Marker Assisted Breeding for Disease Resistance in Vegetables

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Marker-assisted selection is an indirect method that facilitates the selection of target traits using tightly linked DNA markers. Marker-assisted selection (MAS) is unlikely to completely supplant phenotypic selection (PS), particularly in the realm of disease resistance, as a final evaluation of breeding lines is always required, irrespective of how closely a marker is linked to a gene or quantitative trait loci (QTL). Marker-assisted selection (MAS) is a powerful tool that can be used to accelerate the breeding process and improve the efficiency of selecting for desired traits. By using molecular markers linked to specific genes or traits. Marker-assisted selection enables the rapid access, transfer, and combination of resistance genes. There is no longer a requirement to conduct time-consuming and labour-intensive artificial inoculation tests to evaluate the resistant phenotype. There is no necessity to maintain pathogens or pests on the host (or their alternate hosts) when utilizing marker-assisted selection. Marker-Assisted Selection (MAS) is a powerful tool in biotic stress breeding (Hasan et al., 2021). It allows for the selection of traits with low heritability, which are often difficult to identify through traditional phenotypic screening. Additionally, MAS facilitates the easy identification and transfer of recessive genes, reduces the problem of linkage drag, enables the pyramiding of multiple disease resistance genes, accelerates the recovery of the recurrent parent genome in backcross breeding, and allows for the early identification of resistant lines at the seedling stage. MAS enhances breeding efficiency by increasing selection precision and intensity, enabling early-generation selection for resistance genes against prevalent pests and diseases. This ultimately leads to increased genetic gain and reduced costs and time. Various MAS schemes in resistance breeding are marker-assisted backcrossing (MABC), marker-assisted recurrent selection (MARS), marker-assisted gene pyramiding and, genomic selection (GS) (Mehraj et al., 2020).

Marker-assisted backcrossing

The backcrossing approach, pioneered by Harlan and Pope, is a widely adopted plant breeding technique. It is primarily used to transfer one or a few specific traits from a donor parent into an elite variety. The elite variety often possesses numerous desirable attributes but lacks certain characteristics. By repeatedly backcrossing the progeny with the elite parent, the goal is to minimize the contribution of the donor genome while retaining the desired traits Vanitha et al., 2024.

Marker-assisted recurrent selection

Marker-Assisted Recurrent Selection (MARS) is a breeding strategy that utilizes molecular markers at every generation to target all the economically important traits. MARS involves an initial F2 population improvement cycle combining phenotypic and marker-based selection, followed by three marker-based selection cycles. In a biparental population, both parents can contribute favorable alleles to QTL mapping. The resulting genotype carried the mosaic of chromosomal segments of both the parents. To achieve such ideal genotypes, multiple generations of crossing are necessary. MARS is particularly effective for complex traits like abiotic and biotic stress resistance and yield, making it a valuable tool for forward breeding of native genes. The success of MARS depends on factors such as the distribution of favorable alleles, selection efficiency, accuracy, and the strength of marker-trait associations within breeding programs (Singh et al., 2021).

Marker-assisted gene pyramiding

Marker-assisted selection (MAS)-based gene pyramiding is a promising method to combine desired genes from multiple parents into a single genetic background for durable resistance against stresses. By utilizing DNA markers, genes or quantitative trait loci (QTLs) can be identified at each breeding generation, accelerating the gene pyramiding process. Gene pyramiding aims to develop a perfect genotype where favorable alleles are homozygous at all loci. This involves two primary steps: pedigree development and fixation. The pedigree step focuses on accumulating targeted genes from multiple parents into a single root genotype. The subsequent fixation step involves fixing these target genes in a homozygous state, ultimately to create the ideal genotype from a single genotype (Haque et al., 2021).

Genomic selection

GS is a method that uses molecular markers distributed throughout the genome, such as single-nucleotide polymorphisms (SNPs), which is preferred for complex traits that are affected by many genes and are strongly affected by the environment. In the GS approach, QTLs and genes identified are in linkage disequilibrium with at least one marker, reducing the risk of missing small-effect QTLs. This facilitates a more precise understanding of the genetic basis of polygenic resistance to crop diseases. GS is considered a more powerful approach than MARS and may become a crucial tool in future resistance breeding programs (Ahmar et al., 2021).

Table 1: Genes and QTLs are utilized in marker-assisted breeding programs to improve disease resistance in vegetable crops

Vegetable Crop	QTL/gene	Characters	Ch. No.	Marker	Reference
Tomato	*I-3*	Resistance to Fusarium wilt	7	SCAR/CAPC	Zhang et al., 2021
	Ph-2	Resistance to Late blight	10	CAPC	Zhi et al., 2021
	Pto	Resistance to Bacterial speck	5	SCAR/CAPC	Zhang et al., 2021
	Tm-2/Tm-22	Resistance to Tomato mosaic virus	9	CAPS/SCAR/RAPD	Zhang et al., 2021
	QTL	Tolerance to salt	6	SSR	
Pepper	*AnR$_{GO}$5*	Resistance to Anthracnose	5	SCAR	Zhao et al., 2020
Eggplant	*ERs1 (EBWR9)*	Resistance to Ralstonia solanacearum phylotype I	9	SNP	Salgon et al., 2017
Cucumber	*pm5.2*	Resistance to Powdery mildew	5	CAPS	Zhang et al., 2021
	Dm4.1.1	Resistance to Downy mildew	4	551 bp deletion	Berg et al., 2020
	psl	Resistance to Angular leaf spot	5	SNP08	Wang et al., 2019

Marker-assisted selection applications in vegetable breeding

Marker-assisted selection is widely used in vegetable breeding programs to incorporate and stacking genes, especially for developing cultivars with multiple disease resistance traits. SCAR, CAPS, and other PCR-based markers are commonly utilized in both public and private tomato breeding programs to select for major-gene disease resistance traits. Several trait-linked markers have been developed and are actively employed in pepper breeding programs for marker-assisted selection. These include allele-specific CAPS markers for genes such as *pvr1*, *pvr11*, *pvr12*, and *pvr2* (Rubio et al., 2008; Holdsworth and Mazourek, 2015). Additionally, closely linked markers for resistance to diseases in pepper, such as those caused by phytophthora capsici, pepper mottle virus (PePMoV), tomato spotted wilt virus (TSWV), and anthracnose, have been developed for marker-assisted selection (Holdsworth and Mazourek, 2015; Kim et al., 2017c; Zhao et al., 2020). Notably, resistance genes Bs1, Bs2, and Bs3 have been successfully introgressed into various commercial pepper cultivars. Additionally, marker-assisted gene pyramiding of Bs5 and Bs6 has provided broad-spectrum resistance against Xanthomonas spp. (Vallejos et al., 2010). Major QTLs for resistance to bacterial wilt have been mapped to chromosome 1 (from Capsicum accession LS2341),

linked to SSR marker CAMS451 (Mimura et al., 2009), and chromosome 10 (from *C. annuum BVRC1*), linked to marker ID10-194305124 (Du et al., 2019). Genes and QTLs are utilized in marker-assisted breeding programs for disease resistance in vegetable crops are listed below Table 1.

References

Ahmar, S., Ballesta, P., Ali, M. and Mora-Poblete, F. (2021). Achievements and challenges of genomics-assisted breeding in forest trees: From marker-assisted selection to genome editing. International Journal of Molecular Sciences. 22(19), 10583.

Du, H., Wen, C., Zhang, X., Xu, X., Yang, J., Chen, B. and Geng, S. (2019). Identification of a major QTL (qRRs-10.1) that confers resistance to Ralstonia solanacearum in pepper (Capsicum annuum) using SLAF-BSA and QTL mapping. IJMS 20: 5887.

Haque, M. A., Rafii, M. Y., Yusoff, M. M., Ali, N. S., Yusuff, O., Datta, D. R., ... and 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.

Hasan, N., Choudhary, S., Naaz, N., Sharma, N. and Laskar, R. A. (2021). Recent advancements in molecular marker-assisted selection and applications in plant breeding programmes. Journal of Genetic Engineering and Biotechnology. 19(1), 128.

Holdsworth, W. L. and Mazourek, M. (2015). Development of user-friendly markers for the pvr1 and Bs3 disease resistance genes in pepper. Mol. Breed. 35: 28.

Kim, S. B., Kang, W. H., Huy, H. N., Yeom, S. I., An, J. T., Kim, S., Kang, M. Y., Kim, H. J., Jo, Y. D., Ha, Y., Choi, D. and Kang, B. C. (2017). Divergent evolution of multiple virus-resistance genes from a progenitor in Capsicum spp. New Phytol. 213: 886–899.

Mehraj, H., Akter, A., Miyaji, N., Miyazaki, J., Shea, D. J., Fujimoto, R. and Doullah, M. A. U. (2020). Genetics of clubroot and Fusarium wilt disease resistance in Brassica vegetables: The application of marker assisted breeding for disease resistance. Plants. 9(6), 726.

Mimura, Y., Kageyama, T., Minamiyama, Y. and Hirai, M. (2009). QTL analysis for resistance to Ralstonia solanacearum in Capsicum accession 'LS2341'. J. Japan. Soc. Hort. Sci. 78: 307–313.

Rubio, M., Caranta, C. and Palloix, A. 2008. Functional markers for selection of potyvirus resistance alleles at the pvr2-eIF4E locus in pepper using tetra-primer ARMSPCR. Genome. 51: 767–771.

Salgon, S., Jourda, C., Sauvage, C., Daunay, M. C., Reynaud, B., Wicker, E. and Dintinger, J. (2017). Eggplant resistance to the Ralstonia solanacearum species complex involves CRITICAL REVIEWS IN PLANT SCIENCES 357 both broad-spectrum and strain-specific quantitative trait loci. Front. Plant Sci. 8: 828.

Singh, M., Nara, U., Kumar, A., Thapa, S., Jaswal, C. and Singh, H. (2021). Enhancing genetic gains through marker-assisted recurrent selection: from phenotyping to genotyping. Cereal Research Communications. 1-16.

Vallejos, C. E., Jones, V., Stall, R. E., Jones, J. B., Minsavage, G. V., Schultz, D. C., Rodrigues, R., Olsen, L. E. and Mazourek, M. (2010). Characterization of two recessive genes controlling resistance to all races of bacterial spot in peppers. Theor. Appl. Genet. 121: 37–46.

Vanitha, J., Mahendran, R., Raveendran, M. and Jegadeeswaran, M. (2024). Marker assisted backcross analysis for high temperature tolerance in rice. Vegetos. 37(2), 731-737.

Zhang, C., Badri Anarjan, M., Win, K. T., Begum, S. and Lee, S. (2021). QTL-seq analysis of powdery mildew resistance in a Korean cucumber inbred line. Theoretical and applied genetics. 134, 435-451.

Zhang, J. and Panthee, D. R. (2021). Development of codominant SCAR markers to detect the Pto, Tm22, I3 and Sw5 genes in tomato (Solanum lycopersicum). Plant Breeding. 140(2), 342-348.

Zhao, Y., Liu, Y., Zhang, Z., Cao, Y., Yu, H., Ma, W., Zhang, B., Wang, R., Gao, J. and Wang, L. (2020). Fine mapping of the major anthracnose resistance QTL AnRGO5 in Capsicum chinense 'PBC932'. BMC Plant Biol. 20: 189.

Zhao, Y., Liu, Y., Zhang, Z., Cao, Y., Yu, H., Ma, W., Zhang, B., Wang, R., Gao, J. and Wang, L.

(2020). Fine mapping of the major anthracnose resistance QTL AnRGO5 in Capsicum chinense 'PBC932'. BMC Plant Biol. 20: 189.

Zhi, X., Shu, J., Zheng, Z., Li, T., Sun, X., Bai, J., ... and Li, J. (2021). Fine mapping of the Ph-2 gene conferring resistance to late blight (Phytophthora infestans) in tomato. Plant Disease. 105(4), 851-858.

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