

## INNOVATIVE WAYS TO BREED PLANTS WITH THE GOAL OF FEEDING THE WHOLE WORLD

### Abstract

The four problems threatening future food security are demand growth, supply contraction, and the need for robust and sustainable production. Crop breeding is an ongoing process whose primary goal is to improve the genome in order to meet rising demand. Faster breeding and shorter breeding cycles are two of the most efficient ways to create new varieties that are climate-adapted. Rapid Generation Advance (RGA) is a faster, simpler, and less expensive breeding technique than other breeding techniques. Haplodiploids significantly shorten the line fixation stage because they produce fully homozygous lines right away. Because many field locations have different environmental factors and diseases, the shuttle breeding system is advantageous because it allows for better selection. Future speed breeding efforts should focus on underutilised nutrient-rich crops, and biofortification is critical for combating global hunger. When conventional hybridization fails, mutation breeding is required. The use of DNA markers has reduced the time required for varietal development by several years. However, the possibility of recombination between the marker and the target gene can result in false positives. Using gene pyramiding, multiple resistance genes can be inserted into a plant at the same time. Instead of focusing on specific genes or quantitative trait loci, genomic selection focuses on making genomic predictions from a large number of DNA markers. Traditional genomic selection models can be outperformed by machine learning-based genomic selection models. Lack of resources, particularly in developing countries, is a major impediment to the development of novel breeding techniques. Marker assisted selection frequently

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necessitates large upfront investments in equipment and operating costs. When discussing public breeding programmes, RGA should be prioritised based on factors such as cost, resource availability, and technical complexity.

**Keywords:** Food security, crop breeding, speed breeding, genes, genomic selection

## I. INTRODUCTION

Food insecurity usually affects one billion people worldwide. The United States Agency for International Development (USAID) clarifies food security as the potential to always have physical and financial access to enough food to meet dietary requirements for a successful and healthy life. Hunger levels remain surprisingly high around the world. According to the Global Report on Food Crises 2022, they broke all previous records in 2021, with nearly 193 million people experiencing acute food insecurity—nearly 40 million more than the previous peak in 2020. There are currently 195 million undernourished people in India. In India, chronic undernutrition or stunting prevents 4 out of 10 children, or nearly 47 million people, from reaching their full potential. India's agricultural sector is extremely underproductive. According to the World Bank, India's cereal yield is 2,992 kg per hectare, while North America's yield is 7,318.4 kg per hectare.

The two biggest threats to food supply in the present and future are population increase and climate change. Due to urbanisation, the population explosion is accelerating, expanding worldwide demand, and placing strain on land. D.Satterthwaite and colleagues (2010) Economic growth is crucial in alleviating hunger (both chronic and hidden) (T. Godecke et al.,2018) and poverty (D. Dollar et al.,2013), but it may not be sufficient to accelerate reductions in hunger and malnutrition (FAO ,2012). As a result of climate change, extreme weather phenomena like droughts and floods are also growing more frequent (M.M.Q. Mirza, 2011; J.E. Hayettal., 2018). Future food security will face four challenges: increasing demand, decreasing supply, and the need for resilient and sustainable production (P. Smith,2013). However, the current rate of yield increase may not be sufficient to meet future cereal crop demand (Dk. Ray,2013). Possible strategies for increasing future food availability include (i) dietary changes (K.F. Davis et al., 2016) (ii) reducing food waste (H.C.J. Godfray et al.,2010) (iii) reducing yield disparities through improved agronomy (H.C.J. Godfray et al., 2010) (iv) increased arable land (B. Kampman et al., 2008); and (v) increased productivity. Productivity gains are critically dependent on both the development and dissemination of new technologies (for example, new crop varieties, precision agriculture, and so on).

Speedy breeding is a workable partial answer to the problems that still need to be solved. Breeding is the logical place to start, but a multidisciplinary strategy (including agronomy, pathology, extension, seed production, and post-harvest technology) will undoubtedly be needed. As a result, we'll go over a number of tried-and-true traditional and biotechnological breeding techniques that don't include gene editing or genetic engineering. The viability of short-term adoption by national agricultural research and extension systems (NARES) in developing nations with constrained capability to execute cutting-edge technology is given particular consideration. We examine the advantages and disadvantages of accelerated breeding, more especially rapid generation advance (RGA), as a response to problems with future food security.

## II. STRATEGIES

**1. Methods of non-molecular breeding:** Fundamental selection theory in plant breeding states that the rate of genetic gain is increased by reducing the time needed for line

development, or the creation of new breeding lines, regardless of the technique. Notably, one of the simplest and most efficient ways to create new varieties that are adapted to existing climates in to mitigate the consequences of climate change is through faster breeding and shorter breeding cycles. (G.N. Atlin et al. 2017, S. Acharjee et al., 2021, A. Sunny et al. 2022)

According to a recent global survey, approximately 78 percent of rice breeders worldwide use the pedigree breeding method (B. Lenaerts et al., 2018). While this is a tried and true rice breeding method, it is based on growing all plant populations in the field during the normal growing seasons.

- **Rapid advancement in generation (RGA):** Breeders of cereal crops have been using rapid generation advance (RGA), also known as single seed descent (SSD), as a quicker breeding technique for fifty years. In essence, this strategy promotes quick line fixing by modifying plant growth circumstances to hasten flowering and seed germination during a regular crop growing season. Another efficient and resource-saving breeding method is bulk-population breeding. It does not, however, result in time savings. RGA has advantages over other breeding methods in terms of speed, technical simplicity, resource requirements, and cost. This strategy, which was empirically tested and shown to be superior to the pedigree method, was widely used in the IRRI's irrigated breeding programme. This resulted in a two-year reduction in the period needed for variety creation and breeding.
- **Haplodiploids:** By triggering chromosome doubling from pollen grains, regenerating plants produce doubled haploid (DH) populations, which significantly shortens the line fixation stage since totally homozygous lines are formed right away (R. Mishra et al.,2016). Only species that can be cultured can be used for this, which is done in tissue culture labs (e.g. cereal species including rice). Similar to RGA, this technique has been utilised for decades in rice breeding and has led to the introduction of numerous rice cultivars (J. Pauk et al., 2009). However, due to biological reasons, it has been more challenging to produce doubled haploid populations for the *indica* subspecies than for the *japonica* subspecies (D. Grewal et al.,2011).
- **Shuttle breeding:** Japanese researchers began a shuttle breeding experiment for rice in 1982. (D.J. Mackill et al.,2013). However, there have been several practical problems with shipping seed across international boundaries over the years, mostly because of concerns about intellectual property and national germplasm protection. Despite these obstacles, the private sector makes use of off-season nurseries (especially in temperate climates). As the field locations varied for a variety of diseases and environmental situations, this technique also improved selection (R. Ortiz et al.,2007). Soil is important to plant growth in speed breeding's high-cost growing chambers. Hydroponics uses water for growth (V. Page and U. Feller 2013). Using solar-powered light and temperature control, disused shipping containers and refrigerators can be converted into fast breeding capsules (BBC, 2018). These tablets boost research in underdeveloped countries and low-fertile zones. Speed breeding relies heavily on lengthy photoperiods for rapid generation development, with LEDs playing a vital role in the flowering of long day and short day crops. LASER's

monochromatic light converts 40 to 60% of its light spectrum energy usage (Ooi, et al. 2016). Future speed breeding should focus on underexploited nutritious crops to address global starvation. Future vertical farming will save room.

- 2. Mutation breeding:** Mutation breeding is important when traditional hybridization is inadequate. Mutation breeding creates polygenic mutations, generates ideotypes for various agro-climatic conditions, and corrects flaws in advanced breeding lines and cultivars. Agronomic traits like straw stiffness, maturity, adaptability, shatter resistance, disease resistance, protein content, baking quality, and malting quality can all be improved by induced mutation (N.R. Chakraborty and P.C. Kole 2014, Z. Imam et al. 2021). Mutation breeding tackles traits not favoured by natural selection or previous plant breeding. N.R. Chakraborty and A. Paul (2012) demonstrated induced mutation's importance in crop improvement.

Mutation breeding's downsides include pleiotropic gene activity and simultaneous mutation of closely linked genes. Most induced mutations are harmful, although useful mutants can be retrieved. Even a few favourable mutations in high-yield types can become homozygous within a few generations after induction in M2 or M3, compared to F6 or F7 in hybridization (A. Kant et al. 2020, A. Kant and N.R. Chakraborty 2021A, 2021B).

Mutations can complement natural variation and hybridization. Induced mutations may be identical to natural mutations or may have never happened or been lost in the natural population. Modern agriculture can maintain favourable mutations with careful selection (Z. Imam et al. 2021).

- 3. Molecular breeding techniques:** Marker-based screening is frequently more effective than conventional methods, allowing for screening that would not be achievable using conventional phenotyping techniques while also improving accuracy or saving money or time.
  - Marker-assisted backcrossing:** "Target gene" is frequently inserted into an established variety by backcrossing. The parent that is used for backcrossing usually possesses most of the desirable qualities and is lacking in only a few. Utilizing DNA markers dramatically improves backcrossing selection efficiency. Marker-assisted backcrossing (MABC) effectively identifies the target gene or quantitative trait locus while preserving the recipient variety's original significant qualities and "enhancing" the original variety in terms of traits that are lacking (B.C.Y. Collard and D.J. Mackill, 2008). MAB can improve the effectiveness of backcross breeding in three ways: 1. If the desired gene's phenotype from the donor parent cannot be clearly assessed, one option is to select backcross offspring with a marker allele from the donor parent at a locus close to the target gene (foreground selection). 2. Backcross progeny can be protected from inheriting high levels of donor parent germplasm located outside the target zone by using markers (background selection). 3. Linkage drag can be alleviated by using markers to choose rare progeny that result from recombination near to the target gene (recombinant selection). The time needed for varietal development to occur has been reduced by several decades because of the use of DNA markers. Marker-assisted backcrossing has been utilised in rice breeding

programmes for drought, flood, and salinity tolerance (N. Sandhu and A. Kumar, 2017).

- **Pyramiding of genes:** Pyramiding is the practise of simultaneously combining several quantitative trait loci (QTLs) or genes into a single genotype. Conventional breeding can make it happen, but the first few generations can be challenging or perhaps impossible. Individual plants should be investigated for all phenotypic traits in classical phenotypic selection. Due to this, it is more difficult to assess particular plants, populations (such as F<sub>2</sub>), or features (using destructive bioassays). DNA markers are frequently used in plant breeding, but one of their most important uses is marker-assisted gene pyramiding (MAGP). It is used to simultaneously introduce many resistance genes into a plant for long-term defence. Gene pyramids have been developed to guard rice from bacterial blight and blast (N. Huang et al., 1997; S. Singh et al., 2001; Y. Luo et al., 2012). In order to increase barley's resistance to stripe rust, qualitative genes and QTLs were pyramided (A.J. Castro et al., 2003). Common pyramiding techniques include backcrossing, recurrent selection, multiple-parent crossing, or complicated crossing. The number of genes/QTLs necessary for trait improvement, the number of parents with the necessary genes/QTLs, the heritability of the desired characteristics, and other parameters all affect the suitability of a MAGP breeding plan. Three-way, four-way, or double crossing can be used to pyramid three or four desired genes/QTLs. Pyramiding of more than four genes may be preferred to complex or multiple crossing and/or recurrent selection, while it can also be performed through convergent backcrossing or stepwise backcrossing.
- **Molecular selection:** All quantitative trait loci (QTL) are placed in linkage disequilibrium with at least one marker when utilising genetic markers that span the entire genome; this procedure is known as "genomic selection."

A similar strategy to MAS called genomic selection focuses on making genomic judgments from a large number of DNA markers rather than on particular genes or quantitative trait loci (Z.A. Desta and R.Ortiz, 2014, Seth et al. 2019). However, the implementation of genomic selection in public sector breeding programmes in developing countries is prevented by significant obstacles of technical and economic nature. Furthermore, before employing genomic selection, the most cost-effective and efficient method must be determined. P. Rajsic et al. 2016).

4. **Genomic forecasting:** Because of advancements in sequencing technologies, genotyping has become more efficient, faster, and cost-effective. Nowadays, genotyping a breeding line at a high density is less expensive than determining how effective it is in the field. Genotypic information can be utilised in breeding operations by creating sequencing and genotyping technology that is more inexpensive and effective. Using innovative, affordable genome-wide sequencing in conjunction with precise phenotype data, genomic estimated breeding values (GEBVs) can be produced to help breeders pick offspring that can act as parents for the following generation (improvement cycle). The rate of genetic gain in breeding is anticipated to increase with the use of GEBVs in the context of genome-wide prediction (P. Sinha et al., 2021). When comparing traditional selection with MAS techniques for genomic prediction, an accuracy of 0.5 in maize and wheat

leads to a two- to three-fold improvement in genetic gains each year (E.L. Heffner et al., 2011). For Fusarium head blight resistance in wheat, multiple-trait genomic prediction outperformed single-trait genomic prediction (A.W. Schulthess et al., 2017).

### III. DISCUSSION

The lack of resources, especially in developing nations, is a major barrier to the development of novel breeding techniques. It has been determined that a fundamental obstacle limiting rice growers from adopting RGA as their principal breeding approach is the inadequacy of a greenhouse (B. Lenaerts et al., 2018). RGA and MABC often demand large up-front expenditures for infrastructure as well as ongoing operating costs. Economic analysis of breeding technology investments must consider both the costs and the benefits. This is consistent with the discovery that not all expenditures related to investment projects are recoverable. It is sometimes necessary to convert markers into more reliable and "breeder-friendly" markers. MAS may be more expensive than traditional methods, particularly in terms of startup costs and labour costs (K. Dreher et al., 2003; M. Morris et al., 2003). False positives could be caused by the marker and the gene of interest recombining.

In order to speed up the rate of genetic gain and shorten the time needed to breed new varieties of crops, scientists have turned to Rapid Generation Advancement (RGA) protocols, which increase the number of crop generations per year and allow for the rapid generation of homozygous lines. Fast-tracking breeding pipelines will allow ICRISAT, ICARDA, and partner breeding institutions to deliver improved chickpea and lentil cultivars faster and with greater resource efficiency. Saved time: For generation advancement, the single-seed descent (SSD) method of RGA uses a single seed and requires less space and time (less than two months to complete a cycle ). Adoption by the scientific community is simple: Early generation selection is laborious, and there is a risk of losing valuable genotypes due to unfavourable linkages. RGA does not have this issue because selection is not used until the F5-6 generations. Researchers with greenhouse facilities can use the RGA protocol to advance breeding populations on a small scale by utilising existing infrastructure. Under various bilateral projects, ICRISAT and ICARDA are disseminating technology to researchers. When grown under field conditions, integrating RapidGen with crop breeding provides tremendous opportunities to overcome the limitations of seasons and photoperiods. Breeding tools like marker-assisted selection (MAS) and genomic selection (GS) can easily be integrated with RGA technology to modernise breeding programmes and achieve higher genetic gains in respective crops (Samineni S et al.,2020). The problems are a lack of information on an individual's or population's potential during RGA processing, possible genetic drifts, and a decrease in population size per generation.

When chromosomes double in haploid cells, a genotype termed as a doubled haploid (DH) is generated. The development of artificially doubled haploids is crucial to plant breeding. In contrast to doubled haploidy, conventional inbreeding takes six generations to reach about full homozygosity. (Jain and others, 1996) Breeding initiatives involving diploid wild relatives of agricultural plants may benefit from the utilisation of dihaploid plants generated from tetraploid crop plants. Genes, which have minor but cumulative impacts, govern the majority of economic features. Although the potential of DH populations in quantitative genetics has long been understood, it wasn't until the development of molecular

marker maps that their application in locating loci governing quantitative traits really gained off. Accurate phenotyping with replicated trials is necessary because QTL effects are modest and heavily influenced by environmental factors. As a result of their actual breeding nature and ease of mass production, doubled haploidy organisms make this achievable. The biggest drawback of the DH population is the inability to perform selection. In contrast, selection can be used in conventional breeding to enhance desired traits in the population across numerous generations. In haploids created from a different culture, some plants are aneuploids, while others are hybrid haploid-diploid genotypes. The high cost of designing tissue culture and growing facilities is another drawback of double haploidy. Genetic diversity may be decreased by overusing doubled haploidy in breeding material. As a result, there are a number of things to take into account when using doubled haploidy in breeding programmes.

Despite the fact that genomic selection has a great deal of potential for sustainable agriculture, there are still a number of obstacles preventing its direct application. It is necessary to refocus efforts in order to overcome constraints in genomic selection in order to maximise its potential for crop improvement and food security. Non-GM genomic selection products are more widely accepted by farmers and consumers. If constraints are removed, genomic selection has the potential to contribute to long-term agricultural development by assisting in the feeding of the world's growing population. With MAS-based gene pyramiding, the breeder can now conduct multiple rounds of selections per year. Gene pyramiding with marker technology can be integrated into existing plant breeding programmes all over the world, allowing researchers to access, transfer, and combine genes at previously unheard-of speeds and precision. However, a number of issues remain in this field. Some of the challenges encountered stem from the need for improved scoring methods, larger population sizes, multiple replications and environments, appropriate quantitative genetic analysis, diverse genetic backgrounds, and independent verification through advanced generations.

When nonadditive changes had a significant impact on predictions produced using genome-wide ML approaches, the machine learning based "deepGS" outperformed more conventional genomic selection (GS) models. The characterization of genomic areas and genome function, the inference of regulatory networks, and the understanding of the complexity of plant responses to stressors are just a few of the many uses of machine learning in plant science and breeding. The current lack of high-quality labelled data on large populations is the biggest obstacle preventing machine learning from being used to accelerate crop breeding. The use of automatic machine learning methods and synthetic data generation could reduce this bottleneck. The impacts of genotype environment interaction on single trait genomic prediction for hybrids less related to the estimate set might be reduced by multiple trait genomic selection if a good indicator trait was available (S. Debnath et al., 2022; A.W. Schulthess et al., 2018).

Crop breeding is a continuous process that primarily aims to improve the genome to meet emerging situations and problems. Long-term crops such as paddy, wheat, and others with tall structures and low yields were grown in the 1960s and 1970s. When it was discovered that such varieties were not producing enough to sustain the growing population, short duration high yielding varieties were developed and released into the field (N.R. Chakraborty and A. Paul, 2012). The introduction of short-term Mexican wheat in Punjab



during India's famous green revolution in the 1970s to produce a bumper crop to meet the food requirements of the hungry Indian population is a classic example. Breeding is generally done to increase crop yield, to sustain adverse climatic, soil, and water conditions, such as developing saline resistant, flood resistant varieties, disease and pest resistant varieties, and so on. Man's spice is variety. As a result, when consumer tastes/preferences shift, breeders work to develop new varieties to meet the demand. However, many logistical issues regarding difficulties in moving seed across international borders have been encountered over the years, primarily due to intellectual property issues and national germplasm protection. Despite these limitations, the private sector (particularly in temperate regions) makes use of off-season nurseries.

#### **IV. CONCLUSION**

Despite being a very helpful tool, conventional plant breeding has drawbacks. To begin with, breeding can only take place between two sexually compatible plants. This restricts the amount of additional features that can be added to a species' existing traits.

Due to technological advancements, double haploid protocols are now available for the vast majority of plant genera. In only a few decades, the number of species that can undergo doubled haploidy has skyrocketed to an astounding 250. With the gradual removal of species from the recalcitrant category, response efficiency has also improved. Therefore, it will increase the efficiency of plant breeding. However, the cost of establishing tissue culture and growth facilities is higher in double haploidy. When used excessively, doubled haploidy can decrease the range of genes available for selection in breeding stock. As a result, before employing doubled haploidy in breeding programmes, several factors must be considered. Shuttle breeding posed several practical difficulties for the transportation of seeds across international borders due to concerns about copyrighted material and the safeguarding of national biodiversity. Notwithstanding these limitations, off-season nurseries are used by the private sector, especially in temperate areas. Field rapid generation advance is an efficient technique that uses few resources. Accelerated breeding to maintain food security through climate manipulation is possible due to improvements in genetic gain rate, decreased breeding programme costs, saved time, and widespread acceptance by the scientific community. Molecular breeding methods necessitate sophisticated technologies, which are comparatively more expensive in the public sector. Not only are the infrastructure facilities expensive, but so are the input costs. These facilities necessitate a lot of upkeep. All of these factors make it difficult for the public sector to use molecular breeding methods on a large scale.

Whether or not a proposed new method or technology is practically possible is an important consideration before committing to its implementation. The following factors should be taken into account when discussing public sector breeding: expense, resource availability, and technical proficiency. Due to its greatest potential for rapid adoption across the board in public sector programmes, we believe RGA to be the optimal strategy.

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