

Agricultural Biotechnology and Crop Improvement: A Review

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Abstract: To meet the needs of a predicted worldwide population of nine billion people in the year 2050, agricultural biotechnology's promise of sustainable crop production improvements is critical. Climate change, scarcity of land for agriculture, and social issues are the factors that limit agricultural production and productivity, resulting in poverty, starvation, malnutrition, and deaths for millions of people throughout the world, particularly in sub-Saharan Africa and South Asia. In most developing countries, including Africa, agricultural production and productivity systems are not supported by modern technology. Nowadays, advanced agricultural biotechnology techniques such as genetic modification and transformation of plants play a crucial role in crop improvement by introducing advantageous novel gene(s) or inhibiting the transmission of existing traits in the plants. Crop resilience to abiotic and biotic variables, quality of the grain, and crop design will all contribute considerably to the community's adoption of genome-edited crops in order to advance the lines of breeding and utilize distinct environmental responses. Herbicide tolerance, insect resistance, abiotic stress tolerance, disease resistance, and nutritional improvement are all characteristics of genetically modified crops. Therefore, crop improvement using agricultural biotechnology is the best and most efficient way in agriculture to overcome food insecurity and climate change disasters globally.

Keywords: Agricultural Biotechnology, Crop Improvement, Genetic Transformation, Genome Editing, GM Crops

1. Introduction

Food security is one of the biggest and most pressing issues confronting population survival in the world. To meet the needs of an estimated 9 billion individuals by 2050, the globe will require about two times the amount of food delivered right away. To properly attain this objective, agricultural production must be substantially raised on current cultivable land while tackling the obstacles posed by climate change. Thus, biotech has the potential to improve global food supply and accessibility in a sustainable way. Crop breeding strategies and better management practices have resulted in steady improvements in agricultural yields over the last five decades. The pace of production growth, however, has slowed [1]. The very minor yearly productivity increases (wheat yields increasing at a non-compounding average of 0.9% per annum; at these speeds, worldwide supply rises by 38%) are insufficient to satisfy the anticipated demand by 2050. Developing more effective, higher-yielding plants is thus the optimum method to pursue right away [2]. Agricultural

biotechnology is the utilization of plants and animals or their cellular parts in agricultural products. Tissue culture, traditional breeding, molecular marker-assisted breeding, genetic engineering, gene editing, and GMOs are all now in use in agriculture. Genetic improvements enable agriculture to achieve larger yields while meeting the demands of growing numbers of people who have restricted resources such as water and land. Advanced agricultural biotechnology refers to biotechnology procedures that go above regular developmental boundaries to change DNA and fuse cells. Genetic engineering, for example, uses "transgenic" technology to make genetically modified organisms (GMOs) by inserting or deleting genes. The artificially created manipulation of genetic material is known as genetic engineering, sometimes known as genetic transformation. It includes extracting and cutting a gene at a precise spot with the help of enzymes. Targeted fragments of DNA can then be delivered into the cells of the intended organism. *Agrobacterium tumefaciens* as a vector for disseminating the genetic characteristic [3]. Plants can be modified genetically to improve flavor, pest and disease

resistance, or growth in harsh environments. Biosafety and genetic engineering programs in Africa have been launched in the past few years with the goal of bringing GM crops into Africa's agricultural systems. Countries such as South Africa, Egypt, and Burkina Faso have already made commercial GMOs, and a number of others have established the ability to perform studies and advances in modern agricultural biotechnology [4]. The term "green biotechnology" refers to the application of ecologically sound alternatives in agricultural, horticultural, and livestock breeding activities [5].

2. Agricultural Biotechnology Techniques in Crop Improvement

2.1. Somaclonal Variation

Somaclonal variation refers to variability between crops produced in vitro through any type of somatic cell or tissue culture. It is a novel and changing technique for enhancing genetic diversity, widening the genome base, and, as a result, genetic enrichment in order to achieve considerable and significant improvements in agriculture [6, 7]. It contains DNA-related hereditary or genetic changes that cause traits to differ from those of the initial parents. Extended in vitro culturing, tissue culture medium substances, the existence of chemical compounds, and some other mechanical factors during culture are all main contributors [8]. Nevertheless, because in vitro genetic change does not always result in favorable results, somaclonal variation has several challenges

connected to in vitro cloning and plant material maintenance, as in vitro genetic alteration cannot usually produce useful, favorable, and steady results. Moreover, its application is limited by genotype reliance and genomic stability [9]. Plants grown from tissue culture, on the other hand, are not faithful to type [10].

In regular or stressful settings, variations in phenotype are most often seen in plants. Such unusual and abnormal variants can be DNA or epigenetic in origin, resulting from changes in genes, abnormalities in genomic rearrangements, modifications, and transposed components [11]. Culture-induced genetic changes are inherited, whereas epigenetic alterations are typically non-heritable, unstable, and eliminated when crop reproduction is sexual. Molecular techniques such as DNA markers and reversed-phase HPLC (RP-HPLC) can be used to assess this genetic and epigenetic diversity. Furthermore, the methyl-sensitive amplifying fragment length polymorphism (metAFLP) enabled the simultaneous detection of structural variations as well as modifications in DNA methylation trends [8, 12]. Various culture procedures are also responsible for somaclonal diversity in the regenerated plantlets. Somaclonal variation can be characterized as gametoclonal, androclonal, gynoclonal, protoclonal, or calliclinal according to the tissue from which it arises [13]. The following is an overview of how to use plant tissue culture or in vitro procedures to produce various sorts of variability in order to extend and improve the genetic basis. (Figure 1).

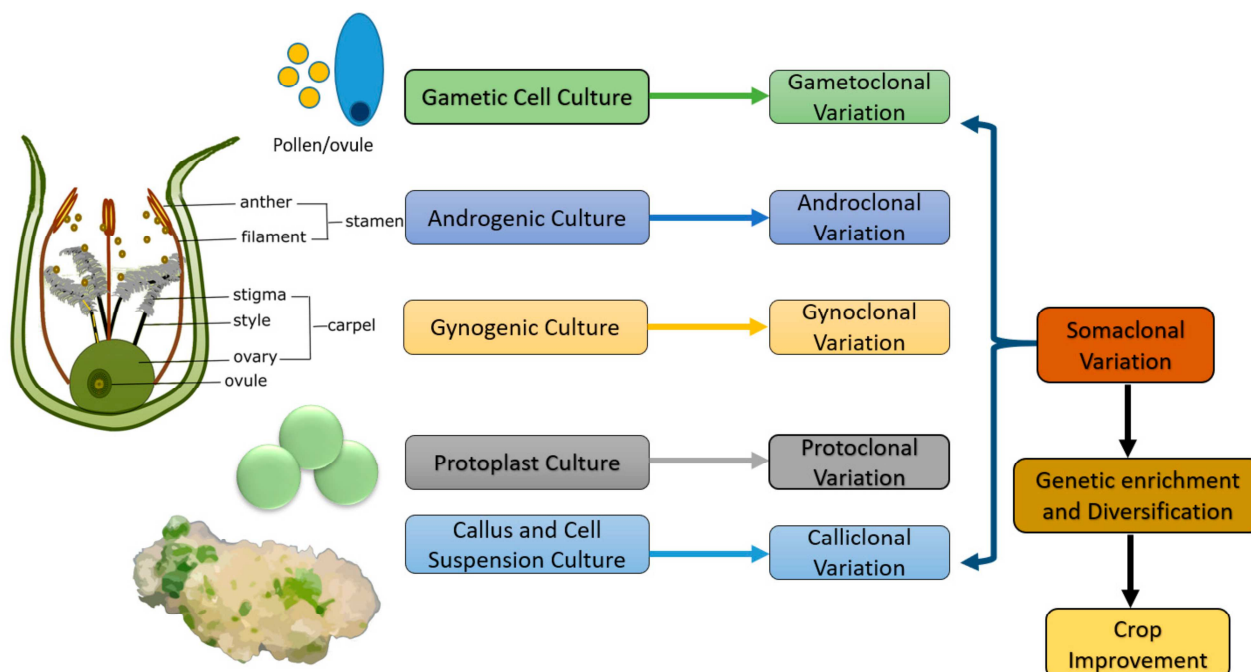


Figure 1. Types of somaclonal variations. (Source: Akila et al., 2022).

2.2. Genetic Transformation

Plant genetic transformation enables the immediate

introduction of crucial agricultural traits into the main cereals. It is a critical technique in plant breeding for creating distinctive and genetically diverse crops. The transferred

gene is referred to as a "transgene," and the living things produced as an outcome of the accurate transfer of genes are referred to as "transgenics" [14]. Many genes in the system of delivery employ various methods to convey genetic materials into functional cell hosts.

2.3. Molecular Breeding

Over the last ten years, major advancements have been achieved in the discipline of genetics in rice [15–17], poplar (*Populus trichocarpa*) [18], sorghum (*Sorghum bicolor*) [19], maize [20], and soybean (*Glycine max*) [21]. Moreover, the introduction of so-called 'next-generation sequencing' (NGS) technologies has made it feasible to sequence the gene pools or chromosomes of all living things (and for a wide range of organisms) reasonably promptly and inexpensively [22]. Consequently, the sequencing of genomes is now accessible to understudied plants such as cucumber (*Cucumis sativus*) [23], pigeon pea (*Cajanus cajan*) (<http://www.icrisat.org/gt-bt/IIPG/home.html>), and huge and intricate species such as wheat (<http://www.genomeweb.com/sequencing/wheat-genome-sequenced-roches-454>) and barley (*Hordeum vulgare*) (<http://barleygenome.org/>).

2.4. Genetic Engineering

Genetic engineering, specifically, has enormous opportunities to improve crop improvement performance. Over the last decade, the quick growth of genetic data and the application of accompanying scientific computation methodologies have resulted in the discovery of signaling pathways, regulation genes, and networks regulating intricate traits connected with environmental challenges. The interaction of crops GE with signal mechanisms and transcription factors (TFs) results in the production of their target transcriptome, which includes numerous genes associated with stress adaptation. Overexpression of the *LOS5/ABA3* genes, which encode a molybdenum cofactor sulfurase necessary for ABA synthesizing, provided improved resistance to drought in genetically engineered rice plants in natural circumstances [24]. Furthermore, the upregulation of rice *AP37* (an *APETALA2*-type TF) expression led to an upsurge in the synthesis of numerous desired traits and a 16–57% increase in crop output under drought-stressed conditions [25]. As a result, transcriptional construction promises the development of natural factors resilient to stress crops.

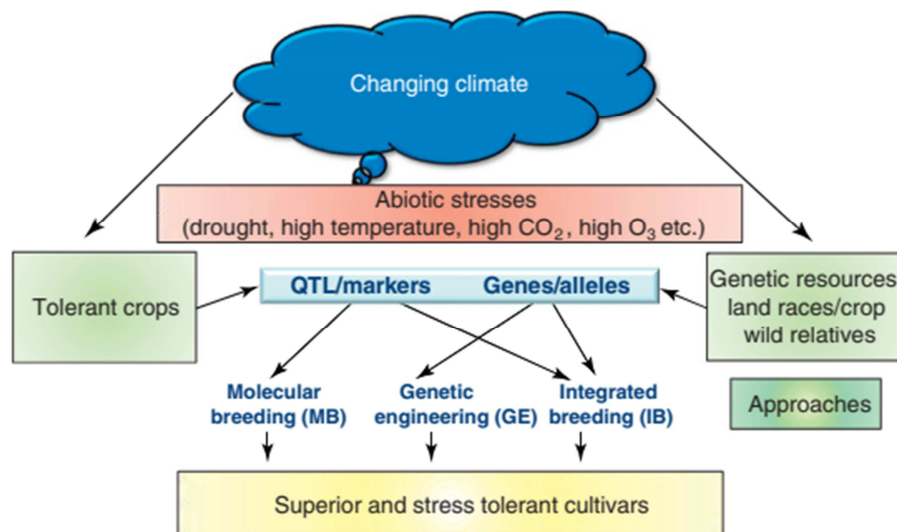


Figure 2. An integrated approach to developing crops those are better adapted to abiotic stresses. (Source: Varshney et al., 2011).

2.5. Mutation Breeding

Mutation breeding involves employing either chemicals or physical factors to induce variety in plants. Mutagenesis, which also results from these chemicals, is frequently employed in improving crops, and foods produced from this method are commonly consumed [26]. Nearly two thousand agricultural types of plants developed by mutation breeding were produced in the previous seventy years, possibly through direct mutations or as progenitors for developing novel strains. The majority of mutant breeding projects intend to change features like the height of plants and resistance to disease in suitable crop types. Mutation breeding is an approach that is commonly employed in crops such as rice, barley, wheat, chickpeas, and soybeans [27].

Around 400 enhanced varieties of rice have resulted from this approach [27]. Of these, a mutation in the semi-dwarf cultivar 'Calrose 76' substantially assisted in rice improvements. The *Sd 1* (*semidwarf1*) gene is down-regulated in this cultivar via gamma-ray mutagenesis. Two high-yielding and semi-dwarf cultivars, particularly 'Golden Promise' and 'Diamant,' which were also developed via forced mutations, played important roles in the growth of the European brewing industry. Mutation breeding also helps neglected cereals. Mutation breeding, for example, was responsible for the introduction of early-maturing and virus-resistant mung beans and high-yielding and blight-resistant chickpeas [26, 27]. Furthermore, in order to improve orphan crops, the FAOIAEA project "Genetic improvement of exploited and skipped crops in low-income food-deficit

countries" (LIFDCs) used irradiated and associated approaches [26].

2.6. GM Crops

Genetically modified (GM) crops are agricultural plants with genomes that are being transformed using the techniques of genetic engineering to enhance present characteristics or introduce additional characteristics that do not occur normally in the original plant variety. Transgenic crops are those in which particular portions of foreign nucleic acids or sequences of genes have been incorporated into the genetic code using techniques for transformation (such as *Agrobacterium*-mediated transformation or direct gene transfer) [28]. In developed nations, genetically engineered crops are widely used. Such crops have an outstanding capacity to provide additional nutrition compared to conventional crops [29].

2.7. Genomic Selection

Genomic selection (GS) is one of the most promising developments for next-generation sequencing selection, allowing for rapid improvement of crops requiring considerable genetic study. The estimation of genomic estimated breeding values (GEBVs) for distinct components in a phenotyped and genotyped developed population is the foundation of GS. As a consequence, a population for breeding might be constructed from a population sample and maintained over consecutive generations with no requirement for extra laborious traits of morphology. As demonstrated by computational methods with the grazing grass *Lolium perenne*, GS reduces the breeding season by 4 years when compared to traditional breeding. Empirical studies of GS in the oil palm industry have demonstrated its utility in enhancing the breeding process [30]. Cassava GS concentration in both performance and yield metrics indicated conceptual gains ranging from 39.42 percent to 73.96 percent as compared to phenotypic selection for this crop [31], which is potentially exceptionally adaptive to upcoming climate change [32]. Crop scientists have begun to undertake empirical GS studies in wheat using GBS techniques [33].

2.8. Genome Editing

The CRISPR/Cas9 System for Crop Genome Engineering

The clustered regularly interspaced short palindromic repeat (CRISPR)/CRISPR-associated protein (Cas9) approach for direct modification of genes is an inexpensive and powerful tool. The growing acceptance of this innovative technology has sparked "CRISPR fever," with significant implications for plant gene editing for basic research and agricultural advancement [34]. CRISPR/Cas9 gene editing has an impressive degree of accuracy, which can be enhanced with Cas9 nickase [35]. In fact, cleavage effectiveness and precision can be greater than with other genome editing techniques. Over the last three years, CRISPR-Cas9 technology has been demonstrated to be effective on a wide

range of crop varieties, including maize, orange, potato, rice, sorghum, tobacco, tomato, and wheat. The vast majority of developing approaches depend on intrinsic variation in genes or modification platforms to introduce advantageous loci into superior genotypes through tedious backcrossing operations. Though CRISPR offers unrivaled crop improvement opportunities, applying a CRISPR approach requires in-depth knowledge of the target gene(s), its purpose, and its activity.

3. Conclusion

Solving global issues of increasing populations, worldwide warming and related biotic and abiotic stress factors, limited land for agriculture, and depleting natural resources through sustainable improvement in agricultural production and productivity has become a priority area. More than 800 million people worldwide struggle to have access to adequate food every day. The global population is expected to rise from seven billion to 9.8 billion by the year 2050. Producers will have to generate at least 50% of their food sources in order to feed everyone. The improvement of crop varieties with increased production, resilience to both abiotic and biotic stresses, and improved quality of food was made possible by agricultural biotechnology.

Conflict of Interest

The author has not declared any conflict of interests.

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References

- [1] Grassini, P.; Eskridge, K. M.; Cassman, K. G. (2013). Distinguishing between yield advances and yield plateaus in historical crop production trends. *Nat. Commun.* 2013, 4, 2918. [CrossRef].
- [2] 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* 2013, 8, e66428. [CrossRef] [PubMed].
- [3] Johanson A, Ives CL, (2001). An inventory of the agricultural biotechnology for Eastern and Central Africa region. Michigan State University. p. 62.
- [4] Mayet M (2007). The new green revolution in Africa: Trojan Horse for GMO? A paper presented at a Workshop: "Can Africa feed itself"? – Poverty, Agriculture and Environment – Challenges for Africa. 6-9th June 2007, Oslo, Norway. Center for African Biosafety (www.biosafetyafrica.net).
- [5] Treasury, H. M. (2009). Green biotechnology and climate change. *European Biology*, 12. Retrieved from <http://www.docstoc.com/docs/15021072/Green-Biotechnology-and-Climate-Change>

- [6] Gosal, S. S.; Wani, S. H. (2018). Cell and Tissue Culture Approaches in Relation to Crop Improvement. In *Biotechnologies of Crop Improvement*; Gosal, S. S., Wani, S. H., Eds.; Springer International Publishing: Cham, Switzerland, 2018; Volume 1, pp. 1–55; ISBN 978-3-319-78283-6. [CrossRef].
- [7] Stelpflug, S. C.; Eichten, S. R.; Hermanson, P. J.; Springer, N. M.; Kaeppler, S. M. (2014). Consistent and Heritable Alterations of DNA Methylation Are Induced by Tissue Culture in Maize. *Genetics* 2014, 198, 209–218. [CrossRef].
- [8] Ranghoo-Sanmukhiya, V. M. (2021). Somaclonal Variation and Methods Used for Its Detection. In *Propagation and Genetic Manipulation of Plants*; Siddique, I., Ed.; Springer: Singapore, 2021; pp. 1–18; ISBN 9789811577369.
- [9] Bridgen, M. P.; Van Houtven, W.; Eeckhaut, T. (2018). Plant Tissue Culture Techniques for Breeding. In *Ornamental Crops*; VanHuylenbroeck, J., Ed.; Handbook of Plant Breeding; Springer International Publishing: Cham, Switzerland, 2018; pp. 127–144; ISBN 978-3-319-90698-0.
- [10] Zhang, D.; Wang, Z.; Wang, N.; Gao, Y.; Liu, Y.; Wu, Y.; Bai, Y.; Zhang, Z.; Lin, X.; Dong, Y.; et al. (2014). Tissue Culture-Induced Heritable Genomic Variation in Rice, and Their Phenotypic Implications. *PLoS ONE* 2014, 9, e96879. [CrossRef].
- [11] Krishna, H.; Alizadeh, M.; Singh, D.; Singh, U.; Chauhan, N.; Eftekhari, M.; Sadh, R. K. (2016). Somaclonal variations and their applications in horticultural crops improvement. *Biotech* 2016, 6, 1–18. [CrossRef].
- [12] Machczynska, J.; Orłowska, R.; Zimny, J.; Bednarek, P. T. (2014). Extended metaFLP approach in studies of tissue culture induced variation (TCIV) in triticale. *Mol. Breed.* 2014, 34, 845–854. [CrossRef] [PubMed].
- [13] Bhojwani, S. S.; Dantu, P. K. (2013). *Plant Tissue Culture: An Introductory Text*; Springer: New Delhi, India, 2013; ISBN 978-81-322-1025-2.
- [14] Keshavareddy, G.; Kumar, A.; Ramu, V. S. (2018). Methods of Plant Transformation—A Review. *Int. J. Curr. Microbiol. Appl. Sci.* 2018, 7, 2656–2668. [CrossRef].
- [15] Goff, S. A. et al. (2002). A draft sequence of the rice genome (*Oryza sativa* L. ssp. *japonica*). *Science* 296, 92–100 23.
- [16] Yu, J. et al. (2002). A draft sequence of the rice genome (*Oryza sativa* L. ssp. *indica*). *Science* 296, 79–92 24.
- [17] IRGSP (International Rice Genome Sequencing Project) (2005). The Map-Based Sequence of the Rice Genome. *Nature*, 436, 793–800.
- [18] Tuskan, G. A. et al. (2006). The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). *Science* 313, 1596–1604.
- [19] Paterson, A. H. et al. (2009). The *Sorghum bicolor* genome and the diversification of grasses. *Nature* 457, 551–556 27.
- [20] Schnable, P. S. et al. (2009). The B73 maize genome: complexity, diversity, and dynamics. *Science* 326, 1112–1115 28.
- [21] Schmutz, J. et al. (2010). Genome sequence of the paleopolyploid soybean. *Nature* 463, 178–183.
- [22] Varshney, R. K. et al. (2009). Next-generation sequencing technologies and their implications for crop genetics and breeding. *Trends Biotechnol.* 27, 522–530 30.
- [23] Huang, S. et al. (2009). The genome of the cucumber, *Cucumis sativus* L. *Nat. Genet.* 41, 1275–1281.
- [24] Xiao, B. Z. et al. (2009). Evaluation of seven function-known candidate genes for their effects on improving drought resistance of transgenic rice under field conditions. *Mol. Plant* 2, 73–83.
- [25] Oh, S. J. et al. (2009). Overexpression of the transcription factor AP37 in rice improves grain yield under drought conditions. *Plant Physiol.* 150, 1368–1379.
- [26] Jain SM (2009) Mutation induced genetic improvement of neglected crops. In: Tadele Z (ed) New approaches to plant breeding of orphan crops in Africa. In: Proceedings of an International Conference, Bern, Switzerland. Stämpfli AG, Bern, 19–21 Sept 2007.
- [27] Ahloowalia BS, Maluszynski M, Nichterlein K (2004). Global impact of mutation-derived varieties. *Euphytica* 135: 187–204.
- [28] Griffiths AJF, Wessler SR, Lewontin RC, Gelbart WM, Suzuki DT, Miller JH (2005). Introduction to genetic analysis. 8th (ed.) FreemanWH, New York. https://www.bio.bg.ac.rs/materijali_predmeta/med-eng-griffiths-an-introduction-to-genetic-analysis.pdf
- [29] Kumar K, Gambhir G, Dass A et al (2020). Genetically modified crops: current status and future prospects. *Planta* 251: 91. <https://doi.org/10.1007/s00425-020-03372-8>
- [30] Cros, D., M. Denis, L. Sánchez, B. Cochard, A. Flori, T. Durand-Gasselin, et al. (2015). Genomic selection prediction accuracy in a perennial crop: Case study of oil palm (*Elaeis guineensis* Jacq.). *Theor. Appl. Genet.* 128 (3): 397–410. doi: 10.1007/s00122-014-2439-z.
- [31] De Oliveira E. J, de Resende M. D. V., Santos V. D., et al. (2012). Genome-wide selection in cassava. *Euphytica*. 187: 263-276.
- [32] Jarvis A, Ramirez-Villegas Campo B. V. H, et al. (2012). Is cassava the answer to African climate change adaptation? *Trop. Plant Biol.* 5: 9-29.
- [33] Poland J, Endelman J, Dawson J, et al. (2012). Genomic selection in wheat breeding using genotyping-by-sequencing. *Plant Genome*. 5: 103-113.
- [34] Belhaj K, Chaparro-Garcia A, Kamoun, Patron NJ, Nekrasov V (2015). Editing plant genomes with CRISPR/Cas9. *Curr Opin Biotechnol*; 32: 76-84. doi: 10.1016/j.copbio.2014.11.007. Epub 2014 Nov 29.
- [35] Shen B, Zhang W. S, Zhang J, et al. (2014). Efficient genome modification by CRISPR-Cas9 nickase with minimal off-target effects. *Nat. Meth.* 11: 399-402.