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## Genomic selection in crop plants: An overview

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### Abstract

Genomic selection involves future breeding aimed at increasing genetic gain in crops plants. Molecular markers and other genetic markers are applied to the conventional phenotypic selection strategies for increasing genetic gain of the crop plants is referred to as genomic selection. Although, genomic selection is more favourable than marker-assisted selection (MAS) as it allows a more significant number of QTL than MAS. Additionally, it aids in the early identification of the most qualified candidates for selection based on the plant's entire genome. While the field of high-throughput phenotyping is still in its infancy, it is showing signs of maturity, with the capacity to assess features more rapidly and correctly than was previously thought possible. The synergy between genomic and phenotypic data will usher in an age unlike any other in human history of inbreeding and functional genomics. Here, we have discussed the application of genomic selection to crop plants with significant development in the field.

**Keywords:** Genomic selection, genetics, breeding, genes, genome

### Introduction

More than 7 billion people live on the planet, and the global population clock is constantly ticking upward [1-5]. According to United Nations (UN) projections, this development pattern will continue until roughly 2050, when the world's population is expected to reach a remarkable 9.1 billion inhabitants. The fact that thousands of years were required to expand the world population to the first 2 billion people is noteworthy. However, it is also important to note that another 2 billion people will be added to the globe in the following twenty-five years. Given the enormous problem of feeding the world's population, scientists are attempting to develop more effective ways of food production. As a result, various innovations are being implemented into food production in order to fulfil the increased demand, including precision farming, the use of micronutrients, protected cultivation, and integrated crop management, to name a few. The production of cultivars via plant genetic breeding is regarded as one of the most significant advances in agriculture. It has been responsible for more than half of the improvements in crop yields over the previous century. Plant breeding may be accomplished using two sorts of methods: traditional breeding and marker-assisted breeding (MAB) [6-12].

Since the 1990s, marker-assisted selection (MAS) has been utilised in plant development initiatives to encourage research findings for tagging genes and mapping quantitative trait loci (QTL) [13, 14] recommended the use of MAS to produce quicker gains and enhance selection efficiency when compared to selection based only on phenotypic data. Genetic linkage with specific loci affecting quantitative features is achieved by using morphological data and molecular markers in MAS (quantitative trait loci, QTL). MAS and association genetics have been employed in the discovery of underlying significant genes in gene pools and introducing these genes into breeding programmes to enhance the qualities of the offspring. Nonetheless, they have shown several limitations, primarily due to the lengthy selection cycles and the inability to search for solid marker-QTL relationships to capture 'minor' gene effects [16-18]. It was initially suggested by [19] and is an example of molecular-marker aided selection. Hundreds or thousands of DNA markers are used to concurrently anticipate the genetic effects on hundreds or thousands of markers' phenotypes [20]. In linkage disequilibrium (LD) with the QTL, these markers may have both big and minor effects, and they can account for virtually all of the genetic variation within a quantitative trait (see Figure1) [21-26].

Furthermore, whole-genome prediction is more accurate than single-genome prediction because it better accommodates the variance caused by Mendelian segregation during gamete production than single-genome prediction [27-30]. In recent years, the growing availability and lowering prices of molecular markers covering the whole genome have enabled large-scale

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genomic selection in breeding programmes for various species [31]. GWS has the potential to be used in breeding programmes because it allows for the efficient selection of traits with low heritability, allows for the most efficient use of available genetic resources by selecting appropriate genetic crosses, and increases genetic gain per unit time by enabling the identification of the best individuals for selection early in the breeding process [32-35]. Therefore, here we have compiled the information regarding genomic selection of crop plants.

### **Plant breeding in the traditional manner**

Traditional plant breeding requires patience since it often takes 8 to 12 years to develop a new cultivar owing to the several procedures involved, such as cross-breeding to determine cultivar value for cultivation and usage. Genomic techniques, at the very least, allow for a decrease in the selection time because, unlike classical breeding, which does not allow for phenotyping in all generations, selection may be undertaken by genotyping in all generations. The merging of traditional breeding techniques with genomic technologies might be beneficial in this situation. Even with the new technologies, genotyping procedures must be first modified to be compatible with phenotyping, a time-consuming and expensive process that takes a long time [36-41]. It is important to note that molecular tools do not take the place of traditional breeding procedures.

Integrating both fields to increase selection accuracy while simultaneously decreasing the intervals between selection generations is of particular interest. Plant breeding is an art, a science, and a business that has only been around for a little over a century. Breeders have created agronomically better cultivars mainly via techniques that were established in the past century or so. Plant breeding must adapt and absorb new information as the difficulties to agricultural food supply become more challenging to overcome. Because of this progressive integration of molecular tools into ordinary breeding procedures, the accuracy, speed, and efficiency of breeding processes will improve. Even though the obstacles are significant, the opportunities are much bigger.

### **Breeding development is most effectively accomplished with the use of molecular markers**

In building genetic maps for distinct species, the use of molecular markers or polymorphic DNA sequences as chromosomal references is the fundamental technology [42] that underpins the process. Until the late 1980s, the great majority of species, with the exception of a few model organisms, did not have genetic map information available to them. As a result, there has been a significant revolution in the amount of information available on linkage groups in the genomes of diverse species in a brief period of time. Additionally, it should be highlighted that various disciplines of genetics, like population genetics, which lacks in-depth experimental data due to the use of molecular markers, have profited from the massive volumes of data created by the use of molecular markers.

### **Marker-assisted selection (MAS) and genome-wide selection (GWS) are two types of selection (GWS)**

Selection based on MAS has the following characteristics: it necessitates the establishment of marker-QTL associations (linkage analysis) for each family under investigation in other words, the identification of associations that are useful for

selection only within each mapped family must explain a significant proportion of the genetic variation for a quantitative trait that is controlled by a large number of loci with minor effects, and it must present a substantial proportion of the genetic variation for a quantitative trait that is in actuality but this conclusion is not confirmed, owing to the polygenic nature of quantitative characteristics and the significant influence of the environment on these traits, among other reasons [43-48]. A result of these issues is the identification of only a few QTLs with large effects, and these are insufficient to fully explain the genetic variation, MAS is only significantly better than selection by looking at phenotypic data when the studied family has been genotyped for a large number of individuals (on the order of 500 or more). Because of these characteristics, the deployment of MAS has been restricted, and the efficiency improvements have been relatively minor [49].

The attraction of molecular genetics for the benefit of applied genetic improvement is the direct use of DNA information for selection, which allows for high selection efficiency, highly rapid achievement of genetic gains from selection, and low cost when compared to traditional selection based on phenotypic data, as well as immediate achievement of genetic gains from selection. As a result, [50] introduced a new selection approach known as genomic selection (GS), sometimes known as genome-wide selection (GWS). GWS can be applied to all families under investigation in genetic improvement programmes. It has a high selectivity accuracy for selection based solely on markers (after their genetic effects have been estimated from phenotypic data in a sample of the selection population). It does not require prior knowledge of QTL positions (map), and it is not subject to type II errors associated with the selection of markers in linkage with QTLs [51].

### **Selection based on genomic information**

Gene set analysis (GS) is a highly effective approach that takes use of the linkage disequilibrium (LD) between markers and quantitative trait loci (QTL), as shown by [53-57]. Genotyping and phenotyping are performed on a training population, which is then used to estimate the marker effects that will be utilised to calculate the genomic breeding value (GEBV) of additional genotyped animals in the prediction population after they have been bred. The accuracy of the GEBV is critical for GS deployment [58]. The accuracy of GEBV depends on four factors: the level of linkage disequilibrium (LD) between the single nucleotide polymorphism (SNP) and the quantitative trait locus (QTL); the distribution of QTL effects; the size of the training data set; and the trait's heritability ( $h^2$ ) [59, 60].

### **Selection based on Genomic Information**

Genomic selection refers to strategies that employ genotypic data from throughout the whole genome to predict any attribute with sufficient precision to enable selection based only on that prediction. The possibilities for speeding the breeding cycle and the increase in selection intensity that may be achieved are mind-blowing [61]. A four-year breeding cycle, which includes three years of field testing, may be condensed into the four months it takes to develop and cross a single plant. There are thousands of qualified people who can be examined without ever stepping foot on a field [62].

In the case of GS, it is common practise to employ

populations that are distinct from the initial reference group. It is common practise to use both a training and validation dataset in combination with each other <sup>[36]</sup> while doing genomic selection <sup>[63]</sup>. There are three pieces to this puzzle: (1) phenotypic data from appropriate breeding material examined under a variety of environmental conditions, (2) molecular marker scores, and (3) information on ancestry or blood relations. As a result, the marker effect is evaluated, and the genomic breeding value or genetic values of new genotypes are only predicted on the basis of the marker effect using certain statistical methodologies. Candidate genotyping (but not phenotyping) was performed on the validation set's selection candidates (derived from the reference population) based on marker effects calculated in the training set <sup>[64]</sup>. Selection candidates are also included in the validation set (derived from the reference population).

Selecting for quantitative characteristics solely based on marker effects has had a significant impact on normal breeding procedures in both plant and animal breeding. However, in public plant breeding initiatives, the advantages of GS have only been examined via computer modelling rather than in-person experiments. In an applied plant breeding programme, genotyping is now less expensive than phenotyping because marker technology is constantly lowering the cost per data point and increasing the number of accessible markers <sup>[65]</sup>. Along with the ability to speed up the selection cycles, GS also provides the option to boost the selection gains achieved per unit of time. As a result, it is anticipated that alternating progeny field testing with selection based only on markers would maximise the genetic gains per unit of time. However, there are still some unanswered problems, such as how much (if any) genetic diversity would be lost due to the combination of phenotypic and genetic selection <sup>[66]</sup>.

Genomic selection is a strategy for determining the breeding value of individuals in a population by using genome-wide markers. A genotyped and phenotyped population is used to train or calibrate a statistical model, which is then used to anticipate breeding or genotypic values of non-phenotyped selection candidates for the purpose of performing GS. The training population (TP) is a genotyped and phenotyped population used for research purposes. When referring to the second group of individuals that have been genotyped but not phenotyped, it is referred to as "the breeding population" (BP). As a result, allelic association with loci linked with phenotypic diversity in the TP's performance is utilised to predict the BP's performance for a variety of qualities. According to the results of this work, a collection of diverse lines from a breeding programme that have been carefully phenotyped and genotyped may be used as a good training set for robust calibration models <sup>[67-70]</sup>.

It is generated from a mix of advantageous loci revealed in the genomes of individual patients with BP. This technique enables a direct estimation of the probability that each individual will have a superior genotype (i.e., high breeding value). The GEBV is used to determine which new breeding parents should be selected for the following generation of animals. The breeding cycle time is reduced since it is no longer required to wait for late filial generations (usually F6 or later in the case of wheat) before phenotyping quantitative measurements such as yield and its components. There is now complete genotyping and phenotyping of the third group of individuals, dubbed the validation population (VP). The GS

model's validity is assessed by computing the GEBV for the VP and correlating this value to the actual phenotypic value <sup>[71, 72]</sup>.

GS is defined as  $G = irA/y$ , where  $I$  represents selection intensity,  $r$  symbolises selection accuracy,  $A$  denotes additive genetic variation, and  $y$  is the time required to complete one breeding cycle (in years). Even if both genetic and phenotypic selection have equal selection intensities and genetic variance, it is possible to achieve greater gains per unit of time if the reduction in breeding cycle duration caused by genetic selection (GS) more than compensates for the reduction in selection accuracy caused by phenotypic selection (PS). When reasonable assumptions regarding selection accuracy, breeding cycle lengths, and selection intensities are employed, comparing genetic selection (GS) to traditional breeding may boost annual genetic gain in both animal and crop breeding <sup>[73-75]</sup>. When reasonable assumptions regarding selection accuracy, breeding cycle lengths, and selection intensities are adopted, genetic selection may boost annual genetic gain in both animal and crop breeding. For traits with a long generation time or that are difficult to evaluate (for example, insect resistance, bread-making quality, and others), GS becomes more cost effective or easier to perform than PS, allowing for the characterization of a greater number of candidates at a given cost and, as a result, an increase in the selection process's intensity <sup>[76]</sup>.

The GEBV is calculated by combining beneficial loci in each individual's genome, and it offers a direct estimate of the probability that each individual will have a better phenotype than the rest of the population (i.e., high breeding value). Because it is no longer necessary to wait for late filial generations (typically F6 or later in the case of wheat) to phenotype quantitative traits such as yield, susceptibility to biotic and abiotic stresses, or other phenotypic traits, GEBV-based selection of new breeding parents results in a shorter breeding cycle duration. As suitable assumptions regarding selection accuracies, breeding cycle durations, and selection intensities are made, genetic selection (GS) may significantly boost annual genetic gain in animal and crop breeding when compared to traditional breeding <sup>[77-80]</sup>. When compared to traditional breeding, genetic selection (GS) has the ability to boost the genetic gain each year in both animal and crop breeding. For traits with a long generation time or that are difficult to evaluate (for example, insect resistance, bread-making quality, and others), GS becomes more cost effective or easier to perform than PS, allowing for the characterization of a greater number of candidates at a given cost and, as a result, an increase in the selection process's intensity. For the purposes of this discussion, genetic selection (GS) has a number of advantages over conventional selection (PS), including a shorter selection duration and an improvement in accuracy, intensity, effectiveness, and gains per unit of time, all of which result in time and money savings. This strategy generates more reliable results while being less damaging to the environment <sup>[81-84]</sup>. This allows the development of new crop kinds to address the challenges posed by climate change and diminishing arable land to proceed much more rapidly and effectively. The computation of GEBVs is the core genetic screening procedure. People with just genotypic data are calculated GEBVs using a model that has been "trained" on individuals with both phenotypic and genotypic data. GEBVs of selection candidates (for example, breeding lines) with only genotypic data are calculated using the "training

population," which consists of individuals with both phenotypic and genotypic data. The training population is used to estimate model parameters that will then be used to calculate GEBVs of selection candidates (for example, breeding lines) with only genetic data. These GEBVs are then used to select individuals for progression in the breeding cycle based on their genetic characteristics. Therefore, the selection of an individual without phenotypic data may be accomplished by developing a model to anticipate the individual's breeding value, which can then be used to make the selection. A training population representative of selecting candidates in the breeding programme to which GS will be applied must be used to ensure the maximum accuracy of GEBV estimations<sup>[85, 86]</sup>.

Future elite and parental lines may be chosen based on their GEBV rather than their phenotypic records from extensive field testing, given the high accuracy of GEBV shown in studies. The most obvious consequence of this situation would be a significant increase in the pace of the breeding cycle, which would result in an increase in selection gains per unit of time. This transition would also have a significant impact on the function of phenotyping in plant breeding. In a GS-driven breeding cycle, phenotyping aims to quantify or re-estimate the impact of genetic markers. At this stage, it is unclear whether it will be more beneficial to review just the best lines or if it will be more advantageous to examine a small number of lines with high replication<sup>[87-90]</sup>.

## Conclusion

The cost per data point for molecular markers has fallen by a factor of two or three since the development of high-throughput genotyping. This reduction was made possible by three parallel advancements: Numerous single nucleotide polymorphism (SNP) markers have been identified in a variety of species; high-throughput technologies such as multiplexing and gel-free DNA arrays for screening SNP polymorphisms have been developed; and automation of the marker-genotyping process, including streamlined DNA extraction procedures, has been developed. Genetic selection can accelerate breeding progress by increasing selection intensity while shortening the breeding cycle. The methodology of genome-wide association studies (GWAS) has progressed to the point where it is now a powerful tool for the analysis of simple traits under additive genetic scenarios and the dissection of complex genetic architectures. Despite its infancy, field-based high-throughput phenotyping shows signs of maturity, with the capacity to quantify features more rapidly and precisely than previously thought possible. The combined power of genomics and phenomics will usher in an age of inbreeding and functional genomics that has never been seen before.

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