International Journal of Biology Sciences

ISSN Print: 2664-9926
ISSN Online: 2664-9934
NAAS Rating (2026): 4.82
IJBS 2026; 8(1): 90-95
www.biologyjournal.net
Received: 25-11-2025
Accepted: 29-12-2025

Lokendra Kumar
Assistant Professor,
Department of Agriculture
Motherhood University,
Roorkee, Haridwar,
Uttarakhand, India

Dr. Soniya Singh
Assistant Professor,
Department of Botany
Motherhood University,
Roorkee, Haridwar,
Uttarakhand, India

Gaurav Tomar
Assistant Professor,
Department of Agriculture,
COER University, Roorkee,
Haridwar, Uttarakhand, India

Dr. Sandeep Kumar
Assistant Professor,
Department of Agriculture,
Mata Gujri College, Fatehgarh
Sahib, Punjab, India

Dr. Mohd. Irfan
Assistant Professor & Head,
Department of Botany,
Chaman Lal Mahavidhyalaya,
Landhora, Haridwar,
Uttarakhand, India

Rishab Chauhan
Assistant Professor,
Department of Agriculture,
Motherhood University,
Roorkee, Haridwar,
Uttarakhand, India

Dheerendra Kumar
Assistant Professor,
Department of Agriculture
Motherhood University,
Roorkee, Haridwar,
Uttarakhand, India

Corresponding Author:
Lokendra Kumar
Assistant Professor,
Department of Agriculture
Motherhood University,
Roorkee, Haridwar,
Uttarakhand, India

Importance of plant genetic resources in sustainable agricultural development

Lokendra Kumar, Soniya Singh, Gaurav Tomar, Sandeep Kumar, Mohd. Irfan, Rishab Chauhan and Dheerendra Kumar

DOI: https://www.doi.org/10.33545/26649926.2026.v8.i1b.548

Abstract
PGR are the foundation of global food and nutritional security, providing the raw material required for crop improvement and adaptation. The term genetic resources comprises landraces, wild relatives, traditional cultivars, and improved varieties that contribute to genetic diversity within agricultural systems. With climate change, emerging pests and diseases, and increase in demand for high-quality food, the importance of PGR is evident. The three key building blocks of sustainable agricultural development are the conservation, characterization, and use of genetic resources for the development of resilient, productive, and climate-smart crop varieties. PGR provide a basis for breeders to incorporate such traits as drought tolerance, disease resistance, nutritional enhancement, and stress adaptation. Both *in-situ* and *ex-situ* conservation strategies, including gene banks, field repositories, and community seed systems, play a vital role in safeguarding this diversity for future generations. Generally, management, documentation, and policy support should be further strengthened to ensure long-term availability and use. Therefore, plant genetic resources will play a crucial role in achieving sustainable agricultural growth, environmental resilience, and global food security.

Keywords: Plant Genetic Resources (PGR) genetic diversity, sustainable agriculture, crop improvement, conservation strategies, *in-situ* conservation, *ex-situ* conservation, climate resilience

Introduction

PGR are the heritable materials contained within and among plant species that are of actual or potential value for food, agriculture, and environmental sustainability. They range from landraces, wild relatives, improved cultivars, breeding lines, and traditional varieties that together form the genetic diversity necessary for crop improvement. With global agriculture facing increasing challenges in the form of climate change, soil degradation, emerging pests and diseases, and a rapidly growing population, the importance of PGR has become more critical than ever. Sustainable agricultural development relies heavily on the availability, conservation, and effective utilization of diverse genetic resources. Genetic variability within crops allows breeders to develop improved varieties that are high-yielding, nutrient-rich, and resilient to climate and other biotic and abiotic stresses. Traditional cultivars and wild species often hold unique adaptive attributes that may be lacking in modern varieties, making them invaluable for breeding programs with objectives of enhancement of resilience and sustainability. Conservation of PGR is done both *in situ* and *ex situ* to prevent genetic erosion that threatens the long-term stability of agricultural systems. Both the *in-situ* and *ex-situ* methods of PGR conservation include gene banks, field gene banks, seed banks, botanical gardens, and community seed systems for safeguarding diversity for future generations. Simultaneously, the documentation, characterization, and evaluation of germplasm ensure its effective use in breeding and research. Thus, Plant Genetic Resources form the backbone of sustainable agricultural development as raw materials for innovation in crop improvement, ensuring food security and ecological balance. Protecting and promoting the use of PGR is one of the key methods to meet present and future agriculture-related challenges.

Concept and Scope of Plant Genetic Resources (PGR)

Plant Genetic Resources (PGR) are heritable materials contained within and among plant species that possess actual or potential value for present and future generations. These resources include the entire spectrum of diversity-from primitive landraces, wild relatives, traditional cultivars, improved varieties, hybrids, and genetically modified crops to specialized breeding lines conserved in gene banks. PGR comprise the basic biological foundation for crop improvement, food security, and ecological robustness in agriculture. The concept of PGR is more than the genetic material itself but also involves knowledge, practices, and cultural heritage associated with the identification, selection, and use of the resources. It includes a traditional knowledge system of farming communities, indigenous methods for seed selection, and localized management of crop diversity, which all make a significant contribution to resources conservation and sustainable use. The scope of PGR is extensive and three-dimensional. It involves exploration, collection, characterization, evaluation, documentation, conservation, and sustainable utilization of plant germplasm. Activities involved range from conservation, where genetic diversity remains within natural or cultivated ecosystems, to *ex situ* conservation through gene banks, botanical gardens, DNA banks, and seed storage facilities. The scope furthermore embraces pre breeding, varietal development, biotechnology applications, and molecular characterization with a view to enhancing the use of diversity. PGR bear immense potential for tackling emerging global challenges, such as climate change, pest and disease outbreaks, nutritional insecurity, land degradation, and the requirement for more sustainable systems of agriculture. It is their utilization that enables the development of stress-tolerant, high yielding, and nutritionally superior crop varieties that are fundamental to achieving agricultural sustainability in the long term. The concept and scope of PGR thus represent the cornerstone of modern and future-oriented agricultural development strategies. Source of Materials for Characterization on Climate Change Adaptation Plant materials used for characterization and evaluation of climate change adaptation traits were sourced from a diverse range of genetic resources to ensure broad variability and representation of adaptive potential. The primary sources of germplasm included: a. National and International Gene Banks-National Bureau of Plant Genetic Resources (NBPGR), New Delhi. Regional gene banks located in major agro-climatic zones. International centres such as CIMMYT, IRRI, and ICRISAT. These sources provided well-documented accessions with passport data useful for tracing ecological origin and potential stress-adaptive traits. b. Indigenous Landraces and Farmers' Varieties-Locally adapted landraces were collected from traditional farming communities in drought-prone, flood-prone, saline, and high-temperature regions. These materials were prioritized due to their natural selection over generations under harsh environmental conditions. c. Wild Relatives and Weedy Forms-Forest margins. Grazing lands. Uncultivated fields. These species exhibit inherent tolerance to environmental stresses and serve as reservoirs of adaptive genes. d. Field Gene Banks and Research Farms. Perennial crops, fruit species, and clonally propagated materials were obtained from field repositories maintained by state agricultural universities and horticultural research stations. These collections offered long-term conserved materials suitable for stress evaluation. e. On-Farm Conservation Sites and Community Seed Banks Materials from community-managed seed banks and farmer-maintained on-farm conservation plots were included to capture traditional knowledge, ecological adaptation, and socio-cultural diversity in crop varieties. f. Breeding Lines and Advanced Genetic Materials-Stress-tolerant breeding lines under development at agricultural research institutions were also considered. These materials provided a reference to compare adaptive performance with traditional germplasm .g. Ecologically Stressed Agro-Climatic Zones-Drought. Salinity and alkalinity. Water logging and submergence Heat and cold stress Erratic rainfall. Such environments naturally select for resilient genotypes, making them valuable sources for adaptive traits.

Role of Plant Genetic Resources in Sustainable Agriculture

Plant Genetic Resources are very important in ensuring that agricultural development will be sustainable. They provide the raw genetic material required to improve the productivity, stability, and resilience of crops. In relation to increasing population, climate change, and other emerging biotic and abiotic stresses, PGR forms the basis for developing agricultural systems that will not only be productive but also ecologically balanced. Firstly, PGR enhance crop improvement programs by offering a wide range of genetic variability that is required for breeding new varieties possessing desirable traits. These include higher yield potential, tolerance to drought, salinity, and temperature extremes, besides resistance to pests and diseases. Wild relatives and landraces are of particular value because they possess genes that have been lost in modern, highly uniform cultivars. Incorporating this type of genetic variability helps develop crop varieties capable of adapting to changing climatic conditions. Secondly, PGR support nutritional security by diversifying crops and varieties with essential vitamins, minerals, and bioactive compounds. By widening the genetic base of cultivated crops, PGR may enable the development of nutritionally enhanced biofortified varieties with the capability of reducing malnutrition and micronutrient deficiencies, especially in developing countries. Thirdly, PGR contribute to agro-ecological sustainability through the promotion of diversified farming systems. Genetic diversity within and among crop species reduces reliance on external chemical inputs, enhances soil health, improves pollinator services, and helps to stabilize agricultural ecosystems. Traditional varieties and landraces are well adapted to local agro-climatic conditions and mostly require fewer resources, hence supporting low-input, environmentally friendly farming practices. In addition, PGR play a crucial role in managing risks and building resilience. Genetic diversity acts like a naturally occurring insurance system against crop failure resulting from extreme weather events, pest outbreaks, and disease epidemics. Maintaining broad genetic bases ensures the long-term stability of food production systems and supports farmers' ability to cope with uncertainties. Finally, the role of PGR relates to biotechnological innovations such as genomics, molecular breeding, and genetic engineering. These advanced tools depend to a great extent on diverse germplasm collections for the identification of useful genes, markers, and traits.

The integration of biotechnology with PGR utilization accelerates the process of developing improved varieties and enhances the efficiency of sustainable agricultural practices. In brief, PGR form the backbone of sustainable agriculture. They ensure productivity, ecological balance, nutritional improvement, and resilience, which are indispensable in achieving long-term agricultural sustainability and global food security.

Diversity, Conservation and Utilization of Plant Genetic Resources (PGR)

Plant Genetic Resources (PGR) embody the full spectrum of genetic variability present within and among plant species that are cultivated or have potential use in agriculture. The diversity, conservation, and utilization of these resources are integral to sustainable agricultural development, ensuring long-term productivity, adaptability, and resilience of cropping systems.

Diversity of PGR: The diversity of PGR is expressed through variations in morphology, physiology, biochemistry, and genetic makeup across plant populations. This diversity can be categorized into:

Wild relatives of crops: Possess valuable genes for tolerance to drought, salinity, pests, and diseases.

Landraces: Locally adapted traditional varieties that exhibit broad genetic bases and resilience under marginal environments.

Modern cultivars and hybrids: Improved varieties developed through scientific breeding, offering high yield and uniformity.

Underutilized and minor crops: Provide nutritional and ecological benefits, contributing to diversified farming systems.

Genetically modified and biotech-derived materials: Contain targeted traits introduced through advanced technologies.

Conservation of PGR: The conservation of plant genetic resources aims to safeguard genetic variability for present and future use. It involves both strategies: *In situ* Conservation. This refers to the preservation of genetic diversity within natural habitats or traditional farming systems. Key approaches include: Conservation of wild relatives in protected areas. On-farm conservation of landraces by local farmers. Maintenance of diverse agro-ecosystems that support natural selection and adaptation. *In situ* conservation allows dynamic evolution of plant populations under changing environmental conditions.

Utilization of PGR-Crop improvement: Breeding programs rely on genetic diversity to incorporate traits such as high yield, stress tolerance, resistance to pests and diseases, and improved quality.

Pre-breeding and genetic enhancement: Introduction of useful genes from wild relatives or landraces into breeding lines to broaden genetic bases.

Biotechnology applications: Genomics, marker-assisted selection, and genetic engineering utilize PGR to accelerate variety development.

Development of climate-resilient varieties: PGR provide adaptive genes essential for coping with heat, drought, salinity, and erratic rainfall.

Promotion of diversified cropping systems: Utilization of underutilized crops and landraces supports ecological sustainability and nutritional diversity.

Restoration of degraded ecosystems: PGR help in reintroducing native species that enhance soil health and agro-ecological stability.

Policy Framework and Institutional Support for PGR Conservation

The conservation and sustainable utilization of Plant Genetic Resources (PGR) are strongly influenced by national and international policy frameworks, as well as institutional support systems dedicated to safeguarding agricultural biodiversity. These policies and institutions provide legal, financial, and technical mechanisms that ensure the long-term availability, equitable access, and responsible use of genetic resources essential for sustainable agricultural development. 1. International Policy Framework-a. Convention on Biological Diversity (CBD), 1992 CBD recognizes the sovereign rights of countries over their biological resources and promotes their conservation, sustainable use, and equitable sharing of benefits arising from their utilization. It provides the legal foundation for national biodiversity strategies and action plans. b. International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), 2001 Also known as the Plant Treaty, it ensures the conservation and free access of key food and fodder crops under a Multilateral System (MLS). It promotes farmers' rights, including seed saving, exchange, and traditional knowledge preservation. c. Nagoya Protocol on Access and Benefit Sharing (ABS), 2010.The protocol establishes clear conditions for access to genetic resources and ensures fair and equitable sharing of benefits with the providers, thereby encouraging responsible utilization of PGR. d. Global Plan of Action (GPA) for PGRFA 2. National Policy Framework (India)a. National Biodiversity Act, 2002. Provides regulations for conservation, sustainable use, and benefit sharing of India's biological resources. It governs access to plant genetic materials by national and international users. b. Protection of Plant Varieties and Farmers' Rights (PPV&FR) Act, 2001 Ensures intellectual property rights for breeders and recognizes farmers' rights to save, use, exchange, and sell farm-saved seeds. It promotes the development of new varieties through equitable benefit sharing. c. Seed Act and Seed Policies Regulate seed production, certification, quality control, and distribution, ensuring availability of diverse and high-quality planting materials. d. National Gene Bank and Long-Term Storage Policies-Provide guidelines for conservation, characterization, and documentation of PGR under secure conditions.3. Institutional Support for PGR Conservation-a. National Bureau of Plant Genetic Resources (NBPGR), India. The apex institution responsible for: Exploration and collection of germplasm. *Ex situ* conservation in National Gene Bank.

Quarantine services. Documentation through databases Distribution of germplasm for research and breeding b. Indian Council of Agricultural Research (ICAR) Supports research institutes and agricultural universities that contribute to characterization, evaluation, and utilization of PGR. c. State Agricultural Universities (SAUs) Conduct crop-specific research, maintain field gene banks, and promote on-farm conservation. d. International Institutions CGIAR Centres such as IRRI, CIMMYT, ICRISAT, and CIP maintain global collections of major crop species and support international collaboration. FAO coordinates global initiatives and capacity-building programs. e. Community and NGO Initiatives Local seed banks, biodiversity management committees, and NGOs play an essential role in preserving indigenous varieties and traditional knowledge. 4. Importance of Policy and Institutional Support Effective policy frameworks and strong institutional support ensure:-Long-term conservation of genetic diversity. Regulated access and benefit sharing. Protection of farmers' and breeders' rights. Promotion of collaborative research and germplasm exchange. Future Prospects and Research Needs. The future of sustainable agricultural development is closely linked to the effective conservation, characterization, and utilization of Plant Genetic Resources (PGR). As global agriculture faces unprecedented challenges—climate variability, shrinking arable land, loss of biodiversity, and increasing food demands—the strategic use of PGR will be crucial for ensuring long-term resilience and productivity. Future prospects lie in the integration of advanced biotechnological tools with traditional breeding approaches. Genomic technologies such as whole-genome sequencing, genome editing (CRISPR/Cas), high-throughput phenotyping, and molecular marker-assisted selection offer immense potential to unlock hidden genetic diversity in landraces, wild relatives, and underutilized crops. These tools can accelerate the identification of genes responsible for stress tolerance, nutritional enhancement, and yield improvement, thereby enabling faster development of resilient crop varieties. Another promising direction is the mainstreaming of climate-resilient crops, including millets, pulses, and indigenous species that are naturally tolerant to harsh environments. Expanding research on these species can diversify global food systems and reduce reliance on a few major crops. Additionally, strengthening community participation in on-farm conservation, establishing local seed banks, and valorising traditional knowledge will promote dynamic conservation and adaptive evolution of plant genetic diversity. Research needs range from a better understanding of genotype-environment interactions, the development of more effective methods for conserving recalcitrant seeds, and increased investment in digital documentation and bioinformatics platforms to catalog global germplasm collections. Full international cooperation, harmonization of access and benefit-sharing policies, and increased financial funding of PGR research are all critical components in underpinning long-term genetic conservation. Ultimately, interdisciplinary research that connects genetics, ecology, climate science, and socio-economics is needed to translate genetic resources into actionable outcomes for sustainable agriculture.

Conclusion

Plant Genetic Resources form the foundational building block of sustainable agricultural development because they provide the fundamental genetic diversity needed to improve crop productivity, resilience, and nutritional quality. Their role is imperative in finding sustainable solutions for emerging global challenges such as climate change, pest and disease outbreaks, soil degradation, and increasing food insecurity. Agricultural systems can be enhanced to better cope with environmental stresses and to sustain long-term productivity through the conservation and effective utilization of rich plant genetic materials, which include wild relatives, landraces, and modern cultivars, including underutilized crops. Integration of appropriate policy frameworks, institutional support, advanced biotechnological tools, and community-based conservation approaches will be crucial in protecting these resources. Further investments in research, conservation infrastructure, and capacity-building will ensure that PGR remain available to future generations. Ultimately, it is the sustainable management and use of plant genetic resources that will dictate the resilience, stability, and sustainability of global agriculture and place plant genetic resources at the center of efforts geared toward achieving food and nutritional security in the coming decades.

References

1. FAO. Second report on the world's plant genetic resources for food and agriculture. Rome, Italy: FAO; 2010. p. 299.
2. McCouch SR, McNally KL, Wang W, *et al*. Genomics of gene banks: a case study in rice. Am J Bot. 2012;99(2):407-423.
3. Treuren R, Hintum TJL. Next-generation genebanking: plant genetic resources management and utilization in the sequencing era. Plant Genet Resour. 2014;12:298-307.
4. Thudi M, Li Y, Jackson SA, *et al*. Current state-of-art of sequencing technologies for plant genomics research. Brief Funct Genomics. 2012;11(1):3-11.
5. Jason DM, Aaron MW, Tam S, *et al*. Long-read genome sequencing identifies causal structural variation in a Mendelian disease. Genet Med. 2018;20(1):159-163.
6. McCoy RC, Taylor RW, Blauwkamp TA, *et al*. Illumina TruSeq synthetic long-reads empower de novo assembly and resolve complex, highly-repetitive transposable elements. PLoS One. 2014;9(9):e106689.
7. Lee H, Gurtowski J, Yoo S, *et al*. Error correction and assembly complexity of single molecule sequencing reads. bioRxiv. 2014. doi: 10.1101/006395.
8. Wambugu P, Furtado A, Waters D, *et al*. Conservation and utilization of African *Oryza* genetic resources. Rice. 2013;6(1):29.
9. Bordoni P, Hodgkin T. Climate change and the conservation of plant genetic resources. J Crop Improv. 2012;26(3):329-345.
10. Sharma S, Upadhyaya HD, Varshney RK, *et al*. Pre-breeding for diversification of primary gene pool and genetic enhancement of grain legumes. Front Plant Sci. 2013;4:309.
11. Wambugu PW, Muthamia ZK. Second report on the state of plant genetic resources for food and agriculture in Kenya. Rome, Italy: FAO; 2009.
12. Khoury C, Laliberte´ B, Guarino L. Trends in *ex situ* conservation of plant genetic resources: a review of

global crop and regional conservation strategies. Genet Resour Crop Evol. 2010;57(4):625-639.
13. Chase MW, Fay MF. Barcoding of plants and fungi. Science. 2009;325(5941):682-683.
14. CBOL Plant Working Group. A DNA barcode for land plants. Proc Natl Acad Sci USA. 2009;106:12794-12797.
15. Lahaye R, van der Bank M, Bogarin D, *et al*. DNA barcoding the floras of biodiversity hotspots. Proc Natl Acad Sci USA. 2008;105(8):2923-2928.
16. Nock CJ, Waters DLE, Edwards MA, *et al*. Chloroplast genome sequences from total DNA for plant identification. Plant Biotechnol J. 2011;9(3):328-333.
17. Parks M, Cronn R, Liston A. Increasing phylogenetic resolution at low taxonomic levels using massively parallel sequencing of chloroplast genomes. BMC Biol. 2009;7(1):84.
18. Yang JB, Tang M, Li HT, *et al*. Complete chloroplast genome of the genus *Cymbidium*: lights into the species identification, phylogenetic implications and population genetic analyses. BMC Evol Biol. 2013;13(1):84.
19. Erickson DL, Spouge J, Resch A, *et al*. DNA barcoding in land plants: developing standards to quantify and maximize success. Taxon. 2008;57(4):1304-1316.
20. Waters DLE, Nock CJ, Ishikawa R, *et al*. Chloroplast genome sequence confirms distinctness of Australian and Asian wild rice. Ecol Evol. 2012;2(1):211-217.
21. McPherson H, van der Merwe M, Delaney SK, *et al*. Capturing chloroplast variation for molecular ecology studies: a simple next generation sequencing approach applied to a rainforest tree. BMC Ecol. 2013;13(1):8.
22. Wambugu PW, Brozynska M, Furtado A, *et al*. Relationships of wild and domesticated rices (*Oryza* AA genome species) based upon whole chloroplast genome sequences. Sci Rep. 2015;5(1):13957.
23. Brozynska M, Omar ES, Furtado A, *et al*. Chloroplast genome of novel rice germplasm identified in Northern Australia. Trop Plant Biol. 2014;7(3-4):111-120.
24. Orjuela J, Sabot F, Che´ron S, *et al*. An extensive analysis of the African rice genetic diversity through a global genotyping. Theor Appl Genet. 2014;127(10):2211-2223.
25. Li S, Xie K, Li W, *et al*. Re-sequencing and genetic variation identification of a rice line with ideal plant architecture. Rice. 2012;5(1):18.
26. Huang X, Huang T, Dong G, *et al*. High-throughput genotyping by whole-genome resequencing. Genome Res. 2009;19(6):1068-1076.
27. Arai-Kichise Y, Shiwa Y, Nagasaki H, *et al*. Discovery of genome-wide DNA polymorphisms in a landrace cultivar of japonica rice by whole-genome sequencing. Plant Cell Physiol. 2011;52(2):274-282.
28. Xu X, Liu X, Ge S, *et al*. Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. Nat Biotechnol. 2012;30(1):105-111.
29. Wang MH, Yu Y, Haberer G, *et al*. The genome sequence of African rice (*Oryza glaberrima*) and evidence for independent domestication. Nat Genet. 2014;46(9):982-988.
30. Li J, He W, Yang G, *et al*. Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. Nat Genet. 2010;42(12):1053-1059.
31. Lu Y, Li J, Buckler ES, *et al*. Genome-wide association studies of 14 agronomic traits in rice landraces. Nat Genet. 2010;42(11):961-967.
32. Huang X, Zhao Y, Wei X, *et al*. Genome-wide association study of flowering time and grain yield traits in a worldwide collection of rice germplasm. Nat Genet. 2012;44(1):32-39.
33. Haseneyer G, Sharma R, Graner A, *et al*. Genome-wide association studies for Agronomical Traits in a world wide Spring Barley Collection. BMC Plant Biol. 2012;12:16.
34. Munoz-Amatriain M, Hayes PM, Muehlbauer GJ, *et al*. The USDA barley core collection: genetic diversity, population structure, and potential for genome-wide association studies. PLoS One. 2014;9(4):e94688.
35. Zhang T, Yu LX, Zheng P, *et al*. Identification of loci associated with drought resistance traits in heterozygous autotetraploid alfalfa (*Medicago sativa* L.) using genome-wide association studies with genotyping by sequencing. PLoS One. 2015;10(9):e0138931.
36. Mora F, Castillo D, Lado B, *et al*. Genome-wide association mapping of agronomic traits and carbon isotope discrimination in a worldwide germplasm collection of spring wheat using SNP markers. Mol Breed. 2015;35(2):69.
37. Tadesse W, Ogbonnaya FC, Jighly A, *et al*. Association mapping of resistance to yellow rust in winter wheat cultivars and elite genotypes. Crop Sci. 2014;54(4):1905-1616.
38. Yu J, Buckler ES. Genetic association mapping and genome organization of maize. Curr Opin Biotechnol. 2006;17(2):155-160.
39. Flint-Garcia SA, Thornsberry JM, Buckler ES, IV. Structure of linkage disequilibrium in plants. Annu Rev Plant Biol. 2003;54:357-374.
40. Utomo H, Wenefrida I, Linscombe S. Progression of DNA Marker and the next generation of crop development. In: Goyal A, editor. Crop Plant. Croatia: InTech; 2012.
41. Jia G, Huang X, Zhi H, *et al*. A haplotype map of genomic variations and genome-wide association studies of agronomic traits in foxtail millet (*Setaria italica*). Nat Genet. 2013;45:957-961.
42. Wu B, Han Z, Xing Y. Genome mapping, markers and QTLs. In: Zhang Q, Wing R, editors. Genetics and Genomics of Rice. New York, NY: Springer-Verlag; 2013.
43. Kilian B, Graner A. NGS technologies for analyzing germplasm diversity in genebanks. Brief Funct Genomics. 2012;11(1):38-50.
44. Schlotterer C, Tobler R, Kofler R, *et al*. Sequencing pools of individuals—mining genome-wide polymorphism data without big funding. Nat Rev Genet. 2014;15(11):749-763.
45. Harakalova M, Mokry M, Hrdlickova B, *et al*. Multiplexed array-based and in-solution genomic enrichment for flexible and cost-effective targeted next-generation sequencing. Nat Protoc. 2011;6(12):1870-1886.
46. Rohland N, Reich D. Cost-effective, high-throughput DNA sequencing libraries for multiplexed target capture. Genome Res. 2012;22(5):939-946.

47. Michelmore RW, Paran I, Kesseli RV. Identification of markers linked to disease-resistance genes by bulked segregant analysis: a rapid method to detect markers in specific genomic regions by using segregating populations. Proc Natl Acad Sci USA. 1991;88(21):9828-9832.
48. Giovannoni J, Wing R, Ganal M, *et al*. Isolation of molecular markers from specific chromosomal intervals using DNA pools from existing mapping populations. Nucleic Acids Res. 1991;19(23):6553-6558.
49. Yang J, Jiang H, Yeh CT, *et al*. Extreme-phenotype genomewide association study (XP-GWAS): a method for identifying trait-associated variants by sequencing pools of individuals selected from a diversity panel. Plant J. 2015;84(3):587-596.
50. Illa-Berenguer E, Van Houten J, Huang Z, *et al*. Rapid and reliable identification of tomato fruit weight and locule number loci by QTL-seq. Theor Appl Genet. 2015;128(7):1329-1342.
51. Han Y, Lv P, Hou S, *et al*. Combining next generation sequencing with bulked segregant analysis to fine map a stem moisture locus in sorghum (*Sorghum bicolor* L. Moench). PLoS One. 2015;10(5):e0127065.
52. Das S, Upadhyaya HD, Bajaj D, *et al*. Deploying QTL-seq for rapid delineation of a potential candidate gene underlying major trait-associated QTL in chickpea. DNA Res. 2015;22:193-203.
53. Lu H, Lin T, Klein J, *et al*. QTL-seq identifies an early flowering QTL located near flowering locus T in cucumber. Theor Appl Genet. 2014;127(7):1491-1499.
54. Yang Z, Huang D, Tang W, *et al*. Mapping of quantitative trait loci underlying cold tolerance in rice seedlings via high-throughput sequencing of pooled extremes. PLoS One. 2013;8(7):e68433.
55. Singh VK, Khan AW, Saxena RK, *et al*. Next-generation sequencing for identification of candidate genes for Fusarium wilt and sterility mosaic disease in pigeonpea (*Cajanus cajan*). Plant Biotechnol J. 2015;14:1183-1194.
56. Henry RJ. Genomics strategies for germplasm characterization and the development of climate resilient crops. Front Plant Sci. 2014;5:68.
57. Stillman JH, Armstrong E. Genomics are transforming our understanding of responses to climate change. BioScience. 2015;65(3):237-246.
58. Vigouroux Y, Ali A, Ndjeunga J, *et al*. Selection for earlier flowering crop associated with climatic variations in the Sahel. PLoS One. 2011;6(5):e19563.
59. Nevo E. Evolution of wild barley and barley improvement. In: Zhang G, Li C, Liu X, editors. Advance in Barley Sciences: Proceedings of 11th International Barley Genetics Symposium. Dordrecht: Springer; 2012. p. 1-23.
60. Franks SJ, Hoffmann AA. Genetics of climate change adaptation. Annu Rev Genet. 2012;46:185-208.
61. Urano K, Kurihara Y, Seki M, *et al*. 'Omics' analyses of regulatory networks in plant abiotic stress responses. Curr Opin Plant Biol. 2010;13(2):132-138.
62. Frankel OH. Genetic perspectives of germplasm conservation. In: Arber WK, Llinensee K, Peacock WJ, editors. Genetic Manipulation: Impact on Man and Society. Cambridge: Cambridge University Press; 1984.
63. McCouch S, Baute GJ, Bradeen J, *et al*. Agriculture: feeding the future. Nature. 2013;499(7456):23-24.
64. Li JY, Wang J, Zeigler RS. The 3,000 rice genomes project: new opportunities and challenges for future rice research. Gigascience. 2014;3:8.
65. Harlan JR, de Wet JMJ. Toward a rational classification of cultivated plants. Taxon. 1971;20(4):509-517.
66. Saka N. A rice (*Oryza sativa* L.) breeding for field resistance to blast disease (*Pyricularia oryzae*) in Mountainous Region Agricultural Research Institute. Plant Prod Sci. 2006;9:3-9.
67. Fukuoka S, Saka N, Koga H, *et al*. Loss of function of a proline containing protein confers durable disease resistance in rice. Science. 2009;325(5943):998-1001.
68. Xu Y. Plant genetic resources: management, evaluation and enhancement. In: Molecular Plant Breeding. Wallingford, UK: CABI; 2010. p. 151-194.
69. Henry RJ, Rice N, Waters DLE, *et al*. Australian *Oryza*: utility and conservation. Rice. 2010;3(4):235-241.
70. McNally KL, Bureau TE, Stokowski R, *et al*. Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. Proc Natl Acad Sci USA. 2009;106(30):12273-12278.
71. Hospital F. Size of donor chromosome segments around introgressed loci and reduction of linkage drag in marker-assisted backcross programs. Genetics. 2001;158(3):1363-1379.
72. Lau WCP, Rafii MY, Ismail MR, *et al*. Review of functional markers for improving cooking, eating and the nutritional qualities of rice. Front Plant Sci. 2015;6:832.
73. Varshney RK, Terauchi R, McCouch SR. Harvesting the promising fruits of genomics: applying genome sequencing technologies to crop breeding. PLoS Biol. 2014;12(6):e1001883-1001888.
74. Hirakawa H, Shirasawa K, Ohyama A, *et al*. Genome-wide SNP genotyping to infer the effects on gene functions in tomato. DNA Res. 2013;20(3):221-233.
75. Frousios K, Iliopoulos CS, Schlitt T, *et al*. Predicting the functional consequences of non-synonymous DNA sequence variants—evaluation of bioinformatics tools and development of a consensus strategy. Genomics. 2013;102(4):223-228.