toward developing varieties that are resistant to all three rust types, adaptable across all agro-ecological zones of Nepal. Similarly, the aggressive stem rust race Ug99 (TTKTT) was reported in Nepal in 2023, alerting the program to prioritize Ug99 resistance breeding. The national wheat breeding program, in coordination with CIMMYT, Mexico, is evaluating advanced breeding lines at the KALRO, Kenya phenotyping platform for Ug99 resistance, and in Jessore, Bangladesh for wheat blast resistance, with support from CIMMYT, Mexico. In addition, the program has placed emphasis on developing aphid-tolerant and FHB resistance wheat lines in coordination with CIMMYT, Mexico. To date, a total of 54 wheat varieties developed by NARC has been released by NSB for cultivation in Nepal. Among them, 41 wheat varieties are currently under cultivation (23 varieties in formal seed system), including two durum wheat varieties (Khajura Durum 1 and Khajura Durum 2), while 13 varieties have been denotified due to genetic deterioration and susceptible to different diseases. The release of six biofortified wheat varieties enriched with zinc and iron (Zinc Gahun 1, Zinc Gahun 2, and Borlaug 2020 for the Terai/plains; Bheriganga, Himganga, and Khumal Shakti for the mid hills) marks a significant milestone for Nepal, not only in ensuring food security but also the nutritional security to combat micronutrient malnutrition among the Nepalese population. The NWRP, Bhairahawa is prioritizing rapid multiplication of nucleus and breeder seed of newly released zinc-enriched wheat varieties. In 2024/25, NWRP produced 43.8 tons of breeder seed, including 20% zinc-enriched varieties. NWRP targets 25–30% coverage of total wheat area with zinc-enriched varieties by 2027. The program has also strengthened its capacity to produce nucleus seed to ensure a sustainable supply of breeder seed by addressing existing challenges in the seed cycle from which foundation, certified, and improved seed classes are generated. Breeder seed production outside the station was initiated in 2022/23 in coordination with nine NARC stations through nucleus seed supply from NWRP, with an annual production target of approximately 70 metric tons (≈70 MT). Our major strategy focuses on varietal development, maintenance breeding and high quality seed dissemination, particularly through the public and private sectors. Furthermore, the NWRP has adopted several strategies, such as mainstreaming the breeding program with zinc and iron enriched materials, strengthened the approach to developing location and product specific varieties and technologies, and placing greater emphasis on abiotic stress breeding to cope with the impacts of climate change (mainly heat stress and drought). Additionally, from our breeding program, four high-yielding and rust-resistant wheat varieties viz; BL 4818, NL 1446, NL 1488, and NL 1179 are candidate varieties to be released soon for cultivation in the Terai and mid-hill regions of Nepal. Future perspectives emphasize molecular-assisted gene pyramiding, and enhanced infrastructure and human capacity to sustain accelerated breeding, ensure resilient and sustainable increase in wheat production for Nepal’s food and nutritional security and self-sufficiency.

Keywords: Wheat Breeding, climate resilience, biofortified, seed scaling, Nepal.

GPS-12

Molecular Diversity Assessment of Nepalese Fine and Aromatic Rice Landraces using SSR markers

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ABSTRACT

The Aromatic rice landraces have great genetic diversity and widely distributed throughout Nepal. The exact information on status of molecular diversity of Nepalese aromatic rice landraces is still unknown. The primary objective of present study is to assess molecular diversity in our aromatic rice landraces with the help of SSR markers. The DNA extraction was carried out employing the CTAB method from the seed samples obtained from National Rice Research Program, Hardinath and PCR was performed in the laboratory of the National Seed Science and Technology Research Center, Khumaltar, Lalitpur during 2021. The diversity assessment was performed in 139 aromatic rice landraces of the Nepal with 37 polymorphic SSR markers. The SSR diversity results reflected that PIC value ranges from 0.01 to 0.74 with an average of 0.48 from the assessment of 139 landraces. Furthermore, 74% of polymorphic loci and 91 total polymorphic alleles were observed with an average of 2.46 alleles per locus. Additionally, PCoA and geographical distribution of landraces constituted three distinct groups of individuals. Both PCoA and geographical data represented 63, 50 and 26 as well as 66, 47 and 26 landraces respectively which almost resembles with each other indicating reliability of SSR allelic data and its robustness in identification of variation in population. The study showed high molecular diversity in Nepalese aromatic rice landraces that could be utilized in the development of high yielding and consumer preferred fine and aromatic rice varieties to increase production and productivity and supports the import substitution in future.

Keywords: Fine and Aromatic rice, Diversity, PIC, Analysis of Molecular Variance, PCoA, SSR marker

GPS-13

Genotype × Environment Interaction of medium grain rice genotypes using additive main effect and multiplicative interaction (AMMI) across different environments of Nepal

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ABSTRACT

In the present study, 19 medium-grain rice genotypes were evaluated across five diverse agro-ecological environments. The experiment was laid out in a randomized complete block design with three replications in 2m^2 plot size for each genotype, keeping a spacing of 20-20 cm (row to row and plant to plant). Traits assessed included plant height (PH), number of tillers per plant (NT), panicle length (PL), and grain yield (GY). The results revealed that location-specific analysis of variance showed significant variation for the studied traits. Similarly, Additive Main Effects and Multiplicative Interaction (AMMI) analysis revealed a significant genotype-environment interaction (GEI), with environments (E), genotypes (G), and GEI accounting 25.37%, 30.05%, and 19.02% of the total variation in grain yield, respectively. The first two principal components of the AMMI (IPCA1–IPCA2) explained 76.30% of GEI. Likewise, based on AMMI and other fourteen stability indices, genotypes CR-Dhan 909 (G03), HKR-47 (G05), Samba Sub-1 Early (G12), and KASP 4.3-R345-212-SST (G18) were the most stable. Among these genotypes, HKR-47 (G05) showed the highest grain yield (6.12 tons/ha), demonstrating both high productivity and stability. The factor analysis revealed that PH and PL were linked with Factor 1 (FA1) and GY was linked with Factor 2 (FA2), with high heritability estimates of 0.844, 0.749, and 0.617, respectively. The findings revealed that stable genotypes could be adapted to diverse environments after further validation or used as parental lines in breeding programs.

Keywords: Genotype, Rice, AMMI, Environment, Stability

GPS-14

SSR marker based genetic diversity assessment of Nepalese wild rice accessions

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ABSTRACT

Wild rice constitutes a critical genetic reservoir for rice improvement; however, its genetic diversity in Nepal remains inadequately characterized, constraining its effective utilization in breeding and conservation. This study was conducted in 2025 at the molecular laboratory of the National Agriculture Genetic Resources Centre (NAGRC), NARC. Genetic diversity among 19 wild rice accessions comprising 18 accessions of *Oryza rufipogon* and one accession of *Oryza nivara* collected from eight districts were characterized and assessed using 52 simple sequence repeat (SSR) markers. DNA was extracted from young seedlings using a modified CTAB protocol, followed by PCR amplification. The SSR bands were scored and data entry was done in Microsoft excel (2016) and analyzed by using MEGA and Gene Alex (6.0) software. The result revealed that among the tested markers 9 were monomorphic, while the remaining 43 exhibited polymorphism. The size of the PCR product ranges from 100-430 base pairs. A total of 153 alleles were detected, with 2-6 alleles per locus and a mean of 3.56 alleles per marker. Polymorphic information content (PIC) values ranged from (0.38-0.74) with mean of 0.53, reflecting moderate to high marker informativeness. Marker RM72 displayed the highest polymorphism (0.75), whereas RM536 exhibited the lowest (0.38). The mean observed heterozygosity (H_o) was 0.6039, while expected heterozygosity (H_e) averaged 0.9486, demonstrating high genetic variability within the germplasm. Marker efficiency analysis revealed a mean resolving power (RP) of 2.08, a mean effective multiplex ratio (EMR) of 2.69, and a mean marker index (MI) of 1.47, with markers such as RM72 and RM263 exhibiting superior discriminatory capacity. Cluster analysis grouped the landraces into two major genetic clusters, while principal coordinate analysis showed that the first two axes explained 31.49% of the total molecular variation. Analysis of molecular variance (AMOVA) indicated that 94% of the genetic variation occurred within populations, compared to 6% among populations. Overall, the results reveal high genetic diversity and heterozygosity among Nepalese wild rice accessions, highlighting their value for conservation and utilization.

Keywords: Amplification**,** Cluster dendrogram, Genetic diversity, Heterozygosity

GPS-15

An Insight into Applied Research and Agricultural Statistics

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ABSTRACT

Rapid advances in applied agricultural science have been driven by technological growth and the increasing complexity of field- and experiment-based research. Agricultural research aims to generate reliable evidence by filling knowledge gaps, developing new methods, and supporting sustainable production and national development. Data science ie sound study design, data collection, and statistical analysis are essential to obtain valid and unbiased results. Statistical science plays a central role through the design of experiments, sampling, data analysis, and interpretation, enabling researchers to understand complex agricultural phenomena and assess the effects of multiple factors. The inherent variability and heterogeneity in agricultural systems have further strengthened the application and evolution of statistical methodologies. The techniques of drawing valid interpretation depend on how the data has been gathered and depending upon the research and variables. This study emphasizes the importance of statistical research design and basic and advanced analytical techniques in agricultural investigations, highlighting their role in minimizing experimental error and bias, and ensuring accurate interpretation. Appropriate use of statistical tools is crucial for advancing agricultural research and informed decision-making.

Keywords*:* Hypothesis testing, Field trials, Agricultural research, Design of experiment, Tools

GPS-16

Screening of Drought Tolerant Rice Genotypes Using SSR Markers

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ABSTRACT

Rice (Oryza sativa L.) is the major staple crop of Nepal, contributing significantly to national food security and rural livelihoods. However, rice production in the country is highly constrained by drought stress due to erratic rainfall patterns and limited irrigation facilities, particularly in rainfed ecosystems. The objective of study was to screen advanced rice genotypes for drought tolerance using Simple Sequence Repeat (SSR) molecular markers at the National Rice Research Program (NRRP), Hardinath, Dhanusha, Nepal in 2025. A total of 32 rice genotypes selected from Advanced Yield Trials (AYT), Participatory Varietal Selection (PVS), Early Composite (E.C.), and released varieties (Sukkhadhan-3,-6, Ghaiya-3, Hardinath-3) were analyzed using three drought-linked SSR markers, namely RM22, RM223, and RM20A. Genomic DNA was extracted from 21-day-old seedlings using the CTAB method and quantified using a NanoDrop spectrophotometer. PCR amplification was performed, and amplified products were resolved through agarose gel electrophoresis. Band sizes were determined using GelAnalyzer software, including polymorphic information content (PIC) were calculated. All three SSR markers produced clear, reproducible, and polymorphic banding patterns, confirming their effectiveness in detecting drought-related genetic variation. The amplified DNA fragments using markers RM 20A, RM 223 and RM 22 ranged 231-266 bp, 161-215 bp, and 205-224 bp, respectively. The marker RM22 exhibited the highest PIC value (0.933), followed by RM223 (0.901) and RM20A (0.893), classifying all markers as highly informative. Well-known drought-tolerant varieties such as Sukkhadhan-3, Sukkhadhan-6, Hardinath-3, and Ghaiya-3 consistently amplified drought-associated alleles, validating their genetic stability. Genotypes G17 to G32 predominantly exhibited larger alleles (~200–224 bp), associated with drought resilience. Overall, finding showed SSR markers RM22, RM223, and RM20A are reliable tools for molecular screening of drought tolerance in rice. The findings support the integration of molecular marker-assisted selection with conventional breeding programs to accelerate the development of drought-tolerant rice varieties suitable for Nepal's rainfed environments.

Keywords: Rice, drought tolerance, CTAB, SSR markers

GPS-17

Optimization of In Vitro Callogenesis and Plant Regeneration in Elite Sugarcane Genotype SRPJ2016 Coll#02

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ABSTRACT

Sugarcane (*Saccharum officinarum* L.) is a major industrial crop of Nepal, accounts for around 60% of the nation's yearly sugar consumption. However, the poor seed multiplication rate and disease transmission linked to conventional vegetative propagation impede faster seed multiplication at the large scale. Plant tissue culture is an effective substitute for quick clonal multiplication and the creation of disease-free planting material. The present study aimed to optimize an in vitro callus induction and plant regeneration protocol for the elite sugarcane genotype SRP2016 Coll#02 using apical meristem explants. A multi-stage experiment was conducted in a Completely Randomized Design (CRD) at the tissue culture laboratory of National Sugarcane Research Program in 2024. Callus induction was evaluated on five different media (0, 1, 2, 3 and 4 mg L^{-1} 2,4-D) followed by shoot regeneration on a standardized regeneration medium and rooting under liquid culture conditions. Among the treatments, MS medium supplemented with 4.0 mg L^{-1} 2,4-D resulted in the highest callus induction (100%) followed by 3.0 mg L^{-1} 2,4-D with 95% induction. For shoot regeneration, calli were transferred to MS medium containing 0.3 mg L^{-1} BAP and 0.5 mg L^{-1} IBA. Calli induced on MS medium supplemented with 3.0 mg L^{-1} 2,4-D in combination with 0.3 mg L^{-1} BAP exhibited the highest regeneration efficiency, producing an average of 43.7 shoots per explant, compared to 23.9 shoots per explant from calli induced with 4.0 mg L^{-1} 2,4-D alone. Among the liquid rooting media tested, MS medium containing 2.0 mg L^{-1} NAA combined with 1.0 mg L^{-1} IBA proved most effective, producing the highest average number of roots (10.0) and maximum root length (2.82 cm). Overall, higher concentrations of 2,4-D were optimal for callus induction, while inclusion of BAP during the callusing phase significantly enhanced shoot regeneration. The combined application of NAA and IBA was superior to NAA alone for rooting. This optimized method provides a reliable foundation for rapid micropropagation, future genetic improvement and somaclonal variation studies in sugarcane.

Keywords: Apical meristem, Callus induction, Micropropagation, Sugarcane

GPS-18

UAV-Based Remote Sensing for Data-Driven Crop Improvement in Plant Breeding

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ABSTRACT

Remote sensing has become a routine tool for high throughput phenotyping in plant breeding trials. Unoccupied aerial vehicles (UAVs) equipped with sensors enable rapid, non-destructive, high-resolution, and repeated measurement of crop status throughout the growing season. Multispectral imagery (MSI) captured through UAVs can be processed to extract vegetation indices that can capture and account for spatial variation observed in the fields. If not accounted for, this spatial variability can confound genetic signal and reduce selection accuracy. Beyond spatial modeling, MSI can also be used to replace or complement manual harvesting through sparse phenotyping, thereby reducing labor and phenotyping costs.This study evaluated the how MSI (phenomics), genomics, and statistical modeling can be integrated to improve selection decisions in alfalfa (*Medicago sativa* L.). Field trials were established at New Mexico State University and included multiple biomass harvests under normal irrigation and early termination treatments during the 2022 and 2023 growing seasons. UAV flights were conducted throughout the season, and vegetation indices were extracted from MSI data. For spatial modeling, univariate yield models were compared with multitrait models integrating MSI and spatial correction. Genomic estimated breeding values (GEBVs) were calculated for each model. Multitrait models incorporating MSI and spatial correction produced more consistent GEBVs across harvests, with correlations of 0.8 to 0.9, compared with models without spatial correction (0.7-0.9) and univariate models (0.6-0.9). For sparse phenotyping, both univariate and multivariate methods were utilized to predict missing replication or entire harvest. Models using MSI collected near harvest dates accurately predicted masked biomass observations, with prediction accuracies ranging from 0.7 to 0.9 across treatments. These results demonstrate that UAVs can be integrated into routine breeding programs for both spatial correction and phenotyping cost reduction, enabling breeders to evaluate more genotypes, increase selection intensity, and improve prediction accuracy in breeding programs.

Keywords: remote sensing, spatial modeling, sparse phenotyping, predictive breeding, multi-omics

GPS-19

Evaluation of Grain Quality Traits of Nepalese Rice Landraces

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ABSTRACT:

Traditional rice (Oryza sativa L.) is the primary staple food crop vital for food security and rural livelihoods, harboring genetic diversity for grain quality traits that remains largely underutilized in breeding programs. This study at the Genetics and Plant Breeding laboratory, Agriculture and Forestry University (AFU), Chitwan, evaluated the variability and breeding potential of 22 Nepalese rice landraces based on 14 grain physical and cooking quality traits. The traits assessed included kernel length and breadth, kernel length-to- breadth ratio, rice grain length and breadth, rice grain length-to-breadth ratio, thousand grain weight, hulling and milling percentages, grain elongation ratio, volume expansion ratio, water uptake, alkali spreading value, gel consistency, chemical test of aroma, and aroma after cooking.Results revealed diversity among the landraces. Kernel and grain dimensions classified most landraces as slender types, with Kernel length ranging from 6.55 mm to 9.30 mm, while grain length varied from 4.34 mm to 7.05 mm. Thousand grain weight ranged from (13.48 to 30.69 g) hulling percentage ranged from (70.89 to 82.29 %) and milling percentage ranged from (65.35 to 74.20 %). Alkali spreading value indicated the presences of high, intermediate, and low gelatinization temperatures. Gel consistency varied from hard to very soft. Aroma ranged from non-aromatic to strongly aromatic types. Cooking quality traits, including grain elongation (0.133 to 0.216), volume expansion rate (3.33 to 8.0), and water uptake (50 to 250 ml) showed broad variability. Cluster analysis based on 13 grain quality traits including kernel length and breadth, grain length and breadth, kernel and grain length-to-breadth ratios, thousand grain weight, hulling and milling percentages, gel consistency, grain elongation ratio, water uptake, and volume expansion ratio and grouped into six distinct clusters. Jagaha, Kalo Basmati, Magar Anadi, and NGRC04968 exhibited superior and distinctive grain quality traits, highlighting their potential for premium quality rice breeding. Overall, this observed variability underscores the rich genetic diversity of Nepalese rice landraces and identifies promising genotypes for breeding consumer preferred and high quality rice.

Keywords: Cluster analysis, Cooking quality, Grain quality, Nepalese rice landraces

GPS-20

Genome wide association mapping of resistance to pre-harvest sprouting in winter wheat

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ABSTRACT

Pre-harvest sprouting (PHS) is a condition that allows the mature kernel to start germinating within the ear itself in the standing crop in response to continuous rain showers overlapping with the harvest period. PHS is a key bottleneck limiting the overall wheat production in recent years causing significant economic losses. An enhanced α-amylase in the sprouted kernel is responsible for altering the flour properties, adversely affecting the end use applications. The main objective of this thesis was to identify potential markers associated with PHS-related traits for future use in marker assisted selection (MAS). Laboratory as well as field-based PHS provocation was done for assessing PHS in 312 European winter wheat genotypes. The experiment was laid out in replicated row-column design. Statistical analysis of the data was done using R studio. For the analysis of phenotypic data, a linear mixed model (LMM) was used but the model was based on general mixed model (GMM). The lines were genotyped using 10464 markers. Using the 'sommer' package in R, GWAS analysis was conducted based on mixed linear model-MLM(Q+K). The repeatability estimated for the evaluated PHS-related traits were found to be moderate to high. The phenotypic correlation between grain sprouting (GS) and head sprouting scoring (HS) was low but positive. The falling number under irrigated replication (HFNi) showed moderate negative correlation to both GS and HS. From the GWAS, 11 significant makers were detected that were most likely to have a connection with the PHS-related traits and majority of the detected QTLs were found on chromosomes 4A (4), 4B, 5A, 7B, 1B, 6D, 2B and 2D. 6 markers were found for the first head sprouting scoring, 4 markers for falling number from non-irrigated replication and 1 marker for grain sprouting. Among all potential QTLs, one QTL located on chromosome 4A was found to be consistent and showed association with all the three PHS-traits.

Keywords: Correlation, Falling number, Grain sprouting, Head sprouting, GWAS, MAS, Markers, QTL, Pre-Harvest Sprouting, Repeatability

GPS-21

Assessment of Induced Mutagenesis as a Tool of Genetic Variance on Seedling Quality Traits in the Local Rice Landrace

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ABSTRACT

Chemical mutagenesis has emerged to be a crucial tool to generate genetic variability and identify novel traits useful in crop varietal improvement program. The research highlights the critical role of mutagenesis in generating genetic variation to be utilized in rice improvement targeting farmer's preferences. In this study, the local rice landrace Taakmaru was subjected to ethyl methanesulfonate (EMS) mutagenesis at National Biotechnology Research Centre in 2025, following International Atomic Energy Agency (IAEA) standard protocol. Five EMS concentrations, alongside two controls were applied to rice seed and subsequent effects on major seed quality traits including germination percentage, root length, shoot length, root-to-shoot ratio, seedling dry weight, etc. were measured to assess mutagenic impact. Results revealed that germination remained unaffected for this genotype upto 30mM EMS but subsequently declined in a significant way at higher doses (90% at 40mM and 83% at 50mM) compared to untreated seed with 98.6% germination. In the same way, shoot length progressively decreased from 16.758 cm in untreated seedlings to 10.937 cm at 50 mM EMS, while root length showed a similar reduction from 17.80 cm to 8.353 cm. The root to shoot ration also declined significantly from 1.0627 in control seedlings to 0.7667 at the highest dose of EMS concentration. These findings demonstrate a dose dependent mutagenic effect, with higher EMS concentrations exerting strong inhibitory impact on seedling vigor. The seedling behaviour under EMS stress provides a valuable baseline for identifying elite mutants for breeding programs. To the nutshell, the study underscores the importance of controlled mutagenesis as a strategic approach for enhancing genetic diversity and unlocking novel traits to be utilized in rice improvement program targeting farmers' demand in Nepal.

Keywords: Crop improvement, ethyl methane sulphonate (EMS), genetic variability, rice mutagenesis, seed quality traits

GPS-22

Evaluation of Grain Quality and Cooking Characteristics of Nepalese Rice (*Oryza Sativa* L.) Landraces

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ABSTRACT:

Rice grain quality is a critical determinant of consumer acceptance, market value, and varietal preference, landraces from Nepal represent an important but underutilized source of quality-related diversity. This study evaluated thirteen grain quality and cooking quality traits of thirty Nepalese rice landraces along with three released check varieties to identify genotypes with promising quality attributes. The experiment was conducted from January to February 2024 at Department of Genetics and Plant Breeding, Agriculture and Forestry University, Rampur, Chitwan, Nepal, under a completely randomized design using standard laboratory protocols set by International Rice Research Institute and Juliano. Significant genotypic variation ($p < 0.01$) was observed for all evaluated grain quality traits. Uncooked grain length ranged from 5.13 to 6.78 mm, while uncooked grain width varied from 1.64 to 1.95 mm. Cooked grain length showed wide variation (7.08 - 10.30 mm), and cooked grain width ranged from 2.87 to 4.01 mm, resulting in cooked length-breadth ratios between 2.11 and 3.30. Optimum cooking time differed markedly among genotypes, ranging from 18 to 35 minutes, with NGRC04957 recording the shortest cooking time, followed by NGRC01962, NGRC03271, and NGRC07913. Water uptake ratio varied from 2.89 to 4.92, while elongation ratio ranged from 1.33 to 1.82, indicating diversity in cooking expansion behavior. Milling quality traits also showed significant variability, with hulling and milling percentages identifying NGRC07925, Ramkumar-11, and NGRC04972 as superior genotypes. Alkali spreading scores identified majority of landraces having intermediate gelatinization temperature. Apparent amylose content spanned from low to high categories, and gel consistency ranged from hard to soft classes, reflecting broad diversity in eating and textural quality. The substantial variation observed across physical, biochemical, and cooking quality traits highlights the breeding potential of Nepalese rice landraces, and these promising genotypes can serve as valuable donor parents for grain quality improvement programs.

Keywords: Amylose content, Cooking time, Grain quality, Rice landraces, Variability

GPS-23

Genetic diversity analysis in fiber related traits of different tossa jute (*Corchorus olitorius* L.) germplasm

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ABSTRACT

An experiment was conducted to examine the magnitude of genetic diversity and characters contributing to genetic diversity among 30 tossa jute genotypes. This study employed a randomized block design to examine and analyze various fiber related traits. Genetic diversity of thirty genotypes of tossa jute was studied through cluster analysis and principal component analysis for 12 quantitative traits related to fiber yield at the research farm of Jute Research Program, Itahari, Sunsari. Cluster mean analysis indicated that the genotypes from cluster I recorded the highest mean performance for plant height (310.36 cm), basal diameter (1.31 cm), fiber thickness (0.12 cm), leaf width (4.56 cm), petiole length (4.37 cm) and green fiber yield (16.20 t ha^{-1}), while the cluster IV showed the minimum mean performance for most of the character. Intra and inter cluster distances among five tossa jute clusters showed the highest inter cluster distance between cluster II and cluster IV (70.53) followed by cluster II and cluster III (61.53), cluster I and cluster V (50.92) and cluster IV and cluster V (40.93) indicating the presence of high genetic divergence between these clusters. The genotypes were grouped into five clusters. Cluster II contained the highest number of genotypes 15 (50%), while cluster III and IV had the lowest number of genotypes 2 (6.66%). The principal component analysis results showed the first seven principal components with cumulative contribution rate of 92.40% indicating that the first seven principal components represented 92.40% of the information of the 12 traits analyzed. Considering the magnitude of cluster distance, cluster means for different characters and contribution of characters towards divergence, the genotypes SRP-7016, SM-1018, SRP-1035, BL/133, SM-024, SRB-061, DS/046, SRB/033 from cluster I and SRB/024, BL/067 from cluster III could be selected as promising parents for hybridization program.

Keywords: Genetic diversity, Cluster analysis, Principle component analysis, Tossa jute

GPS-24

Computational Identification and Characterization of Candidate Catalase Genes in Proso Millet (*Panicum miliaceum* L.) Using TSA Datasets

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ABSTRACT

Abiotic stress plays a major role in growth, development, and yield of any crop, where Catalase (CAT) acts as a key antioxidant enzyme involved in the detoxification of hydrogen peroxide providing a strong hold against plant stress tolerance. *Panicum miliaceum* (Proso millet) is a climate-resilient cereal crop; however, limited genomic information is available regarding its antioxidant defense system. In the present study, a comprehensive computational analysis was performed to identify and characterize catalase genes in *P. miliaceum* using Transcriptome Shotgun Assembly (TSA: GHHA00000000.1) datasets. TSA sequences were retrieved from the NCBI (National Center for Biotechnology Information) database and screened using BLAST analysis. Identified catalase sequences (TSA-GHHA01039779.1, GHHA01007642.1, GHHA01039778.1) were further analyzed for physicochemical properties, conserved domains, and structural features. Further, homology modeling was carried out using SWISS-MODEL, and the quality of the predicted 3D structures was assessed using PROCHECK and ERRAT servers. These results revealed conserved catalase domains and stable structural features, suggesting functional significance in oxidative stress regulation and abiotic stress tolerance. This study provides foundational insights into catalase genes for applying transcriptomics, marker-assisted selection, and genome editing to develop Proso millet cultivars with enhanced yield, and stress resilience.

Keywords: Abiotic stress, BLAST, Catalase, Homology modeling, TSA

GPS-25

Examination of Promising Genotypes of Rajma (*Phaseolus vulgaris* L.) for Variety Release

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ABSTRACT

The area under rajma, french bean (*Phaseolus vulgaris* L.) production is increasing over the years in the Terai and valley regions of Nepal. This crop is mainly cultivated for pulse and green vegetable purposes. To date, the Grain Legumes Research Program (GLRP) under Nepal Agricultural Research Council (NARC), has registered only one variety of rajma, i.e., PDR-14, and there are no varietal options available for farmers for its' cultivation in the country. In this study, different field experiments, such as: Coordinated Varietal Trials (CVT) in Randomized Complete Block Design (RCBD), Disease Screening Trials in Augmented Design (AD), Agronomical Trials in RCBD, and non-replicated Coordinated Farmers' Field Trials were conducted from 2015/16 to 2024/25 at GLRP premises, multi-location trials at different NARC research stations and different out-reach sites. Out of eight genotypes assessed in CVT, two genotypes, namely Arun-2 and Chitra were found to be promising for release. It was found that the days to flowering and maturity, plant height, pods per plant, seeds per pod, hundred seed weight, and grain yield were found 53 and 115 days, 60.5 cm, 19, 5, 32.3g, 1952 kg/ha, respectively, in genotype Arun-2; and 48 and 106 days, 31.2 cm, 15, 4, 35.0 g and 1687 kg/ha, respectively, in genotype Chitra. Similarly, the optimum time of sowing of these varieties is the last week of Ashwin to 1st week of Kartik. The GLRP will submit full proposals for releasing the genotypes Arun-2 and Chitra as the new varieties of rajma for their cultivation in the country.

Keywords: French bean, Variety, Yield, Legumes, Release

GPS-26

Reflection of Agrobiodiversity in Nepalese folk songs

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ABSTRACT

Folk songs are orally acquired repositories of culture, tradition, history, livelihood and lifestyle from generation to generation. Nepalese folk songs reflect so many aspects of diversified society. Nepal is diversified with many ethnic groups which are the sources of rhythms, beats, words, songs and instruments. However, agriculture is the common profession of majority of the ethnic groups. An investigation was carried out to find out the reflection of agrobiodiversity in Nepalese folk songs derived from the several ethnic groups. Many songs released from radio, television, Youtube and practiced among local people were selected as the samples to assess how and at what extent the contents reflect the agrobiodiversity. The results revealed that, generally, the first line of the folk songs contained agricultural commodity as a symbol to make rhyme for the second line to make a stanza of the song. The second line contained the most important abstract or direct message of the song. The meaning of the first line is less important than that of the second line for the audience but it is important for agricultural message. The folk songs contained crop varieties, livestock breeds, fish types, grass types, trees, insects, fruits, vegetables, spices, native species, post-harvest products and other agricultural commodities. These songs were found as oral documents of Nepalese agriculture. These songs should be documented as the evidences of the agricultural commodities for future use.

GPS-27

Experimental Research Design, Sample Survey, and Statistical Analysis Practice in Agricultural Research in Nepal

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ABSTRACT

This paper tries to explore the practice and principles of experimental research design, sample surveys, and statistical analysis in applied agricultural research in Nepal. The required data were collected from a Google Form survey and other secondary sources of review articles. A set of predetermined, self-administered questionnaires covering 31 variables of interest was included. The data was collected over nearly 3 years, from 2080 Baisakh to 2082 Mangsir. Some dummy data, as well as secondary data related to plant breeding and genetics by the same token of mechanical randomization, were used to study the interactive features of typical open-source statistical software and models. The primary objective of this paper is to explore and identify the major issues in experimental design and sample survey, thereby practicing current trends in statistical analysis using open source and proprietary statistical software used by applied researchers who work in agriculture organizations of Nepal.The survey revealed that most researchers working in agricultural research follows design and experiment rather than a sample survey in field experimentation purposes. Out of the 560 researchers, most widely used the split plot design, followed by CRD and RCBD. The Alpha Lattice design was used in special occasions in which high field variability with many treatments. Although 58% of the trials had circumstances that could have benefited from more specialized, efficient designs like Alpha Lattice, researchers primarily used well-known designs like Split Plot and full blocks, according to a study that analyzed 560 agricultural researcher's studies. Remarkably, when it comes to coping with field variance, tradition and perceived complexity are more important than statistical efficiency, as shown by the underutilization. Dummy data with various experimental designs was used to study the various kinds of statistical tools and techniques from open-source statistical Software. The purpose of experimental design used in the special area of plant breeding and genetics in field trial are to minimize the experimental error and thereby increase the precision of genotype comparison. Basic assumptions of normality, homogeneity, independence of error, and additive effects are common in statistical analysis of data. Moreover, to increase confidence in experimental procedures, sample survey and data analysis practice and close this hole, the authors suggest effective training, clearer instructions and ethical guidelines, and up-to-date software.

Keywords: Analysis, Design, Experiment, sample, software, statistical, survey

GPS-28

Assessment of Genetic Variability and Milling Quality of Rice Landraces (*Oryza Sativa* L.) of Nepal

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ABSTRACT

Rice (*Oryza sativa* L.) is a staple food crop and a major contributor to food and nutritional security in Nepal. This study aimed to assess genetic variability and milling quality traits among 30 rice landraces along with three released check varieties of Nepal. The experiment was conducted at the Faculty of Agriculture, Agriculture and Forestry University, Rampur, using an α-lattice design for sixteen agro-morphological traits and a completely randomized design for six milling quality traits. Significant genetic variability was observed among the genotypes. High heritability (>60%) coupled with high genetic advance as a percentage of the mean (>20%) was recorded for plant height, filled grain number per panicle, culm diameter, leaf blade width, panicle primary and secondary branch number, flag leaf width, grain length, dockage percentage, head rice recovery percentage, and broken rice percentage, indicating strong genetic control. Cluster analysis grouped the genotypes into six distinct clusters, with the maximum inter-cluster divergence observed between Clusters IV and VI ($D^2 = 6.09$), reflecting substantial genetic variability. Cluster VI comprised genotypes with superior culm diameter, panicle traits, and yield, suggesting their suitability for use in future breeding programs. Principal Component Analysis revealed that six principal components explained 81.5% of the total variation, with PC1 contributing the most variation through primary branch number, secondary branch number, and filled grain number per panicle, highlighting their primary role in genetic variation. Ramkumar-2 exhibited competitive performance of panicle traits relative to the standard check, while these traits showed strong positive association with yield, supporting their use in indirect selection. NGRC02829 showed superior performance for head rice recovery percentage, suggesting it's potential for future breeding for improving milling quality of rice. These findings emphasize the importance of integrating Nepalese rice landraces into breeding programs to enhance productivity and grain quality.

Keywords: Agro-morphological traits, Cluster analysis, Heritability, Milling quality, Principal Component Analysis, Variability

GPS-29

Genetic Diversity Assessment of Nepalese Chilli *(Capsicum Spp.)* Landraces by Agro-Morphological Characterization

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ABSTRACT

An experiment was conducted at the experimental plots of the National Gene bank, Khumaltar, Lalitpur, Nepal during the summer of 2022/23 to characterize 34 chilli genotypes based on the morphological traits using augmented design. These genotypes were collected from 14 districts of Nepal. A total of 38 morphological characters (both qualitative and quantitative) were characterized based on International Plant Genetic Resources Institute (IPGRI) descriptor for chilli. Leaf width showed a strong and positive correlation with the days of first fruiting, days of first flowering and leaf length. Principle Components Analysis (PCA) explained 67.5% of the total variation, with the first two principal components contributing the most. Principal Component 1 (PC-1) explained52.6% of the variation with immature fruit length and matured fruit length being the major contributors. Principal Component 2 (PC-2) explained 14.9% of the total variation, with mature fruit weight and mature fruit diameter being the most significant factors. Using Euclidian distance and average method, the 34 accessions were divided into two distinct clusters based on their qualitative and quantitative traits. Accessions CO-14179 and CO-14275, which have elongated fruit shapes, were grouped Days of first flowering (DOFF), mature fruit diameter (MFD) and thousand seed weight (TSW) were found to be superior in accessions CO-14275, CO-14646 and CO-14611 respectively. Overall, the genetic variability observed in chilli during this study is essential for further breeding programs.

Keywords: Genotype, Morphological characters, Cluster, Genetic variability

GPS-30

Public Private Community Partnership for Seed Sector Transformation in Nepal

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ABSTRACT

Nepal's seed sector is central to agricultural productivity, food security and agribusiness development as access to quality seed determines much of the yield potential realized at farm level. This research examines Nepal's seed business and market through an integrated conceptual framework that links seed policy, institutional arrangements and international seed system dynamics. Based on recent evidence from FAO, Seed Quality Control Centre (SQCC), National Seed Vision (2013-2026) and relevant research literature, the study analyzed structure and performance of seed systems, supply-demand dynamics and the growing dominance of imported hybrid seeds. Nepal's seed business and market is characterized by the interaction of four core components: (i) policy and regulatory frameworks (Seed Act, National Seed Policy, National Seed Vision), (ii) institutional and research support systems (NARC, SQCC, national gene bank and international research partners), (iii**)** market and value chain actors (public agencies, private seed companies, cooperatives, community seed systems, dealers and farmers) and (iv) international seed structures. The analysis revealed that Nepal's seed market, while expanding in size and diversity, remains constrained by low seed replacement rates, limited domestic hybrid seed research capacity, dependence on imported high-value vegetable and cereal seeds and gaps between policy intent and implementation. Comparative insights from international seed systems highlighted the need for stronger research and development investment, streamlined variety release mechanisms, quality assurance and market-oriented seed production models. In this context, strategic mergers between seed companies and Research and development (R&D) license holders emerge as a critical pathway to accelerate varietal development, enable large-scale production of improved seeds and ensure rapid availability of promising and elite genotypes within a short period of time. Within Nepal's seed system, private seed enterprises therefore play a significant role in implementing policy objectives and research investments in plant breeding into tangible outcomes. The operational model of Muktinath Seed Bank Ltd., a rising public seed company of Nepal, demonstrates how a policy-aligned, market-oriented seed enterprise can strengthen domestic seed production, enhance varietal access and contribute to Nepal's agricultural growth by bridging research, quality seed supply and farmer-focused commercialization.

Keywords: Research and Development (R&D), Seed system, Seed business and market, Seed policy, Private seed companies

GPS-31

Promotion of Climate Resilient Crop Varieties and Technologies in the Gandaki River Basin of Nepal

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ABSTRACT

Gandaki Basin Climate Resilient Project (GBCRP) a seven years project has been implementing in Nepal funding from GCF. The main goal of the project is to enhance the adaptive capacity and resilience of communities and ecosystems to the impacts of climate change in the Gandaki River Basin region. The International Union for Conservation of Nature (IUCN) serves as the GCF-Accredited Entity and implementing entity. The Department of Forest and Soil Conservation (DoFSC) under the Ministry of Forests and Environment (MoFE) and the National Trust for Nature Conservation (NTNC) are the executing entities of the project. The overall goal of the project is to improve climate resilient of poor vulnerable communities and ecosystem in the Gandaki River Basin. Agriculture is the main occupation for the livelihoods of the people in this region. So GBCRP has given priority to promote climate resilient crops and variety specially submergence tolerant and drought tolerant rice variety and other summer crops in terai, inner terai and drought tolerant wheat and other winter crops in mid hills in partnership with Nepal Agricultural Research Council (NARC). For this purpose, MOU has been signed between NTNC and NARC to carryout partnership to increase household income, food security, nutrition, reduce drudgery to women and create employment opportunities to rural women and men of the vulnerable communities and contribute to improve ecosystem. During FY 2081/82, NARC and NTNC, conducted participatory varietal selection (PVS) mother trials, demonstrations and training /interaction program with farmers on main cereal crops including rice, wheat, maize, buckwheat, and finger millet. Climate change is significantly affecting cereal production, which is highly dependent on climatic conditions. Marginalized communities, who rely heavily on cereal production for their livelihood, income, and employment, are the most affected by these climatic changes. The project's aim is to enhance the resilience and sustainability of these communities against climate change impacts by providing optimal varietal options. The project targets 19 districts and 151 Municipalities, across Bagmati, Gandaki, and Lumbini provinces, benefiting approximately 1.9 million people in seven sub-watershed areas of GBCRP. These efforts are expected to result in the avoidance of over 847,000 tons of emissions and serve as a model for climate-resilient development across Nepal. The project specifically aims to enhance resilience in agriculture,

benefiting vulnerable groups including Indigenous Peoples (IPs), Dalits, women, and other marginalized communities.

The Project document has envisaged agricultural intervention in the GRB at the end of the project is above 105,000 ha (38,512 ha rice areas with flood tolerant varieties and 66,749 ha wheat area with drought tolerant varieties) to increase the community resilience. The project interventions such as providing quality seeds, as well as technical and scientific support, to help communities in these high-risk areas select suitable varietal options and adopt effective climate mitigation methods. Such intervention will directly improve food security for marginalized communities in the Gandaki River Basin (GRB), where the crop losses are frequent due to flooding and drought.

The activities under this project reached more than 1000 farmers with a focus on gender and caste inclusion across Gandaki, Bagmati, and Lumbini provinces. Altogether 65 demonstrations of different crop (Rice -22), Wheat (-15), Maize (15), finger millet (12) and Buckwheat (1) and 67 training/ interaction were conducted in FY 2081/82. Key results included successful identification and promotion of high-yielding and stress-tolerant genotypes. In wheat, 15 demonstrations and 2249 kg source seed of 14 newly released and pipeline varieties (18.74 ha) for large plot demonstration was carried out in 15 districts. The three promising genotypes NL 1488, NL 1450, and NL 1446 and newly released varieties Zinc gahun 1, Zinc gahun 2, Bheriganga performed well across the 15 districts. In rice varieties Ganga sagar-1, Bahuguni-2 on submergence rice and Sukha Dhan-2, Sukhha Dhan -3, Hardinath-3 for drought tolerant performed well. Rice variety Bahuguni-1 & Bahuguni-2 performed well for both drought and Submergence condition. In spring rice- IR16L 1769, IR17A 1785, and Chaite 5 and maize varieties Arun -2 Rampur composite, Across- 99402, RH-10, CAH 1511, EEYc1, Manakamana-3, BGBYPOP, EEYC1 preferred by farmers. The dissemination of new varieties along with improved adoption of climate-smart practices has significantly increased the yield along with quality seed for next generation. Community based seed program on maize, rice, finger millet and buckwheat along with complete package of practice was provided in the local level selected by district level workshop organized by NTNC with different agriculture stakeholders in each district. This coordinated effort is expected to enhance varietal adoption in Gandaki River Basin districts, contributing to increased productivity and resilience in Rice/Wheat/Maize based farming systems.

Keywords: Climate resilient agriculture; Climate Change, climate resilient crops variety

GPS-32

Hybrid breeding and varietal development of chili pepper in Nepal

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ABSTRACT

Chili pepper (*Capsicum annuum*) is one of the important commercial vegetables, having a huge prospect of domestic market. Currently, the low varietal option is the main concern among various horticultural issues. Additionally, over 80 percent of varieties being used are hybrid varieties imported from abroad countries, but these are unreliable for their supply and performance. Thus, there is very grave need of developing own hybrid varieties with high yield potential and consumer's preferred fruit qualities as well as tolerance to major diseases and pests. On these context, the National Horticulture Research Centre has developed 15 hybrids using the specific traits of 13 potential inbred lines available in the center. Their initial evaluation has been conducted at NHRC, Khumaltar during summer season in 2081/82. The results revealed that the plant height, canopy width, number of primary branches per plant, and peduncle length were statistically different ($P<0.05$) among the tested F1 hybrids. The plant heights observed among the hybrids ranged from 81.5 cm to 107.4 cm with mean 92.9 cm. The widest canopy was observed at F1 hybrid HRDCHI 012 * HRDCHI 009 (108.25 cm) followed by CO5066-3 * PUSA JWALA (108 cm) among the 15 F1 hybrids. Similarly, the highest number of primary branches per plant was found at CO5063 x Suryamukhi hybrid (10 branches) followed by Thailand x HRDCHI009 (8 branches) and CO5066-3 x Pusa Jwala (8 branches).

GPS-33

Performance of elite local germplasms of barley at HRS Dailekh of Nepal

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ABSTRACT

Barley (*Hordeum vulgare* L.) is an important cereal crop in the mid-hill regions of Nepal. The systematic evaluation of elite local barley germplasm for yield and yield traits remains limited in the western mid-hills of the country. This study was conducted at Horticulture Research Station, Dailekh (HRS), Dailekh, Nepal in two consecutive winter seasons of 2022/23 and 2023/24. Experiment was laid out in RCB design with six treatments and replicated thrice. Crop geometry was maintained row to row 25 cm and plant to plant continuous seed sowing and fertilizers and manure was applied at the rate of 50:30:30 kg N: P_2O_5:K_2O kg/ha + 10 t FYM/ha. Data was analyzed by using Genstat 64-bit release 18.2 version. Analysis of results showed significant variation in yield and yield attributing characters among genotypes. The maximum plant height (98.1 cm) was recorded on genotypes Namule Local followed by Rawatkot local. The genotypes Dharkhola local showed significantly earlier to days to heading (93 days) followed by Rawatkot local, Dullu Local and Pali Local while Rawatkot local showed earlier in day to maturity (139 days). The highest number grains per plant showed by Namule Local and Pali local (64), Similarly longer Spike length and higher thousand grain weight found in Rawatkot Local (7.9 cm and 37.7 gm). The highest grain yield produced by Pali local (5.52t/ha). Based on the significance results of plant height, days to heading, number grain per plant and heads per meter square, spike length, thousand grain weight and grain yield, genotypes Pali local was found superior among the tested genotypes.

Keywords- Barley, local germplasms, grain yield, mid hills, Nepal

GPS-34

Performance and Adaptability of Foxtail Millet (*Setaria Italica* (L.) P. Beauv.) Genotypes in Mid and High Hills of Nepal

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ABSTRACT

Foxtail millet (*Setaria Italica* (L.) P. Beauv.) is the second most widely cultivated millet globally. Nepal is one of the centers of diversity of foxtail millet and has high genetic diversity of this crop. Despite its climate-resilience and nutritional benefits, including low glycemic index, its cultivation and use is declining. The only one registered landrace (*Bariyo Kaguno*) suggests it has not got priority in research. A trail of eight foxtail millet landraces was conducted in three locations (Jumla, Kaski and Lamjung), engaging farmers in identifying preferred traits such as short duration, large grain size, and high yield. The maturity, plant height, panicle length, grain yield and 1000 grain yield were record. The Analysis of Variance revealed significant difference between genotypes and environments. *Kalo Kaguno* (2761.11 kg/ha), *Seto Kaguno* (2472.41 kg/ha) and *Bariyo Kaguno* (2161.36 kg/ha) performed best in Humla, Kaski and Lamjung respectively. The combined analysis of variance over different environments suggested significant relation among grain yield, thousand grain weight and panicle length. The GGE Biplot analysis identified *Pahelo Kaguno, Seto Kaguno and Bariyo Kaguno* as top-performing genotype in Jumla, Kaski and Lamjung respectively. The mean vs. Stability study revealed T1 (NGRC006659) as a stable genotype in all three environments. The study recommended promoting location-specific genotypes over a singly widely adapted variety to enhance foxtail millet cultivation in Nepal.

Keywords: Farmers seed system, G*E interaction, Millet, Agrobiodiversity, local landrace

Posters

PBaGSoN-1

Evaluation of Spring Rice (Chaite Dhan) Genotypes for Growth and Yield Attributes at Belbari, Morang

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ABSTRACT

A field experiment was conducted during the 2025 spring season in Belbari, Morang, Nepal, to evaluate the performance of eleven spring rice (Chaite dhan) genotypes for growth and yield-attributing traits. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications, comprising two check varieties (Hardinath-1 and Chaite-5) and nine advanced IR lines (IR16L 1769, IR17A 1732, IR16L 1411, IR17A 1660, IR17A 1735, IR10L 152, IR16L 1636, IR16L 1831, and IR16L 1619). Data were recorded on growth parameters, phenological traits, yield-attributing characters, and grain yield. Statistical analysis was performed using analysis of variance (ANOVA), and treatment means were separated using Duncan's Multiple Range Test (DMRT). The results revealed highly significant differences ($p < 0.01$) among genotypes for most of the traits studied, indicating substantial variability. IR16L 1411 produced the highest grain yield (8.07 t/ha), followed by Hardinath-1 (7.75 t/ha) and IR10L 152 (7.49 t/ha), whereas IR16L 1831 recorded the lowest yield (5.25 t/ha). IR10L 152 consistently exhibited the tallest plants across growth stages, while IR17A 1660 showed superior tillering ability. The highest thousand-grain weight was observed in IR16L 1831 (29.75 g), followed by IR16L 1636 and IR17A 1735. Harvest index ranged from 39.54% to 61.13%, with Hardinath-1, IR17A 1732, IR17A 1660, and IR16L 1411 exhibiting higher efficiency of biomass partitioning. Grain yield showed significant positive associations with several yield-attributing traits. Based on overall yield performance and favorable harvest index, IR16L 1411 and IR10L 152 were identified as the most promising spring rice genotypes for cultivation under the agro-climatic conditions of Morang district, while other genotypes may serve as valuable genetic resources for specific traits in rice breeding programs.

Keywords: Spring rice, Genotypic variability, Grain yield, Yield attributes, Harvest index, RCBD

PBaGSoN-2

Diversity Assessment and Farmer-Participatory Selection of Proso Millet (*Panicum miliaceum* L.) Accessions in Mid-Hill Conditions of Nepal

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ABSTRACT

Assessment of genetic diversity is fundamental for crop improvement programs, as it helps to identify desirable traits and broaden the genetic base. Thus, research was carried out in rod row design to assess phenotypic diversity and variation among 16 proso millet accessions at Sundarbazar, Lamjung. Shannon Weaver's diversity (H') ranged from 0.66 to 1.58. The maximum H' value was observed in susceptibility to aphids (1.58) and lowest (H' = 0.66) in stigma color and panicle angle of branches. Flag leaf anthocyanin color intensity ($\chi^2 = 6.125$) and spikelet shape ($\chi^2 = 7.625$) were the only traits with significant differences ($p < 0.05$) among the studied accessions. The Coefficient of Variation (CV%) ranged from 9.37% for panicle length to 45.493% for days for 50% germination. The first 6 principal components contribute 85.4% of the total variation. PC1 explained variation in maturity and panicle morphology, PC2 explained ear morphology and panicle compactness, and PC3 accounted for grain and stem morphological traits. NGRC07335, NGRC07336, and NGRC09157 from cluster III were the potential high-yielding and superior accessions. NGRC07335 (4.38), followed by NGRC09157 and NGRC07349 (4.06), were the top-ranked accessions in the participatory varietal selection process. Thus, the current study provides a foundational framework for characterizing and evaluating the diversity of Proso millet accessions with significant potential for genetic enhancement and breeding programs.

Keywords: Diversity, Proso accessions, Preference, Selection, Variation

PBaGSoN-3

Morphophysiological screening of wheat (*Triticum aestivum* L.) genotypes under controlled conditions

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ABSTRACT

Drought is a major abiotic stress that limits wheat yield by affecting morphological and physiological traits; as a result, identifying drought-tolerant wheat genotypes has been crucial. The present study aimed to screen and characterize drought tolerance in 15 wheat genotypes using morpho-physiological indices under controlled conditions. A greenhouse pot experiment was performed using a two-factor factorial completely randomized design with two replications. Genotypes were subjected to two moisture levels: 75% field capacity and 35% field capacity. Drought stress and irrigation schedule were managed based on the gravimetric method. Flag leaf area, hundred seed weight, yield per plant, spike length, SPAD, relative water content and chlorophyll fluorescence parameters were recorded and subjected to data analysis in R Studio. Analysis of variance revealed a significant genotypic difference ($p < 0.05$) for all the studied traits, with the exception of relative water content. Genotypes showed relatively better performance under 75% field capacity. Yield per plant showed the highest reduction under drought stress, while the lowest was observed in maximum PSII photochemical efficiency (F_v/F_m). Owing to high values for spike length, hundred-seed weight, yield per plant, and fluorescence parameters, WK4164 performed best under 35% field capacity, whereas WK4155 showed poor performance. Based on the stress susceptibility index, WK2820, WK4164, and Khumal Shakti were identified as potential drought-tolerant genotypes, while WK1204, WK4155, and WK4158 were identified as drought-susceptible genotypes. Future studies validate the identified drought-tolerant genotypes under field conditions and through molecular markers before their utilization in breeding programs.

Keywords: Abiotic stress, drought, physiology, tolerance, yield

PBaGSoN-4

Participatory Varietal Selection of Potato (*Solanum tuberosum* L.) Varieties at Shivalaya Rural Municipality, Jajarkot

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ABSTRACT

Potato (*Solanum tuberosum* L.) is a major staple and cash crop in the mid- and high-hill regions of Nepal, including Shivalaya Rural Municipality, Jajarkot, where varietal adoption remains low due to limited farmer involvement and poor local adaptation of improved cultivars. This study aimed to identify high-yielding and farmer-preferred potato varieties through a participatory varietal selection (PVS) approach under local agro-ecological conditions. Seven potato varieties Rojita, Kufri Jyoti, Laalgulaab, Desiree, Bajhang Local, Cardinal, and Khumal Seto were evaluated during February–June 2025 using a randomized complete block design with three replications. Farmers actively participated in varietal evaluation based on agronomic performance, tuber quality, and preference traits. Farmers group of 20 farmers took part in assessing the cultivars, according to agromorphological and yield characteristics were measured and preference scoring was done. Significant varietal differences ($p < 0.05$) were observed for emergence, plant height, number of leaves and stems, tuber number, marketable tuber yield, and total yield. Kufri Jyoti produced the highest tuber weight per plant (0.44 kg) and the highest yield (16.91 t ha^{-1}), indicating superior yield potential and adaptability. Bajhang Local recorded the highest total tuber number and marketable tuber count, though it also produced a higher proportion of non-marketable tubers. Rojita showed vigorous early growth and was highly rated by farmers for organoleptic quality. Farmer preference analysis ranked Kufri Jyoti highest overall due to its combined yield performance and tuber quality, followed by Rojita and Bajhang Local for specific traits. This study demonstrates that participatory varietal selection is an effective approach for identifying locally adapted potato varieties. Kufri Jyoti is recommended for cultivation in Shivalaya Rural Municipality, while further multi-location and multi-season evaluations are suggested to support wider dissemination.

Keywords: Participatory varietal selection, potato, Kufri Jyoti, farmer preference, yield performance

PBaGSoN-5

Qualitative Traits Based Diversity Analysis Among Nepalese Foxtail millet [*Setaria italica* (L.) P. Beauv.] Landraces

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ABSTRACT

Foxtail millet (*Setaria italica* (L.) P. Beauv) is among the earliest domesticated, climate-resilient cereal crops with high nutritional value; however, it remains neglected and underutilized in Nepal. This study aimed to evaluate the phenotypic diversity of foxtail millet landraces conserved at the National Agricultural Genetic Resources Center (NAGRC), Khumaltar (1360 m a.s.l.), Lalitpur, Nepal during March-July 2025. Forty-eight landraces were assessed using an augmented design, recording sixteen qualitative traits based on IBPGRI and FAO, 2023 descriptors. Qualitative traits; namely, flag leaf color, growth habit, plant pigmentation at auricle, leaf altitude, leaf sheath intensity of pubescence, inflorescence apical sterility, inflorescence compactness, leaf pigmentation, inflorescence shape, inflorescence lobes, inflorescence bristles inflorescence bristle length, culm branches, panicle branching, leaf senescence and seed color were recorded to assess the intra-specific diversity. Shannon-Weiner diversity indices (H') showed high diversity ranging from 0.101 (panicle branching) to 1.423 (seed color) which indicates that characters were more diverse for seed color while the value of evenness ranged from 0.146 (panicle branching) to 1 (inflorescence apical sterility). Cluster analysis grouped 48 accessions into five clusters based on 16 qualitative traits. Cluster II was the largest cluster with 26 accessions followed by cluster III with 10, cluster IV with 6, cluster II with 4, and cluster V with 2. The genotypes within the same cluster considered to have the similar phenotypic characters. And the genotypes between the clusters are more diverse ones. Therefore, the genotypes of most diverse cluster may be used as parents in hybridization programs.

Keywords: Foxtail millet, Landraces, Accessions, Phenotypic diversity, Cluster analysis

PBaGSoN-6

Agronomic traits characterization of Nepalese Finger Millet (*Eleusine coracana* (L.) Gaertn.) Landraces

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ABSTRACT

Finger millet (*Eleusine coracana* (L.) Gaertn.) is a nutritionally rich and naturally climate-resilient C4 plant. This study aims to characterize the phenotypic diversity of 32 finger millet landraces collected from 20 districts of Nepal. The landraces were evaluated in an augmented block design with two replications at Khumaltar, Lalitpur, Nepal, from August 2025 to January 2026. A total of 22 quantitative and 13 qualitative traits were assessed. The data were analyzed using Microsoft Excel and RStudio, where descriptive statistics, principal component analysis, cluster analysis, and Pearson's correlation analysis were evaluated. Variation was observed across quantitative traits, with CV ranging from 6.69 % to 34.58 %, while the standard deviation also indicated substantial diversity, ranging from 0.09 to 341.94. Principle component analysis revealed that the first seven components with eigenvalue greater than 1 accounted for 84.48% of the total phenotypic variation, with PC1 and PC2 contributing 47.10% with traits such as days to 50% heading, days to 50% flowering, finger width, days to 80% maturity, plant height, ear exsertion, number of leaves per plant, grain yield, peduncle length, and leaf sheath diameter. Cluster analysis was done through the average method, with accessions grouped into 5 clusters based on 22 quantitative traits. Correlation analysis shows that days to heading and days to flowering are strongly correlated with each other, and leaf-related traits were also positively correlated with each other. Accession NGRC 03539 (Jhyapre Kodo) was identified as early maturing, while NGRC 09933 (Nang Katuwa Kodo), NGRC 04852 (Arun Kodo), and NGRC 04817 (Lamre Kodo) were identified as high-yielding landraces. The findings show that these landraces have good phenotypic diversity and molecular, multi-seasonal, and multi locational trial is suggested to further enhance the finger millet breeding programs.

Keywords: Finger millet, landraces, phenotypic diversity, agro-morphological traits

PBaGSoN-7

Evaluation of advance wheat (*Triticum aestivum* l.) lines for yield, agronomic traits, and spot blotch resistance at Rampur, Chitwan

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Abstract

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops, playing a vital role in food and nutritional security. The objective of this study was to evaluate advanced wheat lines for phenological traits, yield performance, and resistance to spot blotch to identify promising genotypes for varietal improvement. The field experiment was conducted at Rampur, Chitwan, Nepal, using a randomized complete block design (RCBD) comprising eighteen wheat genotypes, including seventeen advanced lines and one check variety, with three replications. Observations were recorded for days to booting, heading, anthesis, and maturity, plant height, effective tillers, grains per spike, thousand-grain weight, and grain yield. Spot blotch severity was assessed through the area under the disease progress curve (AUDPC). The collected data were tabulated in MS Excel and analyzed using R Studio, and mean separation among significant traits was performed using the Least Significant Difference (LSD) test at the 5% level of significance. The results revealed significant genetic variability among the genotypes for all traits, indicating strong genotypic influence on phenology, yield, and disease response. Genotype PYT 2024/25-4 produced the highest grain yield (0.284 kg m^{-2}) with moderate susceptibility to spot blotch, whereas PYT 2024/25-12 recorded the highest number of effective tillers m^{-2} (397) and grains per spike (45.35). Early-maturing genotypes such as PYT 2024/25-15 and PYT 2024/25-1 could be suitable for late sowing, while PYT 2024/25-8 and PYT 2024/25-10 matured later due to longer growth duration. A strong negative correlation ($r = -0.83$) between grain yield and AUDPC confirmed the adverse impact of spot blotch on wheat productivity. Overall, PYT 2024/25-4, along with PYT 2024/25-12 and PYT 2024/25-14, showed strong potential for further evaluation and use in wheat breeding programs.

Keywords: wheat, grain yield, phenological traits, AUDPC, spot blotch

PBaGSoN-8

Stability of Fatty Acids in Seed Oil of Soybean Evaluated across Three Growing Seasons at Rampur, Chitwan, Nepal

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ABSTRACT

Soybean [*Glycine max* (L.) Merrill] is a vital oilseed crop and the nutritional quality of its oil is primarily determined by fatty acid composition. Desirable attributes for human health on edible oil include low palmitic and steric acid, low linoleic-to-linolenic acid ratio, and high oleic acid. A total of 14 soybean accessions, including a check (Puja), were evaluated over three consecutive years (2015–2017) at the Agriculture and Forestry University, Chitwan, Nepal, using a randomized complete block design to assess the stability of fatty acid content across different years. Fatty acid profiles were quantified by gas chromatography. Significant variation was observed among accessions, years and accessions × year interactions for all five major fatty acids. Mean concentration percentage were 11.7 palmitic acid, 3.2 stearic, 28.7 oleic, 49.7 linoleic, and 6.6 linolenic where linoleic-to-linolenic acid ratio ranging from 6.8 to 9.3. GGE biplot analysis explained 92.61% of total variability for palmitic acid, 94.74% for steric acid, 98.16% for oleic acid, 98.05% for linoleic and 97.41% for linolenic acid, revealing distinct genotype × environment interactions patterns and stability relationships. Discriminativeness vs. representativeness analysis identified 2016 as the most representative year for palmitic and linolenic acids, 2015 for stearic acid, and both 2015 and 2016 for oleic and linoleic acids. The which-won-where biplot indicated that Puja was the most stable genotype for palmitic, steric, linoleic, and linolenic acid, whereas LS-77-16-16 showed the highest stability for stearic acid. Other stable genotypes included LS-77-16-16, TGX-1993-4FN, TGX-1992-52F, TGX-1989-48FN and TGX-93-4FN for palmitic, steric, oleic, linoleic and linolenic acid, respectively. Puja along with other identified stable genotypes represent valuable genetic resources for soybean breeding programs aiming improved oil quality through optimized fatty acid composition.

Keywords: Fatty acid, linoleic to linolenic acid ratio, GGE biplot, stability, accession

PBaGSoN-9

Agro-Morphological Characterization and Diversity Assessment Of Nepalese Proso Millet (*Panicum miliaceum* L.) Landraces

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Abstract

Proso millet (*Panicum miliaceum* L.), a climate-resilient crop, is an underutilized cereal in Nepal. This study aimed to characterize 21 Nepalese proso millet landraces for key agro-morphological traits to generate baseline information for breeding and conservation programs. The experiment was conducted at the National Agriculture Genetic Resources Centre, Khumaltar from March to June of 2025 using an augmented block design including 3 checks, one of which was *Dudhe Chino,* a registered variety. A total of 23 quantitative and 15 qualitative traits were assessed and the data were analysed. Among the fifteen qualitative traits studied, nine were polymorphic, with highest Shannon-Weaver indices for panicle exsertion and altitude of panicle branches (H' = 1.319) and secondary branching (H' = 0.956). PCA revealed that the first three principal components (PCs) explained 58.33% of total variation, with PC1 explaining 29.89% with plant/panicle architecture traits; PC2 explaining 15.60% with leaf/photosynthetic traits and PC3 explaining 12.83% variation with reproductive/maturity traits. Cluster analysis grouped the landraces into three clusters; with high-yielding types with mean grains/panicle (196.8), higher plant height (49.8cm) and longer inflorescences (21.5cm) falling into the same cluster. Pearson correlation analysis largely validated the PCA structure as plant height, panicle and inflorescence length, peduncle exertion, stem diameter, and grains per panicle, traits with strong positive loadings in PC1, were highly positively correlated ($r > 0.5-0.7$), indicating high-yielding landraces also tend to be structurally more robust. Landraces NGRCO7344, NGRCO7345, NGRCO7343 and NGRCO7352 showed strong potential for future breeding activities due to their superior performance for various traits based on rank sum. This characterization thus reveals valuable agro-morphological diversity in Nepalese proso millet landraces, identifies candidate landraces for breeding and further research, and provides a trait based dataset to support conservation and selection.

Keywords: Characterization, Landraces, Proso millet

PBaGSoN-10

Genetic Variability and Interrelationship among Key Agronomic Traits in Maize Inbred Lines

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ABSTRACT

Genetic variability of inbred lines, relationship among various agronomic traits, nature and extent of their association with grain yield is crucial for developing high-yielding maize hybrids. The present study aimed to dissect the variability, per se performance, relationships among yield contributing traits and identify key determinants of grain yield in maize inbred lines through correlation and path coefficient analysis. A set of twenty-four maize inbred lines was evaluated on two planting dates during the winter of 2024-25, at the National Maize Research Programme, Rampur, Nepal, in an alpha-lattice design with two replications. Twelve agro-morphological and yield traits were measured following CIMMYT maize descriptors. All traits showed significant genetic variation among the inbred lines across both planting dates. High genetic advance as percentage of mean was recorded for grain yield, followed by kernel rows per ear, ear height, and plant height, despite grain yield had medium heritability. Yield contributing traits-number of plants, number of ears, grain yield, and thousand kernel weight-clustered together and showed strong positive genetic correlations, highlighting their close association. Path coefficient analysis identified days to silking, thousand kernel weight, number of ears, and kernel rows per ear as the major determinants of grain yield, while co-heritability analysis showed kernel rows per ear, along with days to 50% anthesis and silking, had strong genetic association with grain yield. The grain yield showed reliable selection potential due to additive gene effects despite environmental influence. RML149, RML95, RML96, RML17, RML98, RML145, CAL14137, CML612, and CML161 exhibited the highest grain yields and are promising parents for hybrid development. The group of RML2, RML18, and RML140 formed a distinct cluster, indicating their suitability for use as tester in future hybrid breeding. Close genetic affinity between RML95 and RML96 explains the poor heterosis observed in the released Rampur Hybrid-16, whereas the greater genetic distance between RML149 and RML18 accounts for the high heterosis recorded in the registered Rampur Hybrid-8. These results provide valuable guidance for maize breeders, highlighting the importance of selecting genetically diverse parental lines to develop high- yielding hybrids through increased heterosis.

Keywords: variability, inbred lines, per se performance, character association, & cluster analysis

PBaGSoN-11

Marker-assisted selection of rust resistance and drought associated genes in wheat

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ABSTRACT

Rusts epidemics and drought stress are the major challenges to wheat production, globally. Deployment of wheat varieties that have durable rusts resistance and drought resilience is the most environment friendly and sustainable strategy to overcome these challenges. A precise and efficient selection of desired recombinant lines from segregating population is crucial for the success of varietal development program. Marker-assisted selection (MAS) is a highly effective approach for selecting multiple genes with major and minor effects; however, its application in wheat breeding programs in Nepal remains limited. In this study, 66 F_3 progenies of wheat (Cross-C021-01) developed at the Department of Genetics and Plant Breeding, AFU were assessed for the recombinants of three major pleiotropic rust resistance genes (*Lr34, Lr46, Lr68)* and drought related gene *TaDreb*-B1 using the gene-specific markers: csLV34, xwmc44/xgwm259, csGS and P40/P18R, respectively. The progenies were analyzed using two sampling strategies in order to maximize the probability of obtaining desirable F_4 recombinant plants (i) bulk sampling of 8-10 plants from each of the 53 progenies and (ii) four individual tagged plants from 13 breeder-identified superior progenies. Leaf samples were collected from the F_3 progeny rows grown in the field. DNA extraction, quantification, PCR assays and gel-electrophoresis were carried out at Plant Molecular Genetics laboratory, Center for Biotechnology, AFU. We identified four progenies and three plants having non-parental recombination for single rust gene and *TaDreb*-B1, 18 progenies and 10 plants for two rust genes and *TaDreb*-B1, and 16 progenies and nine plants for three rust genes and *TaDreb*-B1. Similarly, nine progenies and five plants showed recombination of two rust genes and six progenies and two plant showed recombination of three rust genes. The selection of F_3 recombinant lines for major pleiotropic rust resistance genes and drought associated *TaDreb*-B1 gene and the subsequent generation advancing using MAS provide valuable resource for the development of durable rusts resistant, abiotic stress resilient wheat varieties for Nepal.

Keywords: Marker-assisted selection, Durable rust resistance, Drought resilience, Pleiotropic genes, Recombination

PBaGSoN-12

Agro-Morphological Evaluation of Wheat Varieties Under Late-Sown Condition

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ABSTRACT

Seven different cultivated varieties of wheat, including check variety Gautam, were evaluated for agro-morphological characters, yield, and yield attributing traits at College of Natural Resource Management (CNRM), Sindhuli, Nepal, from December 2080 to April 2081. The experiment was conducted using a Randomized Complete Block Design (RCBD) with three replications. The individual plot size was 3m² (2m×1.5m) and sowing was done on 26th December 2080. The soil of the experimental area was slightly acidic sandy loam. Fertilizer was applied at the rate of 120:50:50 NPK kg/ha. Analysis of variance revealed significant differences between the varieties for days to booting, flag leaf area, peduncle length, spike diameter, number of spikelet per spike, thousand grain weight and grain yield, while, non-significant differences were observed for days to heading, anthesis, flag leaf senescence, physiological maturity, plant height, spike length, spike weight, number of grain per spike, weight of grain per spike, number of tiller per meter square, biological yield and harvest index. The mean grain yield was 3.34 t/ha. Varieties Zinc Gahu-1, NL971, and Banganga out-yielded the check variety Gautam, and the highest yield was observed in Zinc Gahu-1 (4.07t/ha). The highest correlation was observed between days to booting and days to heading (0.901***). Correlation analysis of the studied traits showed positive and significant correlation of harvest index (0.710***), spike weight (0.528*), spike length (0.465*), and days to booting (0.383*) with grain yield. Negative and significant correlation of peduncle length (-0.680**) with grain yield was observed. The study has indicated that harvest index, peduncle length, spike weight, spike length, and days to booting could be valuable traits for higher yield in late-sown conditions of the studied area.

Keywords: Spike, late sown, harvest index, peduncle

PBaGSoN-13

Agro-morphological diversity in Nepalese foxtail millet (*Setaria italica* (l.) P. Beauv.) Landraces

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ABSTRACT

Foxtail millet (*Setaria italica* L.) is a nutrient-dense, climate-resilient cereal with significant untapped potential in Nepal. Despite harboring rich genetic diversity, Nepalese landraces remain poorly characterized, limiting their use in systematic breeding. This study aimed to evaluate agro-morphological diversity and identify superior foxtail millet accessions for breeding and conservation. Forty-nine landraces were evaluated from February to August of the 2023 season at the National Agriculture Genetic Resources Centre (Genebank), Khumaltar, under a randomized complete block design. Data were recorded for 18 quantitative and 29 qualitative traits following IBPGR (1985) descriptors. Shannon-Weaver diversity indices revealed high morphological diversity, particularly for panicle shape (H'=0.92) and seed color (H'=0.89). Significant positive correlations were observed among quantitative traits, including peduncle length with peduncle exertion (0.814**), inflorescence weight with panicle width (0.702**), and grain yield (0.621**). Principal component analysis revealed that the first two principal components accounted for 47.3% of the total variation, with PC-1 being associated with panicle and yield traits, and PC-2 reflecting phenology and plant stature. Cluster analysis grouped accessions into three distinct phenotypic clusters, with Cluster III combining high grain yield (4204 kg/ha) and early maturity (138 days). Superior accessions, such as NGRC05087 (highest yield), NGRC07419 (earliest maturity), NGRC05091 (larger seed size), and NGRC07952 (tallest accession), were identified as potential donors for trait-based breeding. The findings provide a phenotypic foundation for targeted selection, pre-breeding, and in-situ conservation of foxtail millet genetic resources in Nepal, supporting climate-resilient agriculture and nutritional security.

Keywords: Cluster analysis, foxtail millet, genetic diversity, principal component analysis, trait correlations.

PBaGSoN-14

Performance evaluation of finger millet genotypes in Nuwakot

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ABSTRACT

Finger millet (*Eleusine coracana* (L.) Gaertn*)* is a climate-resilient and nutrient-dense crop in Nepal, yet its full potential remains untapped due to low productivity driven by the use of poor-performing genotypes. This study was conducted in Gerkhutar, Nuwakot, to identify high-yielding genotypes suitable for the region by evaluating nine different finger millet genotypes. The key phenological, morphological, and yield-related traits during the 2082 Ashad-Kartik season were assessed using a Randomized Complete Block Design (RCBD) with three replications. The results demonstrated significant variation across all measured parameters. Among the genotypes, Lamre Kodo and Chaure Kodo emerged as the top performers, achieving grain yields of 3.46 t/ha and 3.20 t/ha, respectively. These genotypes significantly outperformed the released variety, Kabre-2, which yielded 2.50 t/ha. Chaure Kodo was the earliest to reach heading (66 days) and flowering (70 days), while Arun Kodo achieved maturity the fastest (117.67 days). Correlation analysis further revealed strong positive associations between grain yield and contributing traits such as the number of effective tillers and thousand-seed weight. While Lamre Kodo and Chaure Kodo demonstrated superior yield potential and favorable agro-morphological traits in this study, these results are based on a single-location and single-season trial. Consequently, further multi-location and multi-year evaluations are essential to validate the yield stability and environmental adaptability of these promising genotypes before they can be recommended for large-scale adoption in the hilly regions of Nepal.

Keywords: Finger millet, genotypes, grain yield

PBaGSoN-15

Wild Rice Diversity in Western Nepal: Conservation Strategies and Ecological Impact for Sustainable Future

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ABSTRACT

Wild rice is an important genetic resource for improving cultivated rice and ensuring long-tern food security under changing climates. This study assessed the diversity, distribution and conservation status of wild rice in western Nepal, covering Kapilvastu, Rupandehi, Palpa, Banke and Kailali districts within a subtropical altitude range of 60-900m. 21 wild rice accessions were explored, collected and characterized. Two species *Oryza nivara & Oryza rufipogon* (AA genome, 2n=24) were recorded. Morphological and ecological comparisons revealed that *O. rufipogon* is a perennial species which thrives in permanent or semi-permanent wetland while *O .nivara* is an annual species adapted to seasonal wetlands and drier conations. These species provide valuable genes for tolerance of drought, flooding and resistance to pest and disease. However, their populations are threatened by habitat destruction, wetland conversion, agricultural pollution and climate change. Current conservation efforts includes both in-situ and ex-situ approaches, with accessions conserved at National Genebank, NARC. Strengthening habitat protection, community-based conservation and utilization of wild rice in climate-resilient breeding program is crucial for sustainable conservation and use of wild rice genetic resources in western Nepal.

PBaGSoN-16

Assessment of Honey Bee Role in Pollination and Productivity of Rapeseed (Brassica campestris var. toria)

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ABSTRACT

Rapeseed (*Brassica campestris* var. *toria*) is a major oilseed crop in Nepal, and the productivity of the crop is low despite the release of improved varieties. Insect pollinators, especially honey bees, are extremely important in determining the quality and quantity of its yield as the crop is an open-pollinated and entomophilous crop. The aim of conducting this study was to determine the benefit of honey bees in improving the productivity and yield properties of rapeseed. The experiment was conducted in Kapilvastu, Nepal, in October-December 2025 using eleven rapeseed accessions in a Randomized Complete Block Design, and the two replications were conducted under two conditions of pollination: open pollination and controlled pollination in the mosquito-net cage. Primary branches, siliques per plant, seeds per siliqua, weight of thousand grains and grain yield were recorded. Duncan Multiple Range Test was used to analyze the data of variance and mean separation at the 5% level. Notably high differences between the genotypes were noted to exist between the traits studied. There were significantly better results in open-pollinated conditions as compared to controlled pollination, and there were significant decrease in the results under caged conditions, especially with regard to thousand-grain weight and grain yield, which decreased by 2.66 g and 0.76 t ha -1, respectively. Madhuwani Tori and Surkhet Tori had the best performance in either pollination conditions, and they were also the best in terms of genotype. The findings clearly demonstrate the significance of honey bees' role in enhancing rapeseed productivity, and how important pollination-friendly management practices, such as the prudent use of pesticides, are to maintain oil production in Nepal.

PBaGSoN-17

Agro-Morphological Characterization and Evaluation of Rapeseed Landraces at Nuwakot

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ABSTRACT

Rapeseed (*Brassica campestris* var. *toria*) is an important oilseed crop in Nepal, but the crop has not been able to yield well despite the availability of released varieties. An agro-morphological assessment of eleven rapeseed accessions was done in the winter of 2025 at Bidur-10, Gerkhutar, Nuwakot, to identify potential high-yielding landraces. The experiment was designed as a two replications Randomized Complete Block Design (RCBD). Records were taken on major quantitative characteristics such as plant height, primary branches, days to maturity, siliquae per plant, seeds per siliqua, thousand grain weight, and grain yield. Most of the traits that contribute to yield showed highly significant differences ($p \leq 0.001$) among the genotypes, which indicated that there was great genetic variability. Gerkhu Red Tori performed well in terms of the greatest number of primary branches, siliquae per plant, seed per siliqua, and yield of grains (1.675 t ha - 1) as followed by Makwane Tori (NGRC02751). The correlation analysis indicated that there were strong positive relationships between primary branches, number of seeds per siliqua, weight of thousand grains, and grain yield. The paper has identified the potential of local landraces, especially Gerkhu Red Tori, in bettering yield and its potential application in future breeding and improvement programs of rapeseed and crops in Nepal.

PBaGSoN-18

Exploring Diversity of Forage and Fodder Species in Nepal

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ABSTRACT

Livestock production in Nepal faces a shortage of seasonal feed imbalance with plenty of green forage during the monsoon, while it is scarce in the spring and winter seasons. Exploitation of diversity of forage crops is vital to cope with this challenge. Around 510 forage species are available, with approximately 275 cultivated plant species recognized as forage species in Nepal. Moreover, over 500 fodder tree species are available in Nepal. Among them, around 250 tree species are considered economically important fodder trees. In the Terai and mid-hill regions, both native and introduced grass species, namely Napier grass (*Pennisetum purpureum*) and fodder oats (*Avena sativa*), are grown by farmers due to higher biomass, palatability, and adaptability. Some pasture species such as ryegrass (*Lolium spp*.), timothy, and Setaria are grown in cooler, high hills regions. Leguminous forages, namely vetch, joint vetch, and forage peanut, are increasingly promoted due to their higher protein content and their biological nitrogen fixing capacity. Some fodder tree and shrub species, namely *Artocarpus lakoocha* (Khanyu), *Ficus semicordata* (Khanayu or Nebharo), and *Premna integrifolia* (Ginderi), are considered integral component to traditional agroforestry and livestock farming systems. This review paper explores the current information on genetic diversity, distribution pattern, and seasonal availability of Nepalese forage and fodder species, highlighting their potential for genetic improvement. Exploitation of diverse forage and fodder species ensures year-round feed availability across different agro-ecological zones in Nepal.

Keywords: Forage crops, fodder trees, genetic resources, livestock, legumes

PBaGSoN-19

Agro-morphological characterization of released and candidate bread wheat genotypes for hills

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Abstract

Bread Wheat (*Triticum aestivum* L.) is a major contributor of national as well as global food security. Genetic improvement of wheat genotypes can be enhanced through effective characterization and utilization of genetic resources. This study aimed to assess the extent of phenotypic diversity for various qualitative agro-morphological traits of the candidate wheat varieties. A total of 29 bread wheat genotypes including released cultivars, were evaluated during winter season of 2024-25 at the research plot of NPBGRC, Khumaltar. Thirteen qualitative traits of ear, spike, peduncle, growth habit, pigmentation, and awn were recorded using standard scoring and analyzed. Frequency distribution and Shannon-Weaver Diversity Index were used to assess phenotypic variation. Multivariate analysis (PCA and hierarchical clustering) was conducted to explore key sources of variation and genotype relationships. The findings revealed considerable variability among spike glaucosity, flag leaf glaucosity, growth habit, kink of the peduncle, and anthocyanin level, whereas anther color and awn presence were relatively less diverse. Shannon Diversity Index indicated a wide range of variation (0.00–1.21), with the highest diversity observed in flag leaf and spike glaucosity and peduncle kink. Cluster analysis grouped genotypes into two groups based on awn presence: 28 awned genotypes and one awnless genotype (Mudule-1). Three sub-clusters of awned genotypes were identified: Sub-cluster I with 16 genotypes, Sub-clusters II and III each comprising six genotypes, reflecting further morphological differentiation. Overall, the study demonstrates the presence of useful phenotypic diversity and highlights important traits and genotypes for future wheat improvement.

Keywords: Agro-morphological traits, Bread wheat, Diversity index, Glaucosity, Principal component analysis

PBaGSoN-20

Accelerating Crop Breeding Cycles through Speed Breeding: Methods, Advances, and Challenges

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ABSTRACT

Due to lengthy generation cycle, climatic unpredictability, and low selection efficiency, conventional crop breeding advances slowly and produces insufficient genetic gain to address the growing global food and climate issues. This paper critically evaluates the idea and use of speed breeding (SB) as an expedited crop-improvement method in order to solve this ongoing bottleneck. In order to conduct a thorough literature synthesis, peer-reviewed articles from key scientific databases were screened, and evidence pertaining to SB methods, environmental alterations, and its integration with molecular breeding techniques was methodically structured. According to the assessment, SB successfully shortens generation times by adjusting photoperiod, temperature, and light intensity. Rapid generation of homozygous lines, mapping populations, and pre-breeding materials are made possible by this method. Furthermore, combining SB with genomic selection, marker-assisted selection, and CRISPR gene editing greatly improves selection accuracy and genetic gain. High energy consumption, the need for dependable electricity and water, limited technical capacity, and the demand to validate complex features in field settings are some of the ongoing issues. Overall, this study comes to the conclusion that SB is a game-changing strategy that has the potential to change crop-breeding pipelines as long as creative facility designs and sustainable energy sources are used to lower operational costs and infrastructure limitations.

Keywords: Controlled environment, Generation times, Genetic gain, Speed breeding

PBaGSoN-21

Assessment of yield parameters of zinc-biofortified wheat genotypes under irrigated condition at Khumaltar

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ABSTRACT

Zinc malnutrition remains a serious public health problem among children and women in the hills and mountain regions of Nepal. Bread wheat (*Triticum aestivum* L.) is second most consumed cereal in Nepal. Identification and deployment of zinc-biofortified wheat varieties is a sustainable approach to address this nutritional challenge. This study evaluated 50 biofortified bread wheat genotypes, bred for enhanced grain zinc concentration, using an alpha lattice design with two replications at Khumaltar during the winter seasons of 2023/24 and 2024/25. Phenological traits, yield and yield-attributing traits, and rust resistance were recorded. Analysis of variance revealed significant differences among genotypes for heading and maturity days, plant height, grain number and weight per spike, thousand grain weight, and grain yield. Grain yield ranged from 2361 kg ha^{-1} (3HZWYTEM-512) to 5996 kg ha^{-1} (3HZWYTEM-507) in 2023/24, and from 3146 kg ha^{-1} (4HZWYTEM-505) to 7061 kg ha^{-1} (3HZWYTEM-546) in 2024/25. Combined analysis across years identified 3HZWYTEM-507 as the most promising genotype with the highest estimated mean grain yield. Genotypes combining superior yield performance, desirable yield components, grain quality, and disease resistance could be advanced for multi-environment testing and utilization in the wheat breeding program.

Keywords: Biofortified, Bread wheat, Grain yield, Yield attributing traits, Zinc malnutrition

PBaGSoN-22

Genetic Variability and Multi-Trait Selection of Groundnut Varieties Using MGIDI in the Tarai of Nepal

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ABSTRACT

Genetic variability and selection are crucial for groundnut breeding program to maximize genetic gain and productivity. This study evaluated 6 groundnut varieties cultivated in the terai regions of Nepal, assessing 8agro-morphological traits. The objective was to identify a superior groundnut variety using a multi-trait analysis approach based on the MGIDI (multi-trait genotype–ideotype distance index. The experiment was conducted in a randomized complete block design (RCBD) with four replications at Madhesh Agricultural University, Rajbiraj, Saptari during 2025 Kharif season. Analysis of variance indicated difference among genotypes were highly significant for the most of traits under studied, this indicated that these genotypes have sufficient amount of variation. PCA analysis showed that only 3 principal components (PCs) exhibited more than 1.00 eigenvalue and showed about87.75% of the total phenotypic variability. It was also found that grain yield, number of pods per plant and hundred seed weight are ideal traits for groundnut improvement through selection in Terai region of Nepal. In this study, a considerable variation was observed for all the studied traits by using PCA analysis. Multi-trait analysis using the MGIDI, which integrated various morpho-agronomical traits, further highlighted Nawalpur Badam-1, Sambridhi, and Baidhahi consistently close to the ideotype 15 % selection intensity. The strengths-weaknesses analysis emphasized their value for targeted improvement. Overall, the findings highlight MGIDI as an effective tool for precise identification of superior groundnut varieties and implementing breeding strategies to improve productivity.

Keywords: Groundnut, PCA, muti-trait, MGIDI, variation

PBaGSoN-23

Role of Community Seed Bank in Strengthening Local Seed Systems and Enhancing Livelihoods of Farmers in Kaski, Nepal

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ABSTRACT

Community Seed Banks (CSB) are increasingly recognized as vital for conserving local crop varieties, enhancing seed security, and supporting sustainable livelihoods. This study, conducted in 2024 in Aarba of Pokhara Metropolitan and Sunpadali of Madi Rural Municipalities, Kaski district, Nepal, aimed to access the role of CSB to Strengthening the local seed systems and improving farmers livelihood. Data were collected from 100 respondents (50 from each site) using surveys, interviews, focus group discussions, Field observations supported by literature review. Purposive sampling was used, with stratification to represent different farmer categories. Results indicated that farmers relied on a mix of agricultural and non-farm income, with 22% fully dependent on farming and 31% combining it with other occupations. Legumes were universally cultivated, followed by cereals and vegetable (80%). Seed sources varied: Agrovets supplied 50% of seeds, while self- saved seeds were more prevalent in Sunpadali (55%) than Aarba (100%) compared to Sunpadali (60%). CSBs contributed to the preservation of local varieties, knowledge exchange, biodiversity conservation, and improved farming practices. Reported benefits included increased crop yield (35%), diversification (95%), income improvement (74%), strengthened collaboration (85%), and enhanced climate resilience (40%). Key challenges included limited resources, inadequate awareness, and logistical constraints. Non- members perceive CSB resources as exclusive to cooperative members. Overall, CSBs are crucial for promoting agricultural diversity, resilience, and food security. Strengthening them through capacity building, community participation, and awareness campaigns can enhance local seed systems and support sustainable rural livelihoods, ensuring their long-term effectiveness and inclusivity in Nepal's agricultural development.

Keywords: Community Seed Bank, Local seed system, Agricultural diversity, Resilience, Food security

PBaGSoN-24

Yield and Yield Attributes Variability of Early Genotypes of Rice in Madhesh Province of Nepal

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ABSTRACT

In Terai and inner Terai region, delayed Monsoon, terminal drought, and the need for multiple cropping systems have increased the demand for early-maturing rice varieties. The objective of this research was to evaluate the performance of 24 early genotypes in Madhesh Province, with a specific focus on yield and yield-attributing characters. This research employed a randomized complete block design (RCBD) with three replications in CNRM Bardibas. Yield and yield attributes were recorded. Data was entered by using MS Excel 2007 and analyzed by R Studio version 2025. Mean differences were compared using DMRT at 5 % level of significance. The genotypes showed highly significant impact on yield and yield attributes ($p<0.01$). The results showed that the highest yield (5.09 t/ha) was achieved by SVIN 372, and the lowest yield (3.11 t/ha) by Genotype IR 17A11089. NR 2325-70-3-2-1-1 showed early maturity (86DAT) and the late maturity by NR2333-33-1-1-1-1 (105 DAT). Genotype SV0054 was superior to their check variety. These results provide valuable insight into the selection and development of rice varieties adapted to the agro-ecological conditions of CNRM Bardibas Nepal.

Keywords: Rice, Early, yield, genotypes, Madhesh

PBaGSoN-25

Evaluation of Phenology, Yield and Yield Attributing Characters of Wheat (Triticum aestivum) Genotypes Under Late Sowing Condition at Bardibas, Mahottari

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ABSTRACT

Wheat is Nepal's third-most important cereal crop after rice and maize. Wheat cultivation in Terai following rice in the prevalent rice-wheat cultivation system is invariably delayed, leading to phenological shifts and yield inconsistency. This investigation assesses the impact of late sowing on key phenological stages, yield, and yield components of selected wheat genotypes. A field experiment was conducted on 2025 wheat growing season at the College of Natural Resource and Management, Bardibas, to evaluate fifty wheat genotypes under late-sown conditions and identify heat-tolerant, high-yielding varieties for the Terai region of Nepal. The trial was laid out in RCBD with three replications. Highly significant variations were found among genotypes for several parameters, indicating considerable genetic variability among genotypes. ADITYA showed maximum plant height (60.16cm) followed by BL-4341 (40.9cm). BL-4341 showed earliest days to heading (54) and early flowering (68.66) and maturity (95.66) than several genotypes. BL-4341 also performed better at spike length (7.41cm) following BORLAUG-2020 (7.93cm), grain per spike (29.33) and thousand grain weight (35,53g). Grain yield varied markedly among genotypes, ranging from 240.58 to 1022.33 kg/ha, with BL-4341(1022.33kg/ha) followed by NL-971 (951.11kg/ha) and MWR-9000(9.3.98kg/ha) emerging as superior yield performers. These high-yielding genotypes also exhibited higher biological yield and harvest index, reflecting efficient translocation of assimilates and adaptability to terminal heat stress. The study concludes that wheat genotypes possessing early maturity, moderate plant height, and optimum leaf area are better suited for late-sown conditions. Genotype BL-4341 can be recommended for further testing of its stability and optimum performance across locations and inclusion in future breeding programs aimed at developing heat-tolerant wheat cultivars for the Terai region.

Keywords: Genotype; Heat stress; Phenology; Wheat; Yield

PBaGSoN-26

Evaluation of Rice (Oryza Sativa L.) Genotypes in Spring under Direct Seeded Cultivation in Janakpur of Nepal

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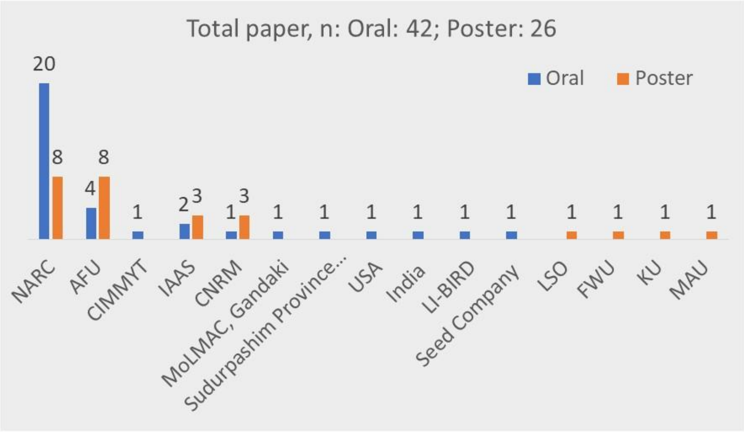
ABSTRACT

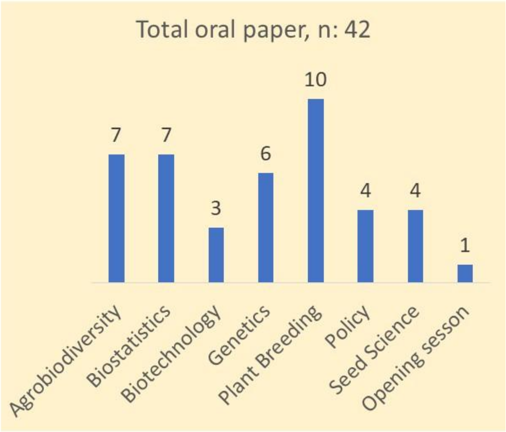
Thirty rice genotypes, including twenty genotypes developed by the International Rice Research Institute (IRRI), four Nepali released varieties as national check and five other variants as international check varieties were selected for action research. Seeds were directly sown in an alpha lattice design with two replications in the field of the National Rice Research Program, Hardinath, Dhanusha, in March of 2023. The primary objective of our research was to evaluate the adaptability, and stability of early maturing rice genotypes bred by IRRI. The secondary objective was to analyse the variation of yield-attributing parameters and drought tolerance among genotypes. The data for ten yield attributing parameters were recorded according to the IRRI protocol. Analysis of variance revealed that most of the traits were significantly different for genotypes except flag leaf area, grain yield (GY) and panicle length. Genotypes IR132084-B-1327-2-1-B-15 (4.16 t/ha), IR13C149 (3.83 t/ha), IR13C149 (3.83 t/ha), IR 132084-B-1327-2-1-B-16 (3.5 t/ha), IR 127152-3-22-18-1-B-B (3.37 t/ha), and IR 132084-B-1327-2-1-B-16 (3.5 t/ha) were found to be superior for their performance based on GY. The genotypes IR13LT799 (23.75 g), IR 132084-B-1202-1-3-B-3 (22.5 g), IR132084-B-1327-2-1-B-15 (23 g), IR13C149 (20 g), and IR 127152-3-22-18-1-B-B (18 g) were recorded to have the highest Thousand Grain Weight (TGW). GY was positively correlated with TGW, plant height and tiller per meter square. The highest broad sense heritability (0.77) was observed for GY, followed by days to heading (0.72). Most of the phenotypic traits had significant positive correlation with GY, revealing that selection pressure on such traits can improve economic yield.

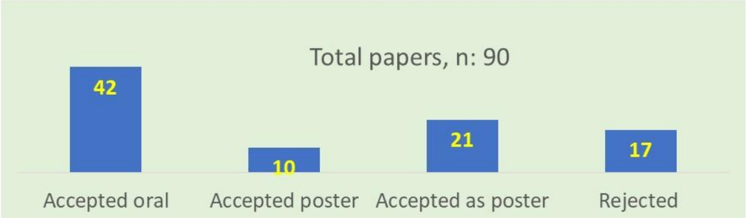
Keywords: Drought, Genotype, Heritability, Nepal, Spring Rice

Paper Status/ Summary in the convention

Papers summary in the **First** National Convention on Genetics, Plant Breeding and Seed Science







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- **Interactive Components**: Group discussions and plenary sessions will be conducted to foster active participation and generate actionable recommendations for the future of GAS-3B.
- **Panel Discussions and Debates**: Interactive panel discussions and debates will be held to explore controversial topics, emerging trends, and policy implications in Genetics, Plant Breeding, Agrobiodiversity, Seed Science, Biotechnology, and Biometrics.
- **Networking Opportunities**: Dedicated networking sessions will be facilitated to encourage interaction and collaboration among participants, including opportunities for young researchers to connect with experienced professionals.
- **Exhibition and Demonstration Stalls**: An exhibition area will be set up where companies, research institutions, and other stakeholders can showcase their products, technologies, and innovations related to GAS-3B.
- **Poster Sessions**: Researchers will present their work through posters, allowing for detailed discussion and feedback from peers and experts.
- **Awards and Recognitions**: The convention will recognize outstanding contributions in the fields of GAS-3B with awards and commendations, encouraging excellence and innovation.

Language

Nepali, English and Hybrid (Nep-Eng)

Guidelines for papers and posters

- Authors should follow the technical details given in the "Authors Guidelines" of journal, Genetics, Plant Breeding and Seed Science of PBaGSoN at https://plantbreeding.org.np/page/journal.html.
- Authors should print poster themselves following standard format and guidelines (free format). All posters will be included in the proceedings.
- Visit website of PBaGSoN at https://plantbreeding.org.np/ or contact the Technical and Publication Team
- Each presenter will get 15-20 minutes for presentation
- Submit abstract, full paper, and poster within given time at pbagson19@gmail.com and sthapromise0584@gmail.com

Best research paper and poster award

Based on their scientific merit, two research papers and two posters will be awarded. There will be separate award category for student on presentation and poster. Poster size should be 24 x 60 inch.

Deadlines

Abstract Submission Deadline: **10 Jan 2026**
Notification of Acceptance: **15 Jan 2026**
Full Paper Submission Deadline: **20 January 2026**
All accepted papers will be presented at the convention and considered for publication in the Proceedings of the National Convention**.**

PARTICIPANTS

Approximately 200 participants are expected at the event, including experts in Genetics, Agrobiodiversity, Seed Science, Plant Breeding, Biotechnology-ag, and Biostatistics-ag (GAS-3B). as well as working in crops, forages and forest plants. Attendees will primarily be researchers, policy makers, students, academicians, extensionists, innovators, farmers, business personal, scientists, etc.

SPONSORSHIP AND EXHIBITION OPPORTUNITIES

The convention invites organizations and companies to participate as sponsors or exhibitors, providing an excellent platform to showcase products, services, and innovations. For sponsorship or exhibition inquiries, please contact Exhibition Team, the President of PBaGSoN or the Director of NARI.

EXPECTED OUTPUTS

- Sharing of advancements and identification of gaps in Genetics, Agrobiodiversity, Seed Science, Plant Breeding, Biotechnology-ag, and Biostatistics-ag (GAS-3B)
- Establishment of interlinkages and collaborative networks among experts, practitioners, and policymakers
- Creation of a mechanism and framework for public-private partnerships in GAS-3B
- Formulation of group recommendations and future directions for GAS-3B
- Compilation of proceedings, including keynotes, theme papers, research papers, and posters

Convention Committees

Organizing committee

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Organizers and partners' brief

PBaGSoN: Plant Breeding and Genetics Society of Nepal, https://plantbreeding.org.np/

The Plant Breeding and Genetics Society of Nepal (PBaGSoN) is a non-governmental, non-political, and non-profit professional organization established to advance genetics, agrobiodiversity, seed science, breeding, biotechnology, and biostatistics (GAS-3B) for strengthening Nepal's agriculture and forestry sectors. Originating from collective efforts of plant breeders since 1999 and formally registered in 2076 BS, PBaGSoN serves as a unified national platform for dispersed experts, fostering collaboration among researchers, farmers, policymakers, and institutions. The society promotes research and innovation, protects professional integrity and rights, supports policy formulation, organizes scientific events, publishes journals and knowledge resources, and provides consultancy services at national and international levels. With over 250 experts and strong engagement within the Nepal Agricultural Federation, PBaGSoN is committed to driving crop improvement, genetic research, and sustainable agricultural transformation, contributing to food, nutrition, health and environment security, economic growth, environmental sustainability, and national resilience.

NARI and NARC: National Agricultural Research Institute, Nepal Agricultural Research Council, https://narc.gov.np/

LI-BIRD: Local Initiatives for Biodiversity, Research and Development, https://libird.org/

Oxfam: Oxfam in Nepal, https://nepal.oxfam.org/

Genebank: National Agri. Genetic Resources Center, https://genebank.narc.gov.np/
The National Agriculture Genetic Resources Center (NAGRC) was established in 2010 under NARC for the conservation and utilization of all agricultural genetic resources which includes six components of agrobiodiversity (crop, forage, livestock, aquatic, insect, and microorganism) and four sub-components (domesticated, semi-domesticated, wild relatives and wild edible). Agricultural genetic resources are managed through four strategies (ex-situ, on-farm, in-situ, and breeding) and deploying 101 good practices across the country. Some of them are seed bank, tissue bank, DNA bank, field genebank, community genebank, livestock farm genebank, aqua pond genebank and cryobank, agro gene sanctuary, insect field genebank, herbal conservation garden, temple garden, etc.

NTNC: National Trust for Nature Conservation, https://www.ntnc.org.np/
The National Trust for Nature Conservation (NTNC), established in 1982 under a Legislative Act, is an autonomous, not-for-profit organization dedicated to nature conservation in Nepal. Over four decades, NTNC has implemented more than 300 projects in biodiversity conservation, climate change and clean energy, cultural heritage protection, ecotourism and sustainable development through strong community participation. Working in close collaboration with the Government of Nepal, NTNC directly manages three mountain protected areas, Central Zoo and supports the management of lowland protected areas nationwide. Its research and field-based intentions have significantly informed evidence-based policy and planning. Operating across Nepal's lowlands, mid-hills and high Himalayan landscapes, NTNC promotes integrated conservation and development approaches that prioritize local livelihoods and community stewardship. In response to emerging global environmental challenges, NTNC is strengthening its engagement in climate change mitigation and adaptation, including pursuing accreditation as a direct access entity to the Green Climate Fund and National Implementing Entity (NIE) to the Adaptation Fund, while partnering with national and international agencies to enhance long-term conservation outcomes.

Supporters
Karma and Sons Traders, https://karmagroups.com/

Nepal Agricultural Federation (NAF), http://naf.org.np/

Seed Entrepreneurs Association of Nepal (SEAN), https://nepalseedassociation.org.np/

Society of Agricultural Scientists Nepal (SAS-Nepal), https://sasnepal.org.np/

Muktinath Seed Bank LTD, https://muktinathseedbank.com.np/

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कृषि सञ्चारको संवाहक

First National Convention on Genetics, Plant Breeding and Seed Science; 20-22 Jan 2026

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