Review Article

Utilizing Crop Genetic Resources in Modern Breeding to Achieve Sustainable Goals in a Changing Climate

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Abstract

Crop improvement has been a vital goal as well as a challenge for human beings since modern cultivation. Farmers and breeders always tried to obtain higher-output food; therefore, they were initially focused on selecting the best-performing plants. They always adopted high-yielding crops and discarded the other types, resulting in a loss of genetic diversity. Developing breeding programs and utilizing crop genetic resources made it possible to achieve sustainable goals in food production and keep increased genetic diversity concerned at different gene banks. Modern plant breeding introduced ways to generate diversity in the crop germplasm, and these newly formed types can also be conserved along with parent lines, landraces, or wild types. So, in this review, we are focused on discussing the utilization and conservation of crop genetic resources using modern breeding tools and conservation strategies.

Keywords: Genetic resources, modern breeding, genetic diversity, climate change, sustainable production

1. Introduction

Agriculture is an occupation in which more than 50% of the world population is directly or indirectly engaged, especially in developing countries where the sole income of poor communities depends on agriculture. The hot topic nowadays is unstable environmental conditions, erratic rainfalls, global warming, and the most recent inclusion is that global cooling is a part of our lives (Hakeem, 2015). There is an increase of 1.0, 1.6. 0.9 and 1.3% in rice, maize, wheat, and soybean production per annum, respectively, which is less than 2.4%, to meet acute hunger and food demand until 2050 (Ray et al., 2013). Considering the current scenario, agricultural production cannot feed the world population, which is increasing so rapidly that it is expected to reach 10 billion in the coming years (Razzaq et al., 2021). This puts additional pressure on sustainable food production.

A growing threat crop faced during the past few decades is dynamic climatic conditions. This is one of the most significant uncontrollable factors affecting agricultural growth and production worldwide (Razzaq et al., 2021; Zafar et al., 2025). Local temperature and precipitation are vital to productivity and crop variety. Due to increased temperature, erratic rainfall, and fluctuations in precipitation, agricultural inputs and outputs vary severely across the globe (Kim, 2012). The farmer must adopt climate-smart agricultural practices according to changing local environmental conditions, which require extra effort and resources.

Furthermore, the effect of these changes cannot be measured. The daunting fluctuations in climate directly and indirectly impact crop yield, irrigation/canal water availability. According to the report issued by the International Food Policy Research Institute (IFPRI) in 2009, the report presented a detailed crop growth modeling report using two climate scenarios to imitate future climate. The outcome suggested the negative impact of a changing climate on human well-being and crops (Nelson et al., 2009). Competing with these climatic factors is necessary to maximize agricultural outcomes. The only way is to create novel variability and a source population within the crop species that can withstand biotic and abiotic climatic effects.

Genetic diversity is a prerequisite to initiating any breeding program (Reddy et al., 2018). The presence of enough genetic variability is the basis for present and future food security. It is essential to break yield barriers and introduce new cultivars to meet the ever-increasing population's hunger (Mashilo et al., 2017). The selection of desired traits requires a wider genetic base to induce a broad sense of heritability in germplasm in changing environmental conditions. DNA-based molecular markers play a vital role in the early identification of required genes that need to be incorporated against climatic stress (Awan et al., 2021; Razzaq et al., 2021). These variations can be achieved by collecting varieties, landraces, and obsolete cultivars through the acclimatization of imported germplasm. If there is not enough variation present, manual efforts like induced mutation, polyploidy, genetic engineering and other modern techniques can serve as a helping hand to create novel variations (Awan et al., 2021).

The Latest research proposes that there is a 21% reduction in total factor productivity for worldwide agriculture since 1961 due to climatic trends (Ortiz-Bobea et al., 2021). Apart from conventional breeding, which needs more duration and further causes genetic erosion and loss of variability because of continuous selection (Abberton et al., 2016) modern breeding approaches like molecular breeding using DNA markers and genome editing tools (CRISPR Cas 9) (Razzaq et al., 2021). Along with innovative agricultural practices and improvement in plant microbiome conditions, it is an excellent way forward to attain desired food production goals. Next-generation breeding tools are a few methods to develop varieties resilient to erratic climatic conditions by utilizing genetic resources. Recent advances in genomic-assisted breeding (GAB) give a full landscape of genetic variability within a crop species to revive the lost gene. A well-known gene editing technique, and still evolving, known as next-generation CRISPR Cas-9 (clustered regularly interspaced short palindromic repeat), has revolutionized the idea that genome editing is restored for crop improvement (Jinek et al., 2012).

Furthermore, the discoveries of Cas orthologs, Cas9, Cas12, Cas13, and Cas14, has strengthened the editing efficacy (Koonin et al., 2017). We should move agriculture toward modernization and automation by adopting climate-smart agronomic practices and speed breeding involving artificial intelligence and machine learning. The amalgamation of genomic and phenomic tools with speed breeding allows us to quickly identify the desired gene. High-throughput phenotyping is a multidisciplinary approach to accelerate next-generation speed breeding and ultimately accelerate crop modification and improvement programs to develop climate-ready crops toward global food security (Fasoula et al., 2020).

This review highlights the use of genetic variability in its conservation with changing climatic trends. The conventional breeding approach no doubt brings novel variability by crossing diverse populations but causes genetic drag, genetic extinction, hybridization bottlenecks, and a laborious selection process. To meet the food demand of this ever-increasing population and to attain the zero hunger goals, we need to adopt modern breeding methods utilizing crop genetic diversity.

2. Genetic Resources to Conserve Biodiversity

Genetic Resources are essential in serving the provisioning ecosystem based on genetic material relevance to humans. They are also involved in improving and domesticating species that can be utilized in food production, drugs, fiber production, and many other food manufacturing for mankind (Nyadanu et al., 2017). Genetic resources also have some gradual and sudden natural and human-induced factors, for example, climate change and fire, that can lead to a big loss. So the proper tools can be used to evaluate genetic resources such as genetic markers, golden trials, seed banks (Dreisigacker et al., 2005), pollen banks, and cryopreservation, and field gene banks (Pastorino & Marchelli, 2021). The advancements in conserving genetic resources for agricultural and food production are increasing day by day and have changed the scope of the conservation of genetic resources. For example, using economic tools (Wellband et al., 2021) such as gene banks, may be highly beneficial for managing genetic resources (Gollin, 2020). The functional food supply is based on plant biodiversity and benefits the resilience of climate change and ecosystem functions. To enhance the values of crop conservation, gene bank management and integration of genomics and phenomics were used, leading to the more sustainable and efficient conservation of resources. For example, Genebanks and the integration of management tools may be involved in the management of genetic conservation data which is a major challenge in plant biodiversity that would be beneficial for breeders and other users (Ebert & Engels, 2020).

A decrease in biodiversity inhibits the capability of ecosystem functions to provide the sustainability of genetic resources and other services like hygienic food and water and also decreases the genetic variability that may potentially reduce the resources required for future use. To overcome this reduction, some measures were used to protect biodiversity; for example, modified habitats, natural habitats, legally protected areas, and invasive alien species (de Boef et al., 2013).

3. Types of Conserving Biodiversity

The sustainability index of the environment is directly proportional to the conservation of biodiversity and in this regard, the preservation of biodiversity should be the priority of all nations (Torchio et al., 2020). It is mandatory to have the centers of diversity information for fragile habitats. Furthermore, the conservation of biodiversity is the obligation and responsibility of every nation for environmental sustainability (Arora, 2018).

The types of biodiversity conservation involve ex-situ and in-situ conservation (Mondal & Palit, 2022)The ex-situ strategy conserves all living organisms in an artful habitat that considers natural living habitats, such as cryopreservation, Botanical gardens, aquariums, zoos, DNA banks, etc. (Kasso & Balakrishnan, 2013). Insitu conservation is the strategy to conserve endangered and wild species and refers to the restoration and protect the population of species and their habitats (Wang & Li, 2021). The examples of in-situ conservation of biodiversity are elaborated in Table 1.

4. Modern tools in plant breeding to boost biodiversity

Before the laws of genetics became known, the art of breeding was already developed. By using the application of the principle of genetics to crops, a phenomenal increase in crop production occurs, particularly in cereal grains (Jeeterwal & Nehra, 2018). But conventional breeding methods may take 10 or more years to transfer a trait from one parent to another cultivar and it also has various limitations in boosting crop biodiversity.

To meet the future demand and boost crop biodiversity, one way of increasing agricultural production might be to breed with or without GMOs, as it requires less water, has better nutrient usage, and is adapted to climate change (Głowacka et al., 2018). But it is the only way to boost biodiversity and in the current situation, the yield enhancement in major crop species (varying from 0.8–1.2%) must be doubled (Li et al., 2018). So, to conserve crop biodiversity, scientists have adapted new techniques and are moving towards modern genetics and breeding of crop plants. Some biodiversity conservation applications have been mentioned that require whole-genome sequences. So, mostly used approaches is reduced representation sequencing (RRS) that targets a relatively large, about 1% unlinked, representative subsequence of the genome, reducing costs per sample and letting more depth of coverage per locus or larger number of individuals (Alex Buerkle & Gompert, 2013). Now in current studies, restriction site-associated DNA sequencing (RADseq) uses sequence fragments adjacent to sites cut by restriction enzymes (Andrews et al., 2016). RADseq use is not restricted to model organisms because it does not require prior genomic information, as microsatellites are obtained from genomic data.

Thousands of genome-wide SNPs can be identified for the cost of developing some microsatellites so they are markers of choice (Kjeldsen et al., 2016). SNPs' main advantage is that they are directly comparable between labs for collaborative studies (De Groot et al., 2016). (Kim et al., 2016) reported the whole-genome sequencing of 137 rice mini core collections, which presented approximately 25,604 rice germplasms in the Korean genebank of the Rural Development Administration (RDA) based on the Nipponbare reference genome, and resequencing data yielded more than 15 million (M) SNPs and 1.3 M INDELs. About 2,046,529 high-quality SNPs were assigned to the accessions of relevant subgroups for the study of rice mini core with phylogenetic and population analysis, as SNPs capture the evolutionary signatures that are present in rice subpopulations. Similarly, by using 201,817 SNPs, a population structure analysis of 300 rapeseed Chinese germplasm with 22 other accessions of different origins was carried out to obtain sequencing (Zhou et al., 2017).

For sequence messenger RNA (RNAseq) the next generation sequencing (NGS) can be used as that is the transcriptome (Todd et al., 2016). It requires the focus on only the functional parts of the genome, and RNA-seq requires high-quality tissue samples, but RNA is rapidly degraded. That’s why its use in conservation studies is restricted. The NGS platforms can be used to assess the methylation of DNA, which is a major mechanism of epigenetic modification (Verhoeven, Vonholdt, & Sork, 2016) The difference can be identified in methylated and unmethylated cytosine bases by sodium bisulfite during sequencing (bsRADseq). Other epigenetic modifications chromatin and histone have a lack of interest in conservation as these are not heritable (Verhoeven et al., 2016).

Over the past two years, CRISPR/Cas9 has displaced other alternative tools such as zinc-finger nucleases and transcription-activator-like effector nucleases (TALENs). It is less cost-effective and simpler to use (Du et al., 2016). Performing in the molecular biology lab, genome editing with CRISPR/Cas9 is very cheap, easy, and versatile, which is the main factor of biodiversity conservation. Some applications are currently being explored in crops (Weeks et al., 2016) and livestock (Reardon, 2016). That have relevance potential in conservation. These crops such as maize (Svitashev et al., 2015), wheat (Sánchez-León et al., 2018), rice (Zhou et al., 2015), tomato (Brooks et al., 2014), soybean (Han et al., 2019), cotton (Zhao et al., 2017) have improved by using different genetic resources. Using these techniques also contributes to biodiversity conservation.

In the future, it should become possible to obtain a complete understanding of the link between genotype, phenotype, and environment by omic technologies (Yug et al., 2016). Although the applications of integrated omics have not yet been developed for conservation (Table 2).

5. Marker-assisted breeding and genome sequencing

The advancements in genomic research are used to identify the genome sequence and loop precisely several genes via linkage to DNA markers. For example, several genes are tightly linked to genetic markers having resistance to virus diseases, drought, salinity, bacterial blight, submergence, and improving the quality of traits (Duitama et al., 2015). Marker-assisted selection can monitor the presence or absence of these genes in breeding populations. This strategy may provide developments for high yield, better quality crop cultivators, and stress-resistant for breeders. Studies were conducted in which the positive aspects of this breeding device utilized, which would be applicable for new crop varieties and provide conversation genetic diversity (Lei et al., 2021; Munda et al., 2022). The marker-assisted selection also provides opportunities to develop high resistance to insects and diseases that would benefit breeders (Haque et al., 2021; Jena & Mackill, 2008). Marker-assisted backcrossing effectively integrates major genes or traits with high effectiveness into different grown varieties (Jena & Mackill, 2008). A study highlights the utilization of marker-assisted backcrossing (MABC) to preserve the important germplasm or genetic resources of rice crops to different types of flooding stress (Panda et al., 2021). Plant breeding is based on selecting phenotypes that require field observations, breeding cycles, and huge resources (Michel et al., 2017). Recurrent selection is a strategy based on population improvement breeding that involves the selection of phenotypes to improve the capability of favorable alleles between individuals through repeated intercrossing (Singh et al., 2021). A study was conducted in China that demonstrated this strategy for the development of new premium varieties of the crop with high quality and disease resistance and varieties can be cultivated in monsoon climate conditions (Wang & Li, 2021).

The advancement of revolutions in genomics is caused by third-generation or long-read sequencing technologies. The main aim of this advancement is to study transcriptomes, metagenomes, and genomes at an unparalleled resolution and can be essential in serving the provisioning ecosystem based on genetic material relevance to humans (Van Dijk et al., 2018). Plant science is taking advantage of the improvements in the field of DNA sequencing that are boosted by biomedical research intensives and influenced biodiversity protection and plant breeding (Delseny et al., 2010). The recent revolutions in genomics with the combination of précised phenotypes and high throughput technology provide the identification of agronomic trait-controlling genes. For example, crop wild relatives (CWRs) provide potential domestication of new individuals. The annotations and assembling of high-quality crop plants provide new research targets such as cis-regulatory regions and long noncoding RNAs (IncRNAs). These advancements may also improve the selection for plant cultivation, and in the future, the crops can approach the demands of the changing climate and growing population (Pourkheirandish et al., 2020).

6. Genome Editing and Mutation Breeding

The main causes of biodiversity degradation are habitat/species loss, invasive species, over-exploitation, pollution, and climate change. Biodiversity conservation, along with innovation in plant breeding, has become a global concern requiring a comprehensive and integrated approach. There are different recently adopted modern techniques and strategies to develop novel plant types and conserve plant biodiversity (Ebert, 2020; Engels & Thormann, 2020). Numerous gene editing tools, such as zinc-finger nucleases (ZFNs) (Basak, Verma, Kumar, & Kumar, 2021), transcription-activator-like effector nucleases (TALENs) (Becker & Boch, 2021) and clustered regulatory interspaced short palindromic repeat (CRISPR)/CRISPR-associated 9 protein (Cas9) systems (Bessoltane et al., 2022). Based on biological cutting techniques, have a wide range of applications in crop breeding and improvement. ZFNs are created by fusing Fok I endonuclease (Osakabe et al., 2010), which has non-specific cutting activity, with a synthetically altered zinc-finger protein (ZFP), which has specific binding activity. A number of the amino acid residues on ZFP's helix directly contribute to the recognition of the target site and can pair with bases nearby (Novak, 2019). Because TALENs use the transcription activator-like effector (TALE) as their binding domain and the binding function mostly depends on highly changeable amino acids at the 12th and 13th positions on the TALE, they vary structurally from ZFPs. A single base can be specifically identified when combined with them (Barnett, 2018). One-guide RNA (sgRNA) and Cas9 were combined to create the CRISPR/Cas9 system. Today’s extensive use of gene editing technology for crop enhancement is largely made possible by the development of the CRISPR/Cas9 system (Zhu et al., 2020). After undergoing particular alteration, the sgRNA can bind to the target location) (Zhang et al., 2021). The Cas9 protein's HNH and RuvC domains can cleave DNA strands with protospacer-associated motif (PAM) sites and are complementary to sgRNA, respectively. The PAM location is close to the cutting site. Base editors (BEs) and prime editors (PEs) have been introduced, which has further enhanced the CRISPR/Cas system (Jacinto, Link, & Ferreira, 2020).

EvolvR system, which can continuously diversify all nucleotides within a tunable window length at user-defined loci in bacteria, has been developed based on nCas9-recruitment of error-prone DNA polymerases. It allows the identification of ribosomal mutations that confer resistance to the antibiotic spectinomycin in *E. coli* (Halperin et al., 2018). CRISPR-Cas13 knocks down RNAs using RNA-guided RNA-targeting CRISPR-Cas effector Cas13a. Direct adenosine-to-inosine deaminase activity performed by ADAR2 (adenosine deaminase acting on RNA type 2) can be targeted toward the transcripts produced by mammalian cells (Matsoukas, 2018). High-throughput mapping of genetic variants can be achieved using CRISPR-enabled trackable genome engineering (CREATE). CREATE cassette designer can be used to design PAM sequences near the target sites of interest It can rapidly design > 105 cassettes, which in turn increases editing efficiency (Ren et al., 2020).

RNA Interference Technology in maize silenced the *Se1* gene, which increased the soluble sugar content by affecting the starch metabolism of the endosperm, making the mutant maize more favorable for intestinal digestion (Zhang et al., 2019). (Pérez et al., 2019) used *MIM168* to inhibit the expression of microRNA168 in rice, increase the expression of the *AGO1* gene, and then increase the number of panicles. Compared with the control rice, the yield was increased by 30–40%. Knockout of the *OsAAP6* gene using the CRISPR/Cas9 system then promoted the rice tillering, thereby increasing rice yield (Lu et al., 2018). (Xiaoyu Zhang et al., 2021) used the CRISPR/Cas9 system to edit the *Ppo* gene of wheat, which affected the expression of polyphenol oxidase, inhibited dough browning, and improved the quality of wheat. These initiatives have advanced the development of gene editing technology and given us a powerful weapon for accelerating the domestication of crops, enlarging the crop gene pool, and enhancing crop output and quality.

7. Future endeavors of plant breeding to achieve sustainable crop production with maximum biodiversity

Climate change is a global phenomenon and a threat to food security in the future. Plant breeders emphasize the higher yield in crop plants with a broader genetic base. To achieve goals in plant breeding, the use of genetic resources is very crucial. It makes it possible to gain maximum genetic diversity to boost crop yield with climate-resilient lines. The idea of climate-resilient crops is growing very fast in the modern era as it protects the future of food security.

Along with a broader genetic base and higher yield in changing climates, breeders are also trying to develop nutrient-enriched crops. For this purpose, wheat, corn, and rice have been improved in the recent past to get nutrient-enriched grains. Flavr Savr and purple tomatoes are other examples of nutrient-enriched crops to fight against climate change. All these developments were only made through the utilization of different genetic resources. Scientists were not interested in conserving genetic resources after developing high-yielding crops, but now they are firstly conserving the genetic base of any breeding material for the future and then focusing on their desired products. So, the application of modern breeding techniques to develop highly efficient crops from genetic resources is the only way to fight future hunger.

8. Conclusion

Conserving and utilizing different genetic resources for crop improvement to cope effects of climate changes on agricultural production. Plant breeders and geneticists play a vital role in this work. Genetic resources are the source of a broad genetic base for any crop to be developed as climate resilient in the future. Modern plant breeding techniques make it more proficient to get higher yield and nutrient enriched crops by utilizing conserved genetic resources to reduce hunger in the scenario of climate change. Recently, different modern techniques have been developed to target a specific trait in a crop or accumulate the desired traits in a single line. In the future, these lines could serve as climate-resilient crops. Genetic resources are also being conserved using different conservation techniques. When a breeder gets germplasm of any crop from genetic resources later, they'll have to submit the equal germplasm after multiplication. So, the conservation of genetic resources and their utilization in modern breeding programs are the ghosts to making highly nutritious, high-yielding crops with a broader genetic base.

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Author Contributions

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Data Availability

The current review article is not available in any repository and has not been submitted before in any journal.

Table 1: In-Situ Conservation of Plant Biodiversity

In-situ Conservation	
Types	**Examples**
Biosphere Reserves These are the sites nominated by national governments having multi-protected areas of an ecosystem open for researchers and the traditional lifestyle of inhabitants (Mengist et al. 2022).	Nanda Devi Sundarban Nokrek Manas
National Parks These are reserves for the conservation of environmental sustainability as well as wildlife maintained by the government.Its limitations are highly demarcated and humans including habitat, cultivation, forestry, and grazing are prohibited (Beissinger et al. 2017).	Kanha National Park Bandipur National Park
Wildlife Sanctuaries The type of conservation biodiversity that involved in the regions where only wild animals and the human activities such as cultivation, harvesting, forest products, and collection of woods are allowed (Rahman 2017).	Abohar Wildlife sanctuary Ghana Bird Sanctuary Mudumalai Wildlife sanctuary

Table 2: Recent studies on utilizing crop genetic resources in breeding and pre-breeding programs

Targeted Crop	**Genetic Resource**	**Technology**	**Outcome**	**References**
Wheat	32 genotypes	RFLP Markers	Assessment of genetic variability and pathogenicity through the identification of 30 unique and 36 shared alleles	(Verma et al. 2020)
Rice	Two rice cultivars (Yukinko-mai and Kaijin) from the Niigata Agricultural Research Institute's Crop Research Center and Iwate Biotechnology Research Center, Japan	SNP marker-assisted selection + speed breeding	Salt tolerance improvement	(Rana et al. 2019)
Rice	SWARNA Sub1, CR Dhan 800	Marker-assisted backcrossing	Submergence tolerance, bacterial blight resistance and high-yielding near-isogenic lines under changing climate	(Mohapatra et al. 2021)
Rice	60 natural assessions	QTL-based- Marker-assisted selection	Identification of genotypes less responsive to Cd toxicity and boosting genotypic effects	(Sun et al. 2022)

Tomato	63 assessions of 14 Spanish Tomato landraces	The specific combination of SNP markers	A high degree of variation in the population, heterozygosity detected spontaneous crossing, genetic fingerprinting of landraces and In-situ conservation of landraces was suggested	(Cortes-Olmos et al. 2015)
Tomato	426 tomato accessions	High-density SNP genotyping	Identification of 7 sub-populations by Principal Component Analysis, linkage disequilibrium in each chromosome of these populations, different patterns of genetic variations,	(Sim et al. 2012)
Tomato	142 F1 cultivars of 4 different classes	SNPs were generated from genotyping by sequencing	Genome-wide SNP discovery, DNA barcoding, variety identification	(Kim et al. 2021)
Cotton	50 representative Pakistani cotton cultivars	SSR primer pairs-based selection	Genetic diversity assessment of cotton genotypes by using SSR markers	(Dahab et al. 2013)
Cotton	25 cotton genotypes	Selection based on SSR and ISSR markers	Genetic diversity determined by SSR and ISSR markers	(Bardak and BÖLEK 2012)
Cotton	12 cotton varieties	RAPD primer series used for selection	Assessment of variability by using RAPD markers	(Bukhari et al. 2021)

Millet	40 accessions of Italian millet	SSR markers developed through SSR- an enriched library from genomic DNA	Development and use of novel SSR markers for molecular genetic diversity	(Zhao et al. 2012)
Chilli	20 local chili accessions of Bangladesh	Selection based on SSR markers	To assess the molecular genetic diversity by SSR markers	(Sharmin et al. 2018)
Sugarcane	PSJT-941, PS-862, and BL varieties	Invitro selection using PEG-selecting agents	In-vitro selection of sugarcane putative mutant for drought stress	(Hartati et al. 2021)
Common bean	IAC Formoso x BRS Perola	Marker-assisted backcrossing	Combining disease resistance and postharvest quality traits by early marker-assisted backcrossing in Carioca beans	(Paulino et al. 2021)
Chickpea	ICCV 92944, ICCV 00108, ICC 4958 (Donor parent)	Marker-assisted backcrossing	Drought tolerance root traits into Kenyan commercial chickpea varieties	(Kosgei et al. 2022)
Wheat	4 cultivars	Backcross selection and marker-assisted selection	To improve stripe rust resistance by backcrossing and marker-assisted selection	(Zhang et al. 2022)
Barley	Garnal x Baisheshek, Natali x Auksiniai	Zinc- Finger Transcription Factors and SNP markers	Use of ZFT Factors and SNP markers for drought tolerance	(Baidyussen et al. 2021)

References

Abberton, M., Batley, J., Bentley, A., Bryant, J., Cai, H., Cockram, J., & De Pace, C. (2016). Global agricultural intensification during climate change: A role for genomics. *Plant Biotechnology Journal, 14*(4), 1095–1098. https://doi.org/10.1111/pbi.12467

Alex Buerkle, C., & Gompert, Z. (2013). Population genomics based on low coverage sequencing: How low should we go? *Molecular Ecology*, *22*(11), 3028–3035. https://doi.org/10.1111/mec.12105

Andrews, K. R., Good, J. M., Miller, M. R., Luikart, G., & Hohenlohe, P. A. (2016). Harnessing the power of RADseq for ecological and evolutionary genomics. *Nature Reviews Genetics*, *17*(2), 81–92. https://doi.org/10.1038/nrg.2015.28

Arora, N. K. (2018). Biodiversity conservation for sustainable future. In *Vol. 1* (pp. 109–111). Springer. https://doi.org/10.1007/978-981-10-6896-0_16

Awan, F. S., Sadia, B., Altaf, J., Habib, M., Hameed, K., & Hussain, S. (2021). Genetic variability through induced mutation. In *Genetic Variation*. IntechOpen. https://doi.org/10.5772/intechopen.95027

Barnett, P. (2018). Transcription activator-like effector nucleases (TALENs): A new, important, and versatile gene editing technique with a growing literature. *Science & Technology Libraries*, *37*(1), 100–112. https://doi.org/10.1080/0194262X.2018.1424114

Basak, N., Verma, V. C., Kumar, R., & Kumar, G. (2021). Mechanism of ZFN-mediated genome editing: Scope and opportunities. In *Genome editing in plants* (pp. 13–27). CRC Press.

Becker, S., & Boch, J. (2021). TALE and TALEN genome editing technologies. *Gene and Genome Editing*, *2*, 100007. https://doi.org/10.1016/j.ggedit.2021.100007

Bessoltane, N., Charlot, F., Guyon-Debast, A., Charif, D., Mara, K., Collonnier, C., & Nogué, F. (2022). Genome-wide specificity of plant genome editing by both CRISPR–Cas9 and TALEN. *Scientific Reports*, *12*(1), 13034. https://doi.org/10.1038/s41598-022-13034-2

Brooks, C., Nekrasov, V., Lippman, Z. B., & Van Eck, J. (2014). Efficient gene editing in tomato in the first generation using the clustered regularly interspaced short palindromic repeats/CRISPR-associated9 system. *Plant Physiology, 166*(3), 1292–1297. https://doi.org/10.1104/pp.114.247148 de Boef, W. S., Subedi, A., Peroni, N., Thijssen, M., & O'Keeffe, E. (2013). *Community biodiversity management: Promoting resilience and the conservation of plant genetic resources*. Routledge.

De Groot, G. A., Nowak, C., Skrbinšek, T., Andersen, L. W., Aspi, J., Fumagalli, L., & Liberg, O. (2016). Decades of population genetic research reveal the need for harmonization of molecular markers: The grey wolf *Canis lupus* as a case study. *Mammal Review*, *46*(1), 44–59. https://doi.org/10.1111/mam.12050

Delseny, M., Han, B., & Hsing, Y. I. (2010). High throughput DNA sequencing: The new sequencing revolution. *Plant Science*, *179*(5), 407–422. https://doi.org/10.1016/j.plantsci.2010.06.011

Dreisigacker, S., Zhang, P., Warburton, M., Skovmand, B., Hoisington, D., & Melchinger, A. (2005). Genetic diversity among and within CIMMYT wheat landrace accessions investigated with SSRs and implications for plant genetic resources management. *Crop Science*, *45*(2), 653–661. https://doi.org/10.2135/cropsci2005.0653

Du, H., Zeng, X., Zhao, M., Cui, X., Wang, Q., Yang, H., & Yu, D. (2016). Efficient targeted mutagenesis in soybean by TALENs and CRISPR/Cas9. *Journal of Biotechnology*, *217*, 90–97. https://doi.org/10.1016/j.jbiotec.2015.11.005

Duitama, J., Silva, A., Sanabria, Y., Cruz, D. F., Quintero, C., Ballen, C., & Torres, E. (2015). Whole genome sequencing of elite rice cultivars as a comprehensive information resource for marker-assisted selection. *PLOS ONE*, *10*(4), e0124617. https://doi.org/10.1371/journal.pone.0124617

Ebert, A. W. (2020). The role of vegetable genetic resources in nutrition security and vegetable breeding. *Plants*, *9*(6), 736. https://doi.org/10.3390/plants9060736

Ebert, A. W., & Engels, J. M. (2020). Plant biodiversity and genetic resources matter! *Plants*, *9*, 1706. https://doi.org/10.3390/plants9121706

Engels, J. M., & Thormann, I. (2020). Main challenges and actions needed to improve conservation and sustainable use of our crop wild relatives. *Plants*, *9*(8), 968. https://doi.org/10.3390/plants9080968

Fasoula, D. A., Ioannides, I. M., & Omirou, M. (2020). Phenotyping and plant breeding: Overcoming the barriers. *Frontiers in Plant Science*, *10*, 1713. https://doi.org/10.3389/fpls.2019.01713

Głowacka, K., Kromdijk, J., Kucera, K., Xie, J., Cavanagh, A. P., Leonelli, L., & Long, S. P. (2018). Photosystem II subunit S overexpression increases the efficiency of water use in a field-grown crop. *Nature Communications, 9*(1), 1–9. https://doi.org/10.1038/s41467-018-03674-z

Gollin, D. (2020). Conserving genetic resources for agriculture: Economic implications of emerging science. *Food Security, 12*(5), 919–927. https://doi.org/10.1007/s12571-020-01054-8

Hakeem, K. R. (2015). *Crop production and global environmental issues*. Springer. https://doi.org/10.1007/978-3-319-23162-4

Halperin, S. O., Tou, C. J., Wong, E. B., Modavi, C., Schaffer, D. V., & Dueber, J. E. (2018). CRISPR-guided DNA polymerases enable diversification of all nucleotides in a tunable window. *Nature, 560*(7717), 248–252. https://doi.org/10.1038/s41586-018-0384-8

Han, J., Guo, B., Guo, Y., Zhang, B., Wang, X., & Qiu, L.-J. (2019). Creation of early flowering germplasm of soybean by CRISPR/Cas9 technology. *Frontiers in Plant Science, 10,* 1446. https://doi.org/10.3389/fpls.2019.01446

Haque, M. A., Rafii, M. Y., Yusoff, M. M., Ali, N. S., Yusuff, O., Datta, D. R., Anisuzzaman, M., & Ikbal, M. F. (2021). Recent advances in rice varietal development for durable resistance to biotic and abiotic stresses through marker-assisted gene pyramiding. *Sustainability, 13*(19), 10806. https://doi.org/10.3390/su131910806

Jacinto, F. V., Link, W., & Ferreira, B. I. (2020). CRISPR/Cas9-mediated genome editing: From basic research to translational medicine. *Journal of Cellular and Molecular Medicine, 24*(7), 3766–3778. https://doi.org/10.1111/jcmm.15118

Jeeterwal, R. C., & Nehra, A. (2018). *Principles of quality seed production of cereal crops*. [Publisher not provided — please supply if known]

Jena, K., & Mackill, D. (2008). Molecular markers and their use in marker-assisted selection in rice. *Crop Science, 48*(4), 1266–1276. https://doi.org/10.2135/cropsci2007.05.0279

Jinek, M., Chylinski, K., Fonfara, I., Hauer, M., Doudna, J. A., & Charpentier, E. (2012). A programmable dual-RNA–guided DNA endonuclease in adaptive bacterial immunity. *Science, 337*(6096), 816–821. https://doi.org/10.1126/science.1225829

Kasso, M., & Balakrishnan, M. (2013). Ex situ conservation of biodiversity with particular emphasis to Ethiopia. *International Scholarly Research Notices, 2013*, 985037. https://doi.org/10.5402/2013/985037

Kim, C. G. (2012). The impact of climate change on the agricultural sector: Implications of the agro-industry for low carbon, green growth strategy and roadmap for the East Asian region. Economic and Social Commission for Asia and the Pacific (ESCAP): Bangkok, Thailand.

Kim, T.-S., He, Q., Kim, K.-W., Yoon, M.-Y., Ra, W.-H., Li, F. P., & Choi, B. (2016). Genome-wide resequencing of KRICE_CORE reveals their potential for future breeding, as well as functional and evolutionary studies in the post-genomic era. *BMC Genomics*, *17*(1), 1–13. https://doi.org/10.1186/s12864-016-2771-4

Kjeldsen, S. R., Zenger, K. R., Leigh, K., Ellis, W., Tobey, J., Phalen, D., & Raadsma, H. W. (2016). Genome-wide SNP loci reveal novel insights into koala (*Phascolarctos cinereus*) population variability across its range. *Conservation Genetics*, *17*(2), 337–353. https://doi.org/10.1007/s10592-015-0785-9

Koonin, E. V., Makarova, K. S., & Zhang, F. (2017). Diversity, classification and evolution of CRISPR-Cas systems. *Current Opinion in Microbiology*, *37*, 67–78. https://doi.org/10.1016/j.mib.2017.05.008

Lei, Q.-Y., Zhou, J.-J., Xiong, Y., Zhang, W.-H., Luo, J., & Long, C.-L. (2021). Genetic diversity evaluation and conservation of Kam fragrant glutinous rice (*Oryza sativa* L.) germplasm in Southeast Guizhou, China. *Plants*, *10*(9), 1898. https://doi.org/10.3390/plants10091898

Li, H., Rasheed, A., Hickey, L. T., & He, Z. (2018). Fast-forwarding genetic gain. *Trends in Plant Science*, *23*(3), 184–186. https://doi.org/10.1016/j.tplants.2018.01.007

Lu, K., Wu, B., Wang, J., Zhu, W., Nie, H., Qian, J., & Fang, Z. (2018). Blocking amino acid transporter OsAAP3 improves grain yield by promoting outgrowth buds and increasing tiller number in rice. *Plant Biotechnology Journal*, *16*(10), 1710–1722. https://doi.org/10.1111/pbi.12907

Mashilo, J., Shimelis, H., & Odindo, A. (2017). Phenotypic and genotypic characterization of bottle gourd [*Lagenaria siceraria* (Molina) Standl.] and implications for breeding: A review. *Scientia Horticulturae*, *222*, 136–144. https://doi.org/10.1016/j.scienta.2017.04.006

Matsoukas, I. G. (2018). Commentary: RNA editing with CRISPR-Cas13. *Frontiers in Genetics*, *9*, 134. https://doi.org/10.3389/fgene.2018.00134

Michel, S., Ametz, C., Gungor, H., Akgöl, B., Epure, D., Grausgruber, H., & Buerstmayr, H. (2017). Genomic assisted selection for enhancing line breeding: Merging genomic and phenotypic selection in winter wheat breeding programs with preliminary yield trials. *Theoretical and Applied Genetics*, *130*(2), 363–376. https://doi.org/10.1007/s00122-016-2820-5

Mondal, S., & Palit, D. (2022). Challenges in natural resource management for ecological sustainability. In *Natural resources conservation and advances for sustainability* (pp. 29–59). Elsevier. https://doi.org/10.1016/B978-0-323-85750-1.00002-4

Munda, S., Saikia, R. J., Begum, T., Bhandari, S., Gogoi, A., Sarma, N., & Lal, M. (2022). Evaluation of genetic diversity based on microsatellites and phytochemical markers of core collection of *Cymbopogon winterianus* Jowitt germplasm. *Plants*, *11*(4), 528. https://doi.org/10.3390/plants11040528

Nelson, E., Mendoza, G., Regetz, J., Polasky, S., Tallis, H., Cameron, D., & Kareiva, P. M. (2009). Modeling multiple ecosystem services, biodiversity conservation, commodity production, and tradeoffs at landscape scales. *Frontiers in Ecology and the Environment*, *7*(1), 4–11. https://doi.org/10.1890/080023

Novak, S. (2019). Plant biotechnology applications of zinc finger technology. In *Transgenic plants* (pp. 295–310). Springer. https://doi.org/10.1007/978-3-030-04904-0_15

Nyadanu, D., Adu Amoah, R., Obeng, B., Kwarteng, A., Akromah, R., Aboagye, L., & Adu-Dapaah, H. (2017). Ethnobotany and analysis of food components of African locust bean (*Parkia biglobosa* (Jacq.) Benth.) in the transitional zone of Ghana: Implications for domestication, conservation, and breeding of improved varieties. *Genetic Resources and Crop Evolution*, *64*(6), 1231–1240. https://doi.org/10.1007/s10722-016-0435-1

Ortiz-Bobea, A., Ault, T. R., Carrillo, C. M., Chambers, R. G., & Lobell, D. B. (2021). Anthropogenic climate change has slowed global agricultural productivity growth. *Nature Climate Change*, *11*(4), 306–312. https://doi.org/10.1038/s41558-021-01000-1

Osakabe, K., Osakabe, Y., & Toki, S. (2010). Site-directed mutagenesis in *Arabidopsis* using custom-designed zinc finger nucleases. *Proceedings of the National Academy of Sciences*, *107*(26), 12034–12039. https://doi.org/10.1073/pnas.1000235107

Panda, D., Barik, J., & Sarkar, R. K. (2021). Recent advances of genetic resources, genes, and genetic approaches for flooding tolerance in rice. *Current Genomics*, *22*(1), 41–58. https://doi.org/10.2174/1389202921999201228150023

Pastorino, M. J., & Marchelli, P. (2021). *Genetic resources: The base material for managing nature* (ISBN 0124095488). [Publisher or URL needed if available]

Pérez, L., Soto, E., Farré, G., Juanos, J., Villorbina, G., Bassie, L., & Rojas, J. A. (2019). CRISPR/Cas9 mutations in the rice Waxy/GBSSI gene induce allele-specific and zygosity-dependent feedback effects on endosperm starch biosynthesis. *Plant Cell Reports*, *38*(3), 417–433. https://doi.org/10.1007/s00299-019-02380-0

Pourkheirandish, M., Golicz, A. A., Bhalla, P. L., & Singh, M. B. (2020). Global role of crop genomics in the face of climate change. *Frontiers in Plant Science*, *11*, 922. https://doi.org/10.3389/fpls.2020.00922

Ray, D. K., Mueller, N. D., West, P. C., & Foley, J. A. (2013). Yield trends are insufficient to double global crop production by 2050. *PLOS ONE*, *8*(6), e66428. https://doi.org/10.1371/journal.pone.0066428

Razzaq, A., Kaur, P., Akhter, N., Wani, S. H., & Saleem, F. (2021). Next-generation breeding strategies for climate-ready crops. *Frontiers in Plant Science*, *12*, 637366. https://doi.org/10.3389/fpls.2021.637366

Reardon, S. (2016). Welcome to the CRISPR zoo. *Nature News*, *531*(7593), 160–163. https://doi.org/10.1038/531160a

Reddy, B. J., Mandal, R., Chakroborty, M., Hijam, L., & Dutta, P. (2018). A Review on Potato (Solanum Tuberosum L.) and its Genetic Diversity. *International Journal of Genetics*, *10*(2), 360. https://doi.org/10.9735/0975-2862.10.2.360-364

Ren, J., Lee, J., & Na, D. (2020). Recent advances in genetic engineering tools based on synthetic biology. *Journal of Microbiology*, *58*(1), 1–10. https://doi.org/10.1007/s12275-020-9381-4

Sánchez-León, S., Gil-Humanes, J., Ozuna, C. V., Giménez, M. J., Sousa, C., Voytas, D. F., & Barro, F. (2018). Low-gluten, nontransgenic wheat engineered with CRISPR/Cas9. *Plant Biotechnology Journal*, *16*(4), 902–910. https://doi.org/10.1111/pbi.12837

Singh, M., Nara, U., Kumar, A., Thapa, S., Jaswal, C., & Singh, H. (2021). Enhancing genetic gains through marker-assisted recurrent selection: From phenotyping to genotyping. *Cereal Research Communications*, 1–16. https://doi.org/10.1007/s42976-021-00142-y

Svitashev, S., Young, J. K., Schwartz, C., Gao, H., Falco, S. C., & Cigan, A. M. (2015). Targeted mutagenesis, precise gene editing, and site-specific gene insertion in maize using Cas9 and guide RNA. *Plant Physiology*, *169*(2), 931–945. https://doi.org/10.1104/pp.15.00793

Todd, E. V., Black, M. A., & Gemmell, N. J. (2016). The power and promise of RNA-seq in ecology and evolution. *Molecular Ecology*, *25*(6), 1224–1241. https://doi.org/10.1111/mec.13526

Torchio, M. F., Lucia, U., & Grisolia, G. (2020). Economic and human features for energy and environmental indicators: A tool to assess countries' progress towards sustainability. *Sustainability*, *12*(22), 9716. https://doi.org/10.3390/su12229716

Van Dijk, E. L., Jaszczyszyn, Y., Naquin, D., & Thermes, C. (2018). The third revolution in sequencing technology. *Trends in Genetics, 34*(9), 666–681. https://doi.org/10.1016/j.tig.2018.05.008

Verhoeven, K. J., Vonholdt, B. M., & Sork, V. L. (2016). Epigenetics in ecology and evolution: What we know and what we need to know. *Molecular Ecology, 25*(8), 1631–1638. https://doi.org/10.1111/mec.13617

Wang, W., & Li, J. (2021). In-situ conservation of biodiversity in China: Advances and prospects. *Biodiversity Science, 29*(2), 133. https://doi.org/10.17520/biods.2021085

Weeks, D. P., Spalding, M. H., & Yang, B. (2016). Use of designer nucleases for targeted gene and genome editing in plants. *Plant Biotechnology Journal, 14*(2), 483–495. https://doi.org/10.1111/pbi.12448

Wellband, K., Baillie, S. M., Bentzen, P., & Bernatchez, L. (2021). Genetic diversity. In *The Lake Charr Salvelinus namaycush: Biology, ecology, distribution, and management* (pp. 119–165). Springer. https://doi.org/10.1007/978-3-030-62203-8_6

Yugi, K., Kubota, H., Hatano, A., & Kuroda, S. (2016). Trans-omics: How to reconstruct biochemical networks across multiple 'omic' layers. *Trends in Biotechnology, 34*(4), 276–290. https://doi.org/10.1016/j.tibtech.2015.12.013

Zafar, M. M., Ijaz, A., Anwar, Z., Iqbal, M. S., Zafar, S., Subhan, M., ... Jiang, X. (2025). Harnessing genetic diversity in cotton for enhanced resilience against salt stress by using agro-physiological characters. *Plant Production Science, 28*(1), 51–68. https://doi.org/10.1080/1343943x.2024.2439874

Zhang, X., Mogel, K. J. H. V., Lor, V. S., Hirsch, C. N., De Vries, B., Kaeppler, H. F., ... Kaeppler, S. M. (2019). Maize sugary enhancer1 (*se1*) is a gene affecting endosperm starch metabolism. *Proceedings of the National Academy of Sciences, 116*(41), 20776–20785. https://doi.org/10.1073/pnas.1912268116

Zhang, X., Xu, G., Cheng, C., Lei, L., Sun, J., Xu, Y., ... Chen, X. (2021). Establishment of an *Agrobacterium*-mediated genetic transformation and CRISPR/Cas9-mediated targeted mutagenesis in hemp (*Cannabis sativa* L.). *Plant Biotechnology Journal, 19*(10), 1979–1987. https://doi.org/10.1111/pbi.13582

Zhao, X., Meng, Z., Wang, Y., Chen, W., Sun, C., Cui, B., ... Guo, S. (2017). Pollen magnetofection for genetic modification with magnetic nanoparticles as gene carriers. *Nature Plants, 3*(12), 956–964. https://doi.org/10.1038/s41477-017-0063-z

Zhou, J., Peng, Z., Long, J., Sosso, D., Liu, B., Eom, J. S., Huang, S., Liu, S., Vera Cruz, C., Frommer, W. B., White, F. F., & Yang, B. (2015). Gene targeting by the TAL effector PthXo2 reveals cryptic resistance gene for bacterial blight of rice. *The Plant Journal : For Cell and Molecular Biology*, *82*(4), 632–643. https://doi.org/10.1111/tpj.12838

Zhou, Q., Zhou, C., Zheng, W., Mason, A. S., Fan, S., Wu, C., ... Huang, Y. (2017). Genome-wide SNP markers based on SLAF-seq uncover breeding traces in rapeseed (*Brassica napus* L.). *Frontiers in Plant Science*, *8*, 648. https://doi.org/10.3389/fpls.2017.00648

Zhu, H., Li, C., & Gao, C. (2020). Applications of CRISPR–Cas in agriculture and plant biotechnology. *Nature Reviews Molecular Cell Biology*, *21*(11), 661–677. https://doi.org/10.1038/s41580-020-00288-x