Crop improvement through Marker Assisted Selection

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**ABSTRACT**

The strong and effective method of marker-assisted selection (MAS) is used in crop improvement to speed up the breeding process and improve the selection of desirable traits. It is the method of choosing agriculturally significant features for crop development utilizing morphological, biochemical, or DNA markers as indirect selection criteria. Traditional breeding techniques are frequently labor- and time-intensive, and there is no assurance that the desired qualities will be obtained. But the development of molecular markers and advancements in genomics have completely changed field of plant breeding. Breeders can drastically cut the length of breeding cycles by locating and utilizing markers that are highly correlated with the trait of interest. In this study, we provide an overview of the benefits of MAS and its most extensively used applications in plant breeding, using different as examples. The big challenge for plant breeders in the coming decades will be to achieve a significant impact on crop improvement using MAS.

**Keywords**: Marker assisted selection, Crop improvement, Trait

1. **INTRODUCTION**

Marker-assisted selection (MAS) is a powerful and sophisticated approach used in crop improvement programmes to accelerate breeding and improve the efficiency of creating superior plant varieties. Traditional breeding procedures can be time-consuming and labor-intensive, necessitating numerous generations to acquire desired crop qualities. DNA marker technology, resulting from studies in molecular genetics and genomics, is one field of biotechnology that has considerable potential for plant breeding. Because of genetic linkage, DNA markers can be employed to detect allelic variation in the genes underlying these traits. The use of DNA markers to aid in plant breeding could considerably improve efficiency and precision. Marker-assisted selection (MAS) involves the use of DNA markers in plant breeding and is a component of the emerging discipline of "molecular breeding." (Collard *et al*., 2008). The basic purpose of crop improvement with MAS is to select plants with specified desirable molecular features. These properties could be connected to yield, disease resistance, stress tolerance, nutritional content, or any other economic or agronomic importance. Traditional breeding takes time and is highly dependent on environmental variables. It takes between eight and twelve years to breed a new variety, and even then, the introduction of an enhanced variety cannot be assured. As a result, breeders are very interested in emerging technologies that could improve the efficiency of this process. By utilising a variety of unique techniques to enhance selection strategies, molecular marker technology provides such a potential. (Akhtar *et al*. 2010). A fundamental challenge that must be addressed is how to improve the efficacy of marker-assisted selection for quantitative features by properly characterising target genes. Fortunately, field design and statistical methodologies for QTL mapping have advanced substantially during the last decade. Field data from diverse settings can be incorporated into a joint analysis to evaluate the QXE and thus identify 'stable' QTLs across environments using the most recent mathematical methodologies, such as composite interval mapping. Furthermore, when combined with a thorough linkage map, composite interval mapping allows for a more exact identification of QTLs in the genome as well as a better identification of coupled QTLs (linked QTLs in which the favorable allele is inherited from the same parental line [3].

**RESULTS AND DISCUSSION**

Marker-assisted selection has been used successfully in a variety of crops, including rice, maize, wheat, soybeans, and many more. Its combination with traditional breeding methods has resulted in the development of enhanced crop varieties that address modern agriculture's difficulties, such as climate change, pest and disease threats, and rising food security requirements.

The late-maturing high-yielding rice variety reeta from the donor parent, Swarna-Sub1, was introgressed with the quantitative trait loci (QTLs) Sub1 for submergence and Pup1 for low phosphorus stress tolerance as well as the narrow-grained trait GW5. The generated lines shared all morphoquality characteristics with the receiving parent, were better yielding, possessed submergence, and had low phosphorus stress-tolerance. Reeta-Panidhan (CR Dhan 413), a prospective pyramided line, has been released for the flood-prone areas of Odisha state using marker assisted breeding [4].

Using MAS giant embryos and golden-like traits combined in colored rice. It proves that for the biofortification purpose, the combination of molecular markers and traditional breeding method can be effectively used. PFR32 and RFR13 can become valuable products and adapt to the current agricultural community [5].

Widespread yield losses from tomato bacterial, fungal, and viral illnesses are to blame, particularly in humid growing settings. The uncommon recombination events that joined these resistance loci into a connected cassette that can be inherited collectively in subsequent crosses were sought after using marker-assisted selection. A novel connection of Xv3/Rx4 and Ty-2 was discovered using a pedigree breeding technique and marker-assisted selection. The results of this study indicate that the trait markers on chromosome 11 are useful for choosing plants that are resistant to the target illnesses because they are closely related to the corresponding resistance loci [2].

The use of markers in selection (MAS) enables breeding to be completed more quickly while using fewer resources. The major fiber quality traits, such as fiber strength, fiber length, fiber uniformity, and micronaire, can be improved by utilizing novel QTLs and SSR markers. The first generation of MAS-derived cotton cultivars in Uzbekistan are the new cultivars "Ravnaq-1/Ravnaq-2," which were registered with the State Variety Testing Commission of Uzbekistan in 2014–2017. These findings demonstrate the potential of MAS in cotton breeding by demonstrating how the LD-block of chromosome 7 and its mapped molecular marker(s) and donor genotypes effectively assisted in the accurate and quick transfer of higher fiber quality QTLs to the commercially cultivated Upland cotton cultivars [6].

In total 23 successful cross combinations, obtained by a half diallel cross among 16 parents, including eight frost-tolerant advanced breeding lines and eight cultivars, were used to map the genetic loci for frost tolerance and to create a molecular marker-assisted selection (MAS) system. Three candidate regions related to frost tolerance on chromosomes II, V, and IX were mapped by bulked segregant analysis (BSA). Furthermore, six SNP markers associated with frost tolerance from candidate regions were developed and validated. Above all, a MAS system for the frost tolerance screening of early breeding offspring was established. The study highlights the practical advantages of applying diallel populations to broaden and improve frost-tolerant germplasm resources using marker assisted selections in potato [7].

Marker assisted selection can be effectively used for resistance breeding in a wheat to control stripe rust. Gene pyramiding is considered to be an effective way to enhance durable disease resistance in wheat. In this experiment, a panel of Yr gene pyramiding lines (consisting of 3–8 Yr genes) with cv. Chuanyu12 as background parent were constructed by using marker assistant selection and evaluated under currently epidemic Pst races. The results showed that the number of pyramided Yr genes was significant correlated with stripe rust resistance (p\0.001). Yr15, Yr62 and Yr65 are effective to the current Pst races. Pyramiding more than four effective or partially effective Yr genes can provide enough resistance to stripe rust. The results showed that the number of pyramided Yr genes was significant correlated with stripe rust resistance (p\0.001). Yr15, Yr62 and Yr65 are effective to the current Pst races. Moreover, the effects of Yr gene pyramids on currently prevalent Pst races and agronomic traits were also evaluated, and Yr-gene pyramiding lines with desirable agronomic traits were obtained for durable controlling Pst in wheat breeding [8].

Powdery mildew, caused by the biotrophic fungus Blumeria graminis (DC.) Speer f. sp. tritici emend. E .J. Marchal, is one of the most destructive diseases that threatens the security production of common wheat (Triticum aestivum L.) [10]. This disease mainly presents on the leaf in the form of white colonies at the seedling stage and also on spikes at later growth stages. Infection by B. graminis f. sp. tritici will reduce chlorophyll content, affect photosynthesis, and typically decrease wheat yield by 10 to 15% and up to 62% in severe cases [11]. The quality of ﬂour will also be affected [10]. Characterization of powdery mildew resistance genes is useful in parental selection and the development of disease-resistant cultivars. KN0816, a Chinese wheat breeding line, exhibits improved agronomic performance and powdery mildew resistance at all growth stages. Genetic investigation of KN0816 populations crossed with susceptible parents revealed that a single dominant gene, tentatively named PmKN0816, gave seedling resistance to various B. graminis f. sp. tritici isolates. PmKN0816 was mapped to the Pm6 interval on chromosomal arm 2BL using polymorphic markers associated to the catalogued genes Pm6, Pm52, and Pm64, and bordered by the markers CISSR02g-6 and CIT02g-2, both with 0.7 cM genetic distances. The marker alleles of PmKN0816 differed from those of other powdery mildew resistance genes on 2BL, including Pm6, Pm33, Pm51, Pm64, and PmQ, according to an analysis of closely connected molecular markers. PmKN0816 is most likely a new powdery mildew resistance gene with effective resistance to all 14 investigated B. graminis f. sp. tritici isolates based on its genetic and physical locations and response pattern to distinct B. graminis f. sp. tritici isolates. PmKN0816 is projected to become an important resistance gene in wheat breeding because to the superior agronomic performance of KN0816 mixed with the resistance. Closely connected markers of PmKN0816 were assessed in order to transfer it to diverse genetic backgrounds using marker- assisted selection (MAS), and four of them (CIT02g-2, CISSR02g-6, CIT02g-10, and CIT02g-17) were verified to be usable for MAS in different genetic backgrounds [9].

Sugar beetroot (Beta vulgaris L.) agriculture is jeopardised by Rhizoctonia solani, which causes Rhizoctonia crown and root rot. Breeding programmes prioritise the production of resistant cultivars aided by marker-assisted selection. The discovery of a single-nucleotide polymorphism (SNP) marker linked to Rhizoctonia resistance using restriction site-associated DNA (RAD) sequencing of two geographically distinct sets of plant materials with varying degrees of resistance/susceptibility, allowing for a more diverse selection of superior genotypes. The SAMtools variant calling method was used, and the resulting raw SNPs from RAD sequencing (15,988 and 22,439 SNPs) explained 13.40% and 25.45% of the phenotypic diversity in the two sets of material from distinct sources of origin, respectively. An association analysis was performed independently on both datasets, and mutually occurring significant SNPs were filtered using principal component analysis (PCA) biplots based on their contribution to the phenotype. To provide a ready-to-use marker for the breeding community, a systematic molecular validation of significant SNPs distributed across the genome was undertaken to combine high-resolution melting, Sanger sequencing, and rhAmp SNP genotyping. We report that RsBv1 located on Chromosome 6 (9,000,093 bp) is significantly associated with Rhizoctonia resistance (p < 0.01) and able to explain 10% of the phenotypic disease variance. The related SNP assay is thus ready for marker-assisted selection in sugar beet breeding for Rhizoctonia resistance [12].

Marker-assisted selection is a frequently used method in tomato resistance breeding. Extensive screening of 964 tomato lines was performed under controlled experimental conditions to determine the resilience of key molecular markers typically employed in MAS. Initially, 36 molecular markers targeting 26 resistance genes (R genes) and 14 important diseases were tested. They used standard molecular biology and bioinformatics approaches for analysis, with polymorphism, accuracy, and clarity of amplicons serving as marker selection criteria. Following an initial examination, 20 of these markers were identified as efficient markers, of which 8 were considered gene-based markers and referred to as ideal markers. Extracted from the PCR results, 18 R genes that control 12 illnesses were classified as efficient markers. On the other hand, grouping breeding lines based on the number of R genes carried indicated that 62% of the lines were devoid of R genes, while 38% had many types of R genes. This gives a way to better understand novel sources of resistance in breeding lines. Finally, these efficient markers and their limited PCR conditions can be proposed as the foundation of a diagnostic kit for MAS applications against 12 major tomato diseases, and the identified resistant breeding lines could be conserved and propagated as different sources of resistance for the development of new resistant varieties. As a result, high efficiency combination of the key R genes and their pyramiding into commercial tomato varieties are proposed to be adopted as a pragmatic method in areas with high disease risk [13].

Sorghum is an essential staple food crop in drought-prone areas of Sub-Saharan Africa, where rainfall is unpredictable and unevenly distributed. Sorghum is a drought-tolerant crop with a reasonable yield when compared to other cereal crops, although abiotic stress reduces output. Stay-green sorghum variants keep green functional leaves during post-anthesis drought stress, making it an important crop for food and nutritional security. Nonetheless, due to climate change caused by human activity, it is difficult to maintain constancy of tolerance through time. Drought in sorghum is addressed by a variety of methods, including breeding drought-tolerant sorghum utilising traditional and molecular technologies. The problem with traditional approaches is that they rely on phenotyping staygreen, which is complicated in sorghum because it is composed of numerous genes and environmental factors. Marker assisted selection, which involves the use of DNA molecular markers to map QTL related with stay-green improvement in sorghum, has been effective to augment stay-green improvement. It entails matching phenotypic field data with QTL mapping related with the stay-green trait for introgression into senescent sorghum varieties by comparing with phenotypic field data. The study used marker-assisted backcrossing to improve the stay-green (STG) properties of farmer-preferred sorghum varieties in Tanzania. A total of 752 individuals from five BC2F1 populations and their parents were genotyped using previously published KASP markers associated to STG 3A and STG 3B QTL. The S35\*Pato background had the most individuals with heterozygous alleles (37) in the BC2F1 populations, while only seven individuals descended from the B35\*Wahi parents' background had heterozygous alleles. In BC2F1 populations, beneficial alleles were found at 18 of the 30 single nucleotide polymorphism (SNP) markers. The B35\*NACO Mtama 1 background population had the maximum grain yield (0.127 kg/panicle) in the BC2F1 generation. The existence of advantageous alleles in homozygous situations at markers loci associated with STG 3A and STG 3B QTLs in BC2F3 populations was shown by genotypic analysis, indicating successful introgression of STG QTLs from donor parents to recurrent parents. The genotype NA316C had the highest mean grain weight (0.068 kg/panicle) across all water irrigation regimes. As a result, our findings show that marker-assisted backcrossing can be used to improve drought resistance in locally adapted sorghum varieties in Africa [14].

Maize is an excellent source of nutrients and is a staple meal in many countries of the world, including India. Creating a maize genotype with increased levels of lysine and tryptophan, as well as -carotene, can help reduce protein-energy malnutrition (PEM) and vitamin A deficiency (VAD). To increase lysine and tryptophan content by transferring the opaque-2 (o2) gene from donor HKI163 to -carotene-rich inbred lines, UMI1200+ and UMI1230+. F1, BC1F1, BC2F1, BC2F2, and BC2F3 plants were created with an o2 line HKI163 and two -carotene-rich inbred lines, UMI1200+ and UMI1230+ as parents. The target genes were chosen via foreground selection with the related marker umc1066 for the o2 gene and the marker crtRB1 3′TE for the crtRB1 gene. The background selection used a total of 236 simple sequence repeat (SSR) markers spread uniformly across the maize genome. Individual plants homozygous at the crtRB1 locus and heterozygous at the o2 locus were selected and backcrossed to produce BC2F1 plants to fix the crtRB1 allele in the BC1F1 stage. In addition, the selected heterozygous BC2F1 plants from both crossings were selfed to produce BC2F2 plants, which were then selected for the target gene and selfed to produce BC2F3 lines. Five improved lines with homozygous marker alleles for the crtRB1 and o2 genes were found from each cross, with RPG recovery ranging from 86.75 to 91.21% in UMI1200+HKI163 and 80.00 to 90.08% in UMI1230+HKI163. The enhanced lines performed well agronomically and exhibited high levels of lysine (0.294-0.332%), tryptophan (0.073-0.081%), and -carotene (6.12-7.38 g/g). These improved lines have the potential to be utilised as genetic resources for maize improvement [15].

**CONCLUSION**

It is crucial that plant breeding keep up its impressive advances in crop development. It appears that contemporary breeding projects are continuing to advance through the use of conventional breeding techniques. Although there hasn't been much of an impact on variety development thus far, MAS could help plant breeders immensely in achieving this goal. Greater breeding programme integration, a thorough understanding of the current obstacles, and the creation of practical solutions are necessary for the potential of MAS to be realised. Utilising the benefits of MAS above traditional breeding could significantly influence fight against biotic and abiotic stresses along with yield and quality improvements. In the near future, the high cost of MAS will remain a significant barrier to its implementation for some crop species and plant breeding in developing nations. To suit particular crops, characteristics, and financial constraints, customised MAS techniques may need to be developed. The price of MAS may be significantly reduced with new marker technology. If the new techniques' efficacy is confirmed and the necessary equipment is easily accessible, MAS should be more broadly useful for crop improvement.

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