Current Agriculture Updates **10(1)12-12(January, 2026)**
www.currentagriculture.com

RESEARCH ARTICLE

Breeding crops for productivity and stability

R. Raj

Birsa Agricultural University, Ranchi- 834006, India

✉ rahulrajranchibau@gmail.com

Manuscript received: December 15,2025; Decision on manuscript: December 29,2025; Manuscript accepted: January 8, 2025

Abstract

Cereal crops, including rice, wheat, and maize, constitute the foundation of global food and nutritional security, yet their productivity is increasingly threatened by climate change–induced stresses. Rising temperatures, erratic precipitation, and expanding pest and disease pressures significantly reduce yield potential and stability. Sustaining cereal productivity under such dynamic conditions requires a balanced focus on high yield and environmental resilience. Genetic variability derived from landraces and wild relatives provides essential allelic resources for stress adaptation and yield stability. Conventional breeding approaches, including selection, hybridization, and mutation breeding, have historically driven genetic gains; however, their efficiency is constrained when targeting complex, polygenic traits. The integration of molecular and genomics-assisted breeding encompassing QTL mapping, marker-assisted selection, genomic selection, and genome editing has enhanced precision and accelerated genetic improvement. Multi-environment testing and stability analyses further support the identification of broadly adapted and climate-resilient genotypes. An integrated breeding framework is therefore essential for developing sustainable, high-yielding cereal cultivars capable of withstanding biotic and abiotic stresses under changing climatic scenarios.

Keywords: Cereal crops, climate change, yield stability, genetic variability, germplasm

Introduction

Importance of cereals in global food security

Cereal crops such as rice, wheat, and maize constitute the primary food source for nearly two-thirds of the global population and form the backbone of food and nutritional security. Their contribution to caloric intake and livelihood security makes them central to global agricultural systems. However, rising global temperatures and increasing climatic variability threaten cereal production systems. A rise of even 1°C in mean global temperature has been estimated to reduce yields by approximately 3.2% in rice, 6.0% in wheat, and 7.4% in maize (Zhao *et al.*, 2017). Such reductions are significant when considered against the backdrop of a rapidly growing global population and finite natural resources. Climate change not only affects productivity directly but also alters land-use patterns, soil health, nutrient dynamics, and ecosystem water balance (Zhao *et al.,* 2017). Furthermore, shifting climatic regimes can modify pest and disease prevalence intensifying biotic pressures on cereal crops (Singh *et al.,* 2018; Luck *et al.,* 2011). Ensuring stable cereal production under these changing conditions is therefore critical for sustaining global food security (Kumar *et al.,* 2024).

Concept of productivity and yield stability

Productivity in cereal crops refers to the capacity of genotypes to produce high yields under given environmental conditions (Kumar *et al.,* 2023). Yield stability, in contrast, reflects the ability of a genotype to maintain consistent performance across diverse and often unpredictable environments**.** Modern cultivars have largely been developed under high-input and favorable environments, prioritizing yield maximization. However, such intensive selection for productivity has often narrowed the genetic base and reduced resilience to environmental stresses. Environmental fluctuations associated with climate change can disrupt phenological processes, including flowering and fruiting time, and influence plant growth dynamics and reproductive efficiency. These shifts frequently result in yield penalties, especially when crops encounter intermittent drought, flooding, salinity, or temperature extremes. The complexity and low heritability of stress-adaptive traits further complicate the improvement of yield stability under adverse conditions (Gaba *et al.,* 2021). Thus, breeding efforts must balance the enhancement of yield potential with the reinforcement of adaptive capacity to ensure sustained productivity.

Emerging breeding challenges under climate change

The changing climate presents multifaceted challenges to cereal breeding. Increased frequency of droughts, floods, salinity, and temperature extremes can significantly reduce crop growth and grain quality (Boraiah *et al.,* 2022 Dudhe *et al.,* 2025). Additionally, altered climatic conditions may expand the habitat range and aggressiveness of pests and pathogens, exacerbating crop losses (Luck *et al.,* 2011). Traditional breeding approaches, though foundational, are often slow and less effective in addressing complex, polygenic traits such as combined stress tolerance (Naqvi *et al.,* 2022). Moreover, the limited resilience of high-yielding cultivars to ecological constraints underscores the need to reintroduce genetic diversity from landraces and wild relatives (Hossain *et al.,* 2022; Neelum et al., 2020). Identifying and incorporating genes or quantitative trait loci (QTL) associated with stress adaptation has therefore become a major focus of modern breeding programs (Snehi *et al.,* 2024). Advances in marker-assisted selection, genomic selection, and gene discovery have accelerated the identification of stress-responsive loci and enabled more precise improvement of climate resilience (Varshney *et al.,* 2021; Naqvi *et al.,* 2022).

Genetic variability and germplasm resources

Role of landraces and genetic diversity

Genetic variability is the cornerstone of sustainable crop improvement and long-term yield stability. The narrowing of the genetic base in modern high-yielding cultivars has increased their vulnerability to abiotic and biotic stresses, particularly under rapidly changing climatic conditions (Kumar *et al.,* 2017). In this context, landraces and wild relatives represent invaluable reservoirs of allelic diversity for stress adaptation and productivity enhancement. Wild and closely related species have been reported to possess significant genetic potential in rice, wheat, maize, potato, tomato, sugarcane, and tobacco (Bakala, 2020; Singh *et al.,* 2020). These genetic resources harbor traits associated with drought tolerance, salinity resistance, disease resistance, and yield stability that are often absent or diminished in elite cultivars (Kumar *et al.,* 2025). The exploitation diversity is essential for broadening the adaptive capacity of breeding populations and mitigating the risks associated with environmental fluctuations (Singh *et al.,* 2020,; Kumar *et al.,* 2017).

Pre-breeding strategies facilitate the systematic transfer of advantageous alleles from wild or exotic germplasm into agronomically acceptable backgrounds (Sukumaran *et al.,* 2021). By introgressing genes from primary, secondary, and tertiary gene pools, pre-breeding enhances genetic diversity and provides improved germplasm for further selection. This approach not only strengthens stress tolerance but also helps in minimizing linkage drag through strategic gene transfer. Consequently, pre-breeding serves as a foundational step in restoring and expanding the genetic variability for resilient crop development.

Molecular characterization and population structure

The advent of molecular tools has significantly improved the ability to characterize genetic resources at the DNA level. The identification and mapping of genes and quantitative trait loci (QTL) associated with biotic and abiotic stresses have led to the development of numerous DNA marker–trait associations. Techniques such as QTL mapping and genome-wide association studies (GWAS) enable the detection of genomic regions linked to complex traits by analyzing phenotypic and genotypic variation within structured populations (Naqvi *et al.,* 2022). GWAS, in particular, utilizes linkage disequilibrium to establish statistically significant associations between markers and traits across diverse germplasm panels (Naqvi *et al.,* 2022). This approach has successfully identified loci associated with tolerance to drought, salinity, chilling, and other stresses (Ma *et al.,* 2016; Pandit *et al.,* 2017; Swamy *et al.,* 2017). Studies have reported multiple QTL associated with drought tolerance in rice landraces (Hoang et al., 2019) and salinity tolerance at different growth stages (Lekklar *et al.,* 2019). Molecular characterization provides insights into population structure, allelic diversity, and the genetic architecture of complex adaptive traits (Das *et al.,* 2025). Through these genomic approaches, breeders can effectively dissect trait variability within germplasm collections and identify superior donor lines for targeted improvement.

Utilization of genetic resources in breeding

The practical use of genetic resources in breeding programs involves integrating identified alleles into elite backgrounds to enhance productivity and stability. Marker-assisted selection (MAS) enables precise introgression of desirable genes associated with stress tolerance (Kumar *et al.,* 2018). Marker-assisted backcross breeding has been widely used to incorporate specific loci such as Sub1 and Saltol and many other genes into popular varieties, resulting in improved tolerance to submergence and salinity without compromising yield under favorable conditions (Singh *et al.,* 2016; Valarmathi *et al.,* 2019; Dar *et al.,* 2018, *et al.,* 2022). QTL pyramiding have further demonstrated enhanced performance under stress environments by combining multiple loci controlling adaptive traits (Shamsudin *et al.,* 2016; Anyaoha *et al.,* 2019; Sandhu *et al.,* 2019). The utilization of genetic diversity through genomics-assisted breeding has thus accelerated the development of climate-resilient cultivars (Varshney *et al.,* 2021). Speed breeding facilitates rapid advancement of generations and efficient screening of diverse germplasm, thereby accelerating the identification and deployment of beneficial alleles from landraces and wild relatives (Bhatta *et al.,* 2021; Cazzola *et al.,* 2021). Collectively, the molecular characterization, and strategic utilization of genetic variability are fundamental to strengthening crop productivity and ensuring yield stability (Kumar *et al.,* 2017).

Breeding strategies for yield improvement

Conventional breeding approaches have historically driven genetic gain in crop productivity through systematic selection and recombination of desirable traits. Methods such as selection and hybridization remain fundamental for improving yield potential and adaptation. In traditional breeding programs, superior plants are selected from large segregating populations, and subsequent generations are evaluated through replicated multi-location trials to assess their genetic potential under diverse environmental conditions (Naqvi *et al.*, 2022). Although effective, these procedures are often time-intensive and resource-demanding, particularly for complex traits influenced by environmental interactions. Mass selection and pedigree-based approaches rely on phenotypic evaluation to identify superior individuals across generations. While these methods have contributed significantly to yield enhancement, their efficiency is limited they are strongly influenced by environmental variability (Gaba *et al.*, 2021). Biometrical techniques like diversity studies and correlation helps in understanding the trait patterns among the genotypes (Maurya *et al.*, 2017; Kumar *et al.*, 2016; Kumar *et al.*, 2017) Hybrid breeding, based on the exploitation of heterosis, has been widely adopted to enhance yield performance (Kumar and Singh, 2019). The success of hybrid development depends on the identification of suitable parental combinations capable of producing superior progenies (Snehi *et al.*, 2024; Singh *et al.*, 2019; Singh *et al.*, 2021). Although conventional hybridization remains central to yield improvement, its progress can be constrained by the complexity of trait inheritance (Naqvi *et al.*, 2022, Das *et al.*, 2021). Mutation breeding has also complemented conventional strategies by generating novel variability. Induced mutations through physical or chemical mutagens have led to the development of improved cultivars with enhanced yield attributes and stress tolerance. For example, the barley variety ‘Diamant’ developed through X-ray irradiation exhibited superior yield characteristics and lodging resistance (Yadav *et al.*, 2016), while gamma irradiation resulted in the dwarf rice cultivar ‘Calrose 76’ (Rutger *et al.*, 1976). Similarly, EMS-induced mutagenesis produced the salt-tolerant rice variety ‘Kaijin’ (Takagi *et al.*, 2015). Hence, conventional breeding strategies continue to form the backbone of yield improvement programs. Despite their limitations, they provide the essential framework upon which modern genomic tools build to accelerate genetic gain.

Multi-environment testing and stability analysis

The performance of crop genotypes is strongly influenced by environmental variability, particularly under the increasing unpredictability associated with climate change. Variations in temperature, precipitation, and atmospheric conditions can significantly alter plant growth, phenology, and yield expression (Zhao *et al.*, 2017). Consequently, genotype × environment (G×E) interactions become a critical factor in determining productivity and yield stability across locations and seasons. Conventional breeding programs routinely evaluate segregating populations and advanced lines through replicated multi-location trials to assess their genetic potential under diverse environmental conditions (Naqvi *et al.*, 2022). Such multi-environment testing enables the identification of genotypes with consistent performance and resilience under varying stress scenarios, including drought, salinity, and temperature extremes (Snehi *et al.*, 2023). Given that many adaptive traits exhibit low heritability and are highly environment-dependent, careful evaluation across environments is essential to ensure reliable selection (Kumar *et al.*, 2020; Singh *et al.*, 2024; Kumar *et al.*, 2025; Yathish et al., 2024; Gaba *et al.*, 2021). Analytical approaches that partition environmental and genotypic effects facilitate a clearer understanding of stability and adaptability. By assessing performance across contrasting conditions, breeders can identify genotypes suited either for broad adaptation exhibiting stable yield across environments or for specific adaptation to particular stress-prone regions. In the context of climate variability, such stability-focused evaluation frameworks are indispensable for developing cultivars capable of sustaining productivity under fluctuating agro-ecological conditions (Mukri *et al.*, 2024; Kumar B *et al.*, 2025).

Breeding for nutritional quality enhancement

Improving the nutritional quality of crop plants is an essential component of sustainable food security, particularly under climate change scenarios that threaten both yield and grain quality. Variations in temperature, precipitation, and atmospheric composition can influence nutrient availability in soil and ultimately affect grain composition (Zhao *et al.,* 2017). Therefore, breeding strategies must integrate productivity with enhanced nutritional attributes to ensure food and nutritional security. Genetic improvement for nutrient enrichment relies on the identification and deployment of genes and quantitative trait loci (QTL) associated with desirable quality traits. Molecular mapping approaches and marker–trait associations facilitate the precise selection of loci governing complex traits, including nutrient accumulation (Naqvi *et al.*, 2022). Marker-assisted selection (MAS) enables efficient introgression of such target loci into elite backgrounds, thereby accelerating the development of nutritionally improved cultivars (Kumar *et al.,* 2018). Genomics-assisted breeding further strengthens these efforts by integrating molecular markers and genomic information to enhance selection accuracy for complex traits (Varshney *et al.,* 2021). QTL pyramiding strategies allow the simultaneous incorporation of multiple favorable loci without compromising agronomic performance under non-stress conditions (Sandhu *et al.,* 2019). Additionally, genome-wide association studies (GWAS) provide high-resolution mapping of marker–trait associations across diverse germplasm, enabling the discovery of alleles linked to quality-related traits (Naqvi *et al.,* 2022; Swamy *et al.*, 2017). Genome editing technologies such as CRISPR/Cas systems offer further opportunities for precise modification of genes controlling quality attributes, thereby enabling targeted enhancement of specific nutritional or specialty traits (Naqvi *et al.,* 2022; Razzaq *et al.,* 2021). Collectively, the integration of conventional breeding with molecular and genomic tools provides a robust framework for improving nutritional quality while maintaining yield stability under dynamic environmental conditions.

Molecular and genomics-assisted breeding

Advances in molecular genetics and genomics have substantially enhanced the precision and efficiency of crop improvement programs. Genomics-assisted breeding (GAB) integrates molecular markers, genetic mapping, and genome-wide analyses to accelerate the development of varieties with improved productivity and stress resilience (Varshney *et al.,* 2021).

QTL mapping and marker-assisted selection

Quantitative trait loci (QTL) mapping enables the identification of genomic regions associated with complex agronomic traits by correlating phenotypic variation with molecular markers. This approach has been widely used to dissect traits such as drought tolerance, heat resistance, and cold tolerance (Kumar *et al.,* 2021; Xiao *et al.,* 2018; Liu *et al.,* 2018). For example, the DRO1 locus in rice, associated with deep rooting and improved performance under drought conditions, has been shown to enhance yield-related attributes (Raj *et al.,* 2023; Choudhary *et al.,* 2021). Similarly, co-expression of DREB2A and APX genes has been reported to strengthen drought tolerance in rice (Sandhya *et al.,* 2021). Marker-assisted selection (MAS) utilizes tightly linked DNA markers to identify and select individuals carrying favorable alleles, thereby increasing selection efficiency compared to conventional phenotypic approaches (Kumar *et al.,* 2018). Genome-wide association studies (GWAS) further complement QTL mapping by detecting marker–trait associations at higher resolution using linkage disequilibrium in diverse germplasm panels (Naqvi *et al.,* 2022; Swamy *et al.,* 2017).

Marker-assisted backcross breeding (MABB)

Marker-assisted backcross breeding (MABB) has emerged as an effective strategy for introgressing specific target genes or QTL into elite cultivars while retaining desirable agronomic backgrounds. Successful incorporation of loci such as Sub1 for submergence tolerance and Saltol for salinity tolerance has led to the development of improved varieties without yield penalties under favorable conditions (Singh *et al.,* 2016; Valarmathi *et al.,* 2019 Valarmathi *et al.,* 2019; Dar *et al.,* 2018).

Valarmathi *et al.,* 2019; Dar et al., 2018). QTL pyramiding through marker-assisted approaches has also enhanced performance under drought stress (Shamsudin *et al.,* 2016; Sandhu *et al.,* 2019).

Genomic selection and high-throughput genotyping

Genomic selection (GS) represents a genome-wide approach in which genomic estimated breeding values (GEBVs) are calculated using dense marker data and phenotypic information (Spindel *et al.,* 2018). Unlike MAS, which targets specific loci, GS captures the cumulative effects of numerous small-effect genes across the genome. This approach enables the prediction of performance of untested individuals and enhances selection for complex, low-heritability traits. The application of high-density molecular markers and genome-wide genotyping platforms has facilitated the implementation of GS in breeding programs, enabling rapid and accurate selection for climate-resilient and high-yielding genotypes (Varshney *et al.,* 2021). Collectively, molecular and genomics-assisted breeding approaches provide powerful tools for accelerating genetic gain, improving stress tolerance, and enhancing productivity under variable environmental conditions.

Breeding for disease resistance and abiotic stress tolerance

Genetic basis of resistance

Understanding the genetic control of stress tolerance is fundamental for developing resilient crop varieties (Kumar *et al.*, 2022). Both biotic and abiotic stress responses are governed by specific genes and quantitative trait loci (QTL), which can be identified through molecular mapping and genomic analyses (Naqvi *et al.,* 2022). Transcriptomic studies have revealed that stress combinations, such as heat and pathogen infection, can alter defense-related gene expression, indicating complex regulatory networks underlying resistance (Rivero *et al.,* 2022; Prasch and Sonnewald, 2013). Such insights facilitate the identification of candidate genes associated with stress adaptation. QTL mapping has identified loci linked to tolerance against drought, cold, and other environmental stresses (Xiao *et al.,* 2018; Liu *et al.,* 2018). For instance, the DRO1 locus in rice contributes to improved root architecture and enhanced performance under drought conditions (Raj *et al.,* 2023; Choudhary *et al.,* 2021). These findings underscore the polygenic and environment-dependent nature of stress resistance traits.

Marker-assisted resistance breeding

Marker-assisted selection (MAS) has enabled precise introgression of resistance-associated loci into elite cultivars (Kumar *et al.,* 2018). Marker-assisted backcross breeding (MABB) has been widely applied to incorporate genes such as Sub1 for submergence tolerance and Saltol for salinity tolerance into popular rice varieties (Singh et al., 2016; Valarmathi *et al.,* 2019; Dar *et al.,* 2018). QTL pyramiding strategies have further strengthened stress resilience by combining multiple adaptive loci within a single genetic background (Shamsudin *et al.,* 2016; Sandhu *et al.,* 2019). Genome-wide association studies (GWAS) have also identified marker–trait associations for resistance to various stresses, enabling high-resolution mapping and effective deployment of favorable alleles from diverse germplasm (Naqvi *et al.,* 2022; Swamy *et al.,* 2017).

Durable resistance and climate-resilient ideotypes

Durable resistance requires the integration of multiple adaptive traits to ensure stable performance under variable environmental conditions. Climate change increases the frequency of drought, salinity, temperature extremes, and pest outbreaks, thereby intensifying the need for resilient ideotypes (Luck *et al.,* 2011; Zhao *et al.,* 2017). Genomics-assisted breeding facilitates the development of such ideotypes by integrating molecular markers, QTL mapping, and genomic selection (Varshney *et al.,* 2021). Genomic selection enables prediction of performance across information, improving selection for complex traits with low heritability (Spindel *et al.,* 2018). Genome editing technologies, including CRISPR/Cas systems, further enhance the precision of breeding by enabling targeted modification of genes involved in stress tolerance (Naqvi *et al.,* 2022; Razzaq et al., 2021). For example, editing of genes such as OsRAV2 and OsDST has demonstrated improved tolerance to salt and drought stress (Gaba *et al.,* 2021; Duan *et al.,* 2016; Santosh *et al.,* 2020).

Collectively, the integration of molecular mapping, marker-assisted breeding, genomic selection, and genome editing provides a comprehensive framework for developing disease-resistant and climate-resilient cereal cultivars capable of sustaining productivity under both biotic and abiotic stress conditions.

Future perspectives and integrated breeding approaches

Future cereal improvement strategies must adopt integrated breeding frameworks to address the complex challenges imposed by climate change. Alterations in temperature, precipitation, and pest dynamics significantly influence crop performance and stability (Zhao *et al.,* 2017; Luck *et al.,* 2011). environments using-genome wide marker Therefore, breeding programs should combine precise phenotypic evaluation across environments with advanced molecular tools to enhance selection efficiency for complex, low-heritability traits (Gaba *et al.,* 2021; Naqvi *et al.,* 2022, Kumar et al., 2024; Kumar R et al., 2024; Kumar et al., 2020). Genomics-assisted breeding integrates QTL mapping, genome-wide association studies (GWAS), and marker-assisted selection (MAS) to identify and deploy favorable alleles associated with stress tolerance and productivity (Naqvi *et al.,* 2022; Swamy *et al.,* 2017; Kumar et al., 2018). Marker- assisted backcross breeding has successfully introgressed adaptive loci such as Sub1 and Saltol into elite cultivars (Singh et al., 2016; Valarmathi *et al.,* 2019; Dar *et al.,* 2018). Genomic selection further enhances genetic gain by predicting genomic estimated breeding values for complex traits across environments (Spindel *et al.,* 2018), while genome editing technologies enable targeted modification of stress-responsive genes (Naqvi *et al.,* 2022; Razzaq *et al.,* 2021).

The integration of conventional and molecular approaches thus provides a coherent pathway for sustainable and climate-smart cereal improvement, ensuring enhanced productivity and yield stability under variable environmental conditions.

References

1. Anyaoha, C.O., Fofana, M., Gracen, V., Tongoona, P. and Mande, S. 2019. Introgression of two drought QTLs into FUNAABOR-2 early generation backcross progenies under drought stress at reproductive stage. Rice Sci., 26 (1): 32 - 41.
2. Bakala, H.S., Singh, G. and Srivastava, P. 2020. Smart breeding for climate resilient agriculture. In: Plant breeding current and future views, IntechOpen.
3. Bhatta, M., Sandro, P., Smith, M.R., Delaney, O., Voss-Fels, K.P., Gutierrez, L. and others 2021. Need for speed: manipulating plant growth to accelerate breeding cycles. Curr. Opin. Plant Biol., 60 : 101986.
4. Boraiah, K.M., Basavaraj, P.S., Halli, H.M., Muhkri, G., Yathish, K.R. and Ranjan, N. 2022. Maize: Impacts and management of abiotic stresses. In: Abiotic Stresses in Agriculture: Impacts and Management, ICAR-National Institute of Abiotic Stress Management, Baramati, Pune, Maharashtra, India, p. 116 - 150.
5. Cazzola, F., Bermejo, C.J., Gatti, I. and Cointry, E. 2021. Speed breeding in pulses: an opportunity to improve the efficiency of breeding programs. Crop Pasture Sci., 72 (3): 165 - 172.

6. Choudhary, P., Pramitha, L., Rana, S., Verma, S., Aggarwal, P.R. and Muthamilarasan, M. 2021. Hormonal crosstalk in regulating salinity stress tolerance in graminaceous crops. Physiologia Plantarum, 173 (4): 1587 - 1596.
7. Dar, M.H., Zaidi, N.W., Waza, S.A., Verulkar, S.B., Ahmed, T., Singh, P.K. and others 2018. No yield penalty under favorable conditions paving the way for successful adoption of flood tolerant rice. Sci. Rep., 8 : 1 - 7.
8. Das, A.K., Choudhary, M., Kumar, P., Karjagi, C.G., Y., K.R., Kumar, R. and Rakshit, S. 2021. Heterosis in genomic era: advances in the molecular understanding and techniques for rapid exploitation. Crit. Rev. Plant Sci., 40 (3): 218 - 242.
9. Das, A.K., Dixit, S., Bhamare, D., Kumar, R., Y., K.R., Singh, S. and Rakshit, S. 2025. Genetic diversity and structure analysis of white maize populations. Range Manag. Agrofor., 46 (1): 62 - 69.
10. Duan, Y.B., Li, J., Qin, R.Y., Xu, R.F., Li, H., Yang, Y.C. and others 2016. Identification of a regulatory element responsible for salt induction of rice OsRAV2 through promoter analysis. Plant Mol. Biol., 90 : 49 - 62.
11. Dudhe, M.Y., Sasikala, R., Ramteke, R.P., Sakthivel, K. and Kumaraswamy, H.H. 2025. Breeding Climate-Resilient Sunflowers in the Climate Change Era: Current Breeding Strategies and Prospects. In: Pandey, M.K., Mallikarjuna, M.G., Lohithaswa, H.C., S. Aski, M., Gupta, S. (eds) Breeding Climate Resilient and Future Ready Oilseed Crops. Springer, Singapore.
12. Gaba, Y., Pareek, A. and Singla-Pareek, S.L. 2021. Raising climate-resilient crops: journey from conventional breeding to new breeding approaches. Curr. Genomics, 22 (6): 450 - 467.
13. Hoang, G.T., Van Dinh, L., Nguyen, T.T., Ta, N.K., Gathignol, F., Mai, C.D. and others 2019. Genome-wide association study of Vietnamese rice landraces reveals new QTLs for water deficit tolerance. Rice, 12 : 1 - 20.
14. Hossain, F., Muthusamy, V., Bhat, J.S., Zunjare, R.U., Kumar, S., Prakash, N.R. and others 2022. Maize breeding. In: Fundamentals of Field Crop Breeding, Springer Nature Singapore, Singapore, p. 221 - 258.
15. Kumar, S., Babu, C., Revathi, S. and Iyanar, K. 2017. Estimation of genetic variability, heritability and association of green fodder yield with contributing traits in fodder pearl millet (Pennisetum glaucum L.). Int. J. Adv. Biol. Res., 7 (1): 119 - 126.
16. Kumar, S., Babu, C., Revathi, S. and Sumathi, P. 2017. Genetic variation delineation among fodder pearl millet accessions and Napier grass germplasm using SSR markers. Indian J. Ecol., 44 : 186 - 189.
17. Kumar, S. and Singh, S.B. 2019. Hybrid seed production technique in maize. Manual on Training Programme-Cum-Exposure Visit on Advancement in Seed Technology and Marketing, 1 : 53 - 60.
18. Kumar, A., Sandhu, N., Dixit, S., Yadav, S., Swamy, B.P.M. and Shamsudin, N.A.A. 2018. Marker-assisted selection strategy to pyramid QTLs for grain yield under drought. Rice, 11 : 1 - 16.
19. Kumar, B., Choudhary, M., Kumar, K., Kumar, P., Kumar, S., Bagaria, P.K. and Rakshit, S. 2022. Maydis leaf blight of maize: update on status, sustainable management and genetic architecture of its resistance. Physiol. Mol. Plant Pathol., 121 : 101889.
20. Kumar, B., Choudhary, M., Kumar, P., Kumar, S., Sravani, D., Kumari, N.V. and Rakshit, S. 2024. GGE biplot analysis and selection indices for yield and stability assessment of maize (Zea mays L.) genotypes under drought and irrigated conditions. Indian J. Genet., 84 (2): 209 - 215.
21. Kumar, B., Kumar, S., Kumar, P., Kumar, A., Jat, S.L., Singh, A.K. and Rakshit, S. 2025. Genotype and genotype by environment interaction (GGE) biplot analysis for assessing genotype stability in grain iron and zinc content of maize across diverse environments. J. Food Compos. Anal., 142 : 107504.

22.Kumar, B., Pushpendra, Kumar, S., Kumar, P., Singh, R., Yankanchi, S. and Jat, H.S. 2025. Understanding the genetic basis of resistance to maydis leaf blight and maturity-related traits in corn. Front. Plant Sci., 16 : 1551940.

23.Kumar, M., Mahato, A., Kumar, S. and Mishra, V.K. 2020. Phenomics-assisted breeding: an emerging way for stress management. In: New frontiers in stress management for durable agriculture, Springer Nature Singapore, Singapore, p. 295 - 310.

24.Kumar, P., Choudhary, M., Jat, B.S., Dagla, M.C., Singh, V., Das, A.K. and Wani, S.H. 2021. Isolation of genes/quantitative trait loci for drought stress tolerance in maize. In: Molecular breeding in wheat, maize and sorghum: strategies for improving abiotic stress tolerance and yield, CABI, Wallingford, UK, p. 267 - 281.

25.Kumar, P., Kumar, S., Choudhary, M., Chikappa, G.K., Kumar, B., Singh, N.K. and Sinha, S.K. 2020. GGE biplot based stability analysis of experimental hybrids for baby corn purpose and green fodder. Range Manag. Agrofor., 41 (1): 60 - 66.

26.Kumar, R., Kumar, S., Das, A.K., Dhonde, S., Kaur, Y., Kumar, S. and Rakshit, S. 2024. Unveiling genotype × environment dynamics for grain yield in QPM hybrids through AMMI, GGE biplot and MTSI approach. Indian J. Genet., 84 (3): 449 - 460.

27.Kumar, S., Babu, C., Revathi, S. and Iyanar, K. 2016. Estimation of per se performance of yield traits in napier grass. Prog. Res., 11 : 4703 - 4707.

28.Kumar, S., Babu, C., Revathi, S. and Iyanar, K. 2017. Estimation of genetic variability, heritability and association of green fodder yield with contributing traits in napier grass (*Pennisetum purpureum* Schum.). Vegetos, 30 (Special): 463 - 468.

29.Kumar, S., Babu, C., Sumathi, P. and Revathi, S. 2017. Estimation of per se performance of yield traits in fodder pearl millet (*Pennisetum glaucum* L.). Environ. Ecol., 35 (3C): 2316 - 2321.

30.Kumar, S., Kasana, R.K., Kumar, S., Gangoliya, S.S. and Rakshit, S. 2018. Identification of resistant sources against turcicum leaf blight of maize (*Zea mays* L.). Maize J., 7 (2): 64 - 71.

31.Kumar, S., Kumar, A., Sen, H., Janeja, H.S., Maity, S., Banerjee, S. and Arun, M.C. 2024. Small millets: a multifunctional crop for achieving sustainable food security under climate change. World, 718 : 863.

32.Kumar, S., Kumar, P., Dhar, B., Kumar, B., Dar, Z.A., Abhijith, K.P. and Nath, V. 2025. Multi-environment evaluation of dual-purpose baby corn hybrids for yield stability and forage biomass in rainfed agro-ecological systems. Front. Sustain. Food Syst., 9 : 1680866.

33.Kumar, S., Singh, P., Devi, U., Yathish, K.R., Saujanya, P.L., Kumar, R. and Mahanta, S.K. 2023. An overview of the current fodder scenario and the potential for improving fodder productivity through genetic interventions in India. Anim. Nutr. Feed Technol., 23 (3): 631 - 644.

34.Lekklar, C., Pongpanich, M., Suriya-Arunroj, D., Chinpongpanich, A., Tsai, H., Comai, L. and others 2019. Genome-wide association study for salinity tolerance at flowering stage in rice. BMC Genom., 20 : 1 - 18.

35.Liu, C., Ou, S., Mao, B., Tang, J., Wang, W., Wang, H. and others 2018. Early selection of bZIP73 facilitated adaptation of japonica rice to cold climates. Nat. Commun., 9 : 3302.

36.Luck, J., Spackman, M., Freeman, A., Trebicki, P., Griffith, W., Finlay, K. and Chakraborty, S. 2011. Climate change and diseases of food crops. Plant Pathol., 60 : 113 - 121.

37.Ma, X., Feng, F., Wei, H., Mei, H., Xu, K., Chen, S. and others 2016. Genome-wide association study for plant height and grain yield in rice under contrasting moisture regimes. Front. Plant Sci., 7 : 1801.

38.Maurya, A.K., Kushwaha, M.L., Jain, S.K. and Kumar, S.K. 2017. Character association and path analysis studies for yield and yield attributes in green chilli (*Capsicum annuum* L.). vegetos. 30 (2), 369-373.

39.Mukri, G., Gowtham, K.V., Gadag, R.N., Sen, R., Kumar, S., Swain, D. and Bhat, J.S. 2024. A combination of analytical methods dissects genotype × environment interaction precisely and facilitates the selection of potential new field corn (*Zea mays* L.) hybrids. Indian J. Genet., 84 (3): 336 - 345.

40.Naqvi, R.Z., Siddiqui, H.A., Mahmood, M.A., Najeebullah, S., Ehsan, A., Azhar, M. and others 2022. Smart breeding approaches in post-genomics era for developing climate-resilient crops. Front. Plant Sci., 13 : 972164.

41.Neelam, S., Tyagi, R.K., Pandey, S., Jacob, S.R., Javaji, C.S., Debnath, M.K. and Kumar, S. 2020. Comprehending the diversity in the regenerated set of maize (*Zea mays* L.) landraces conserved in the Indian National Genebank. Indian J. Plant Genet. Resour., 33 (3): 329 - 333.

42.Pandit, E., Tasleem, S., Barik, S.R., Mohanty, D.P., Nayak, D.K., Mohanty, S.P. and others 2017. Genome-wide association mapping reveals QTLs for seedling stage chilling tolerance in indica rice. Front. Plant Sci., 8 : 552.

43.Prasch, C.M. and Sonnewald, U. 2013. Simultaneous application of heat, drought and virus reveals shifts in signaling networks. Plant Physiol., 162 : 1849 - 1866.

44.Raj, S.R.G. and Nadarajah, K. 2023. QTL and candidate genes in abiotic stress resistance breeding of cereals. Int. J. Mol. Sci., 24 : 6.

45.Razzaq, A., Kaur, P., Akhter, N., Wani, S.H. and Saleem, F. 2021. Next-generation breeding strategies for climate-ready crops. Front. Plant Sci., 12 : 620420.

46.Rivero, R.M., Mittler, R., Blumwald, E. and Zandalinas, S.I. 2022. Developing climate-resilient crops: improving tolerance to stress combinations. Plant J., 109 : 373 - 389.

47.Rutger, J.N., Peterson, M.L., Hu, C.H. and Lehman, W.F. 1976. Induction of useful short stature mutants in japonica rice. Crop Sci., 16 : 631 - 635.

48.Sandhu, N., Dixit, S., Swamy, B.P.M., Raman, A., Kumar, S., Singh, S.P. and others 2019. Marker assisted breeding for flood and drought tolerant rice. Rice, 12 : 1 - 16.

49.Sandhya, J., Ashwini, T., Manisha, R., Vinodha, M. and Srinivas, A. 2021. Drought tolerance enhancement with co-overexpression of DREB2A and APX in rice. Am. J. Plant Sci., 12 : 234 - 258.

50.Kumar, S., V.V., Verma, R.K., Yadav, S.K., Yadav, P., Watts, A., Rao, M.V. and Chinnusamy, V. 2020. CRISPR-Cas9 editing of OsDST gene in rice. Physiol. Mol. Biol. Plants, 26 : 1099 - 1110.

51.Shamsudin, N.A.A., Swamy, B.P.M., Ratnam, W., Cruz, S., Teressa, M., Sandhu, N. and others 2016. Pyramiding of drought yield QTLs into rice cultivar MRQ74. Rice, 9 : 1 - 13.

52.Singh, S.B., Kumar, S., Kasana, R.K. and Singh, S.P. 2019. Combining ability analysis and heterosis for yield and yield attributing traits in late maturing winter maize inbred lines (*Zea mays* L.). Front. Crop Improv., 7 (1): 42 - 51.

53.Singh, G., Singh, I., Taggar, G.K., Rani, U., Sharma, P., Gupta, M. and Singh, S. 2020. Introgression of productivity traits into pigeonpea. Physiol. Mol. Biol. Plants, 26 : 1399 - 1410.

54.Singh, R., Singh, Y., Xalaxo, S., Verulkar, S., Yadav, N., Singh, S. and others 2016. From QTL to variety harnessing tolerance in rice. Plant Sci., 242 : 278 - 287.

55.Singh, S.B., Kasana, R.K., Kumar, S. and Kumar, R. 2020. Assessing genetic diversity of newly developed winter maize (Zea mays L.) inbred lines. Indian J. Plant Genet. Resour., 33 (1): 68 - 76.

56.Singh, S.B., Kumar, P., Kasana, R.K., Choudhary, M., Kumar, S., Kumar, R. and Rakshit, S. 2021. Unveiling combining ability and heterotic grouping of newly developed winter maize (*Zea mays* L.) inbreds. Indian J. Agric. Sci., 91 : 1586 - 1591.

57.Singh, S.B., Kumar, S., Kumar, R., Kumar, P., Yathish, K.R., Jat, B.S. and Kumar, S. 2024. Stability analysis of promising winter maize (*Zea mays* L.) hybrids tested across Bihar using GGE biplot and AMMI model approach. Indian J. Genet., 84 (1): 73 - 80.

58. Snehi, S., Choudhary, M., Kumar, S., Jayaswal, D., Kumar, S. and Prakash, N.R. 2024. Mapping of quantitative trait loci: harnessing genomics revolution for dissecting complex traits. In: Genomics Data Analysis for Crop Improvement, Springer Nature Singapore, Singapore, p. 125 - 157.
59. Snehi, S., Kumar, S., Rathi, S.R. and Prakash, N.R. 2023. Augmenting salinity tolerance in rice through genetic enhancement in the post-genomic era. In: Smart Plant Breeding for Field Crops in Post-genomics Era, Springer Nature Singapore, Singapore, p. 137 - 164.
60. Snehi, S., Prakash, N.R., Pant, U., Singh, P.K., Kumar, S., Jeena, A.S. and Bhajan, R. 2024. Prediction of heterotic combinations using correlation between genetic distance, heterosis and combining ability in yellow sarson (*Brassica rapa* var. yellow sarson Prain). Vegetos, 37 (4): 1552 - 1564.
61. Spindel, J. and Iwata, H. 2018. Genomic selection in rice breeding. In: Rice Genomics, Genetics and Breeding, Springer.
62. Sukumaran, S., Krishna, H., Singh, K., Mottaleb, K.A. and Reynolds, M. 2021. Developing climate resilient wheat using pre-breeding methods. Curr. Genomics, 22 (6): 440.
63. Swamy, B.P.M., Shamsudin, N.A.A., Rahman, S.N.A., Mauleon, R., Ratnam, W., Cruz, S. and others 2017. Association mapping of yield under reproductive stage drought in rice. Rice, 10 : 1 - 13.
64. Takagi, H., Tamiru, M., Abe, A., Yoshida, K., Uemura, A., Yaegashi, H. and others 2015. MutMap accelerates breeding of salt-tolerant rice cultivar. Nat. Biotechnol., 33 : 445 - 449.
65. Valarmathi, M., Sasikala, R., Rahman, H., Jagadeeshselvam, N., Kambale, R. and Raveendran, M. 2019. Development of salinity tolerant rice through marker-assisted backcross breeding. Plant Physiol. Rep., 24 : 262 - 271.
66. Varshney, R.K., Bohra, A., Yu, J., Graner, A., Zhang, Q. and Sorrells, M.E. 2021. Designing future crops: genomics-assisted breeding comes of age. Trends Plant Sci., 26 (6): 631 - 649.
67. Xiao, N., Gao, Y., Qian, H., Gao, Q., Wu, Y., Zhang, D. and others 2018. Identification of genes related to cold tolerance and a functional allele that confers cold tolerance. Plant Physiol., 177 (3): 1108 - 1123.
68. Yadav, P., Kumar, S. and Jain, V. 2016. Recent Advances in Plant Stress Physiology, Daya Publishing House, New Delhi.
69. Yathish, K.R., Karjagi, C.G., Gangoliya, S.S., Kumar, A., Preeti, J., Yadav, H.K. and Gadag, R.N. 2022. Introgression of the low phytic acid locus (lpa2) into elite maize (*Zea mays* L.) inbreds through marker-assisted backcross breeding (MABB). Euphytica, 218 (9): 127.
70. Yathish, K.R., Kumar, S., Rao, T.V., Kumar, P., Karthik, M., Das, A.K. and Rakshit, S. 2024. GGE biplot and AMMI analysis for stability and adaptability of dual purpose maize hybrids tested across multi-environments for baby corn and fodder yield. Range Manag. Agrofor., 45 (1): 49 - 56.
71. Zhao, C., Liu, B., Piao, S., Wang, X., Lobell, D.B., Huang, Y., Huang, M., Yao, Y., Bassu, S., Ciais, P., Durand, J.L., Elliott, J., Ewert, F., Janssens, I.A., Li, T., Lin, E., Liu, Q., Martre, P., Müller, C., Peng, S., Peñuelas, J., Ruane, A.C., Wallach, D., Wang, T., Wu, D., Liu, Z., Zhu, Y., Zhu, Z. and Asseng, S. 2017. Temperature increase reduces global yields of major crops in four independent estimates. Proc. Natl. Acad. Sci., USA 114 (35): 9326 - 9331.