

Review Article**Molecular Markers Improve Abiotic Stress Tolerance in Crops: A Review*****¹Meenajabi Naragund and ²Murtujasab S.****Article Info**^{1,2}Karnataka University
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Publisher's Note: IJABR Press stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.**Copyright:** ©2025 by the author(s). Licensee IJABR Press, India. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution- Share Alike (CC BY -SA) license.**Abstract:**

Plants face various abiotic stresses like temperature extremes (heat and frost), drought, and salinity, which significantly reduce agricultural yields. These environmental factors affect nutrient management, biosynthetic processes, and overall plant growth. Genetically, stress interferes with the full expression of a plant's genetic potential. Several molecular markers, such as RAPD (Random Amplified Polymorphic DNA) and SSR (Simple Sequence Repeat), are used to analyze crop stress tolerance. These markers are also valuable in QTL (Quantitative Trait Loci) mapping for stress-related genes. Genes like dehydrins and saltol regulate drought and salinity responses. Single-gene SNP (Single Nucleotide Polymorphisms) markers are used for genetic mapping and sequencing of stress-related traits in inbred lines, aiding in marker-assisted breeding to enhance stress tolerance.

Keywords: Abiotic stress; genotype; salinity; drought; heat**1. Introduction**

Plants experience various climatic stresses during their growth cycles, including biotic stresses (herbivore attacks, pathogen infections) and abiotic stresses (heat, cold, drought, nutrient deficiencies, high salt levels, and toxic metals like arsenic, cadmium, and aluminum). Temperature extremes, drought, and salinity are the main factors affecting agricultural crop yields and food security. These stresses can alter plant distribution and are worsened by climate change. Plants respond by activating defense mechanisms involving phytohormones (like jasmonic acid, abscisic acid, ethylene, and salicylic acid) and reactive oxygen species (ROS), which reprogram genetic and metabolic systems to reduce damage [8].

Abiotic stresses primarily affect crop production by disrupting plant growth. These stresses trigger three phases: alarm (stress initiation), resistance (defense activation), and exhaustion (stress-induced damage). Salinity hampers growth by disturbing water retention and ion balance, while drought stress reduces plant survival and development, especially when water is scarce or evapotranspiration is high. Environmental changes and global warming intensify these stresses, hindering plant genetic expression [1-3].

DNA markers play a crucial role in genetic analysis, offering insights into genetic diversity, parent identification, and the development of high-resolution genetic linkage maps. Molecular markers, such as PCR-based markers (SNP, SCAR, SSR), are used for gene mapping and identifying stress-resilient traits. These markers enhance breeding strategies and enable the genetic control and screening of stress-resistance traits in crops, providing a pathway for improved agricultural resilience.

2. Abiotic Stress Impact on Agricultural Crops

Heat and drought are major abiotic stresses that reduce crop yields and agricultural productivity. For example, a 40% reduction in water availability can lower maize yields by up to 40% and wheat by 21%. In Africa, drought reduces cowpea yields by 34-68%. These stresses lead to excessive reactive oxygen species (ROS) production, damaging vital plant components, which negatively impacts growth [11]. Abiotic stresses affect 91% of global agricultural land, causing 50% of production losses. Climate change exacerbates these effects, making stress-resistant crop genotypes and improved agronomic practices essential for mitigating the damage.

Heat stress, linked to rising temperatures, reduces germination, photosynthesis, and crop yields. It disrupts reproductive cycles, damaging anther development and pollen viability. Drought stress decreases photosynthetic activity, cell wall elasticity, and stomatal function, affecting nutrient absorption and crop health. Both drought and salinity overlap in their physiological impacts on plants.

To address these challenges, improving plant defenses and adapting stress-tolerant traits is

crucial for maintaining crop production. Molecular genetics can help identify stress defense systems and enhance plant resilience. Despite these efforts, most agricultural land faces stress, and continued focus on improving stress tolerance and resource conservation technologies is necessary.

3. DNA Marker Applications for Abiotic Stress Tolerance

3.1. RAPD Marker Analysis for Salinity and Drought Stresses

Random Amplified Polymorphic DNAs (RAPDs) are PCR-based markers that do not require preliminary sequence data, making them cost-effective and efficient for screening large numbers of samples. RAPDs are useful for identifying salinity stress-tolerant genes in crops. They help differentiate salt-resistant from salt-sensitive genotypes, enabling breeding programs to improve crop resilience. In wheat, RAPDs identified genetic diversity in salt-resistant plants, while in cotton, RAPD markers highlighted DNA variations caused by NaCl stress. RAPD markers are also used to assess genomic template stability (GTS), which measures DNA damage and mutations due to stress. For example, RAPD analysis in cotton showed that salt-resistant varieties had lower GTS values, indicating more stable DNA. Similarly, in wheat, RAPD markers identified genes related to drought resistance, offering insights for breeding drought-resistant crops [7]. In tomatoes, RAPD markers associated with heat resistance were identified, helping to select heat-tolerant genotypes for breeding. These findings demonstrate the utility of RAPDs in identifying stress-resistant traits and advancing

crop improvement under abiotic stress conditions [4].

Table 1. Application of DNA markers in horticultural crops for abiotic stress.

Crop	DNA Marker	Abiotic Stress	Objective	Reference
Citrus	Quantitative trait loci (QTL)	Salinity	Genetic evaluation of salt resistance concerning physiological and vegetative characteristics	Raga et al 2016 [8]
Tomato	RAPD	Heat	To confirm all genotypes by SCAR that had been recorded by RAPD markers	Damra et al 2017 [2]
Cassava	Expressed sequence tags–simple sequence repeat (EST–SSR) markers	Drought	Marker-assisted selection of progeny tolerance to drought stress	Wang et al 2017 [9]

3.2. Stress Tolerance in Hybrids

Marker-assisted selection (MAS) is an effective tool for improving abiotic stress resistance in plants. DNA markers, especially SSR markers, are used to identify stress-resistant genes. SSR analysis, combined with bulked segregant analysis, helps detect molecular markers linked to traits like grain filling and heat tolerance in crops such as wheat. For example, SSR markers Xgwm132, Xgwm617, and Xgwm577 are associated with grain filling in hot environments, aiding in the development of heat-resistant cultivars. In rice, markers RM3586 and RM3735 on chromosomes 3 and 4, respectively, are linked to heat resistance [10]. SSR markers have also

been used to identify drought-resistant cotton hybrids, with significant polymorphism observed in varieties like “Varamin,” “Sayar 314,” and “Nazily.” These findings demonstrate the role of SSR markers in improving drought resistance in crops [5].

3.3. Genetic Diversity Identification under Heat and Frost Stress

Screening for heat-resistant genotypes under field conditions is challenging due to unpredictable climatic influences that affect trial repeatability and precision. Genetic assessment using molecular analysis is essential for identifying adaptive traits and improving crop sustainability under heat stress (Collins et al 2008).

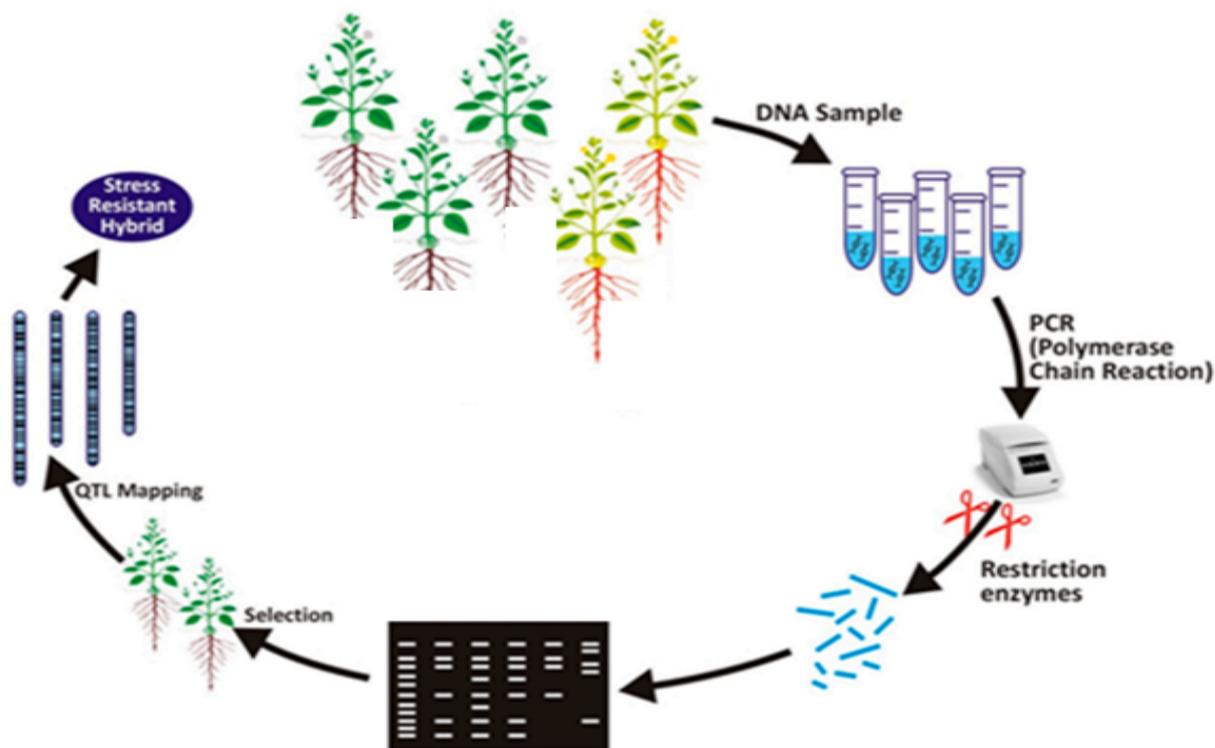


Figure 1. Mechanism of DNA marker-based progeny screening for stress-resistant characteristic.

Heat resistance is a complex, multi-genetic trait controlled by various genes at different growth stages. Sequence-related amplified polymorphism (SRAP) markers are useful for DNA fingerprinting, genetic diversity evaluation, and gene mapping, as they amplify polymorphic alleles. Similarly, target region amplified polymorphism (TRAP) markers, using two DNA primers, are effective for genetic analysis in heat-resistant wheat genotypes. These molecular techniques aid in breeding heat and cold-resistant cultivars [12].

4. Mapping of QTL Genes Related to Abiotic Stresses by DNA Markers

4.1. Saltol

Salt-resistant quantitative trait loci (QTLs), such as the saltol gene on chromosome 1 of rice, have been identified. This gene is linked to low Na⁺ uptake and high K⁺ absorption, resulting in a low Na: K ratio under high salinity conditions. Simple sequence repeat (SSR) markers are

widely used for mapping and evaluating genetic diversity in crops. In rice, SSR markers on chromosome 1 helped identify salinity-resistant genotypes, with the saltol gene linked to the “Pokkali” variety. Using SSR markers RM8094, RM10745, and RM493, successfully screened for salt-resistant rice varieties. Marker-assisted breeding has facilitated the introgression of the saltol gene into popular cultivars, improving their salt tolerance.

4.2. Dehydrin

Dehydration stress triggers molecular changes that reduce water loss, with plant cells producing hydrophilic proteins and dehydrins to respond. Dehydrins, common in crops like barley and wheat, are synthesized during severe dehydration stress (frost, drought, salt) and in the presence of abscisic acid. These proteins protect cells by enhancing enzyme activity under water stress. Research in barley revealed genes related to dehydrin that improve salt and drought resistance. In *Citrullus colocynthis*, DNA marker analysis identified drought-tolerant genes,

including dehydrin, P5CS, and others, aiding in drought resistance evaluation across different locations.

5. QTL Mapping by DNA Markers

Drought is a major stress affecting wheat productivity globally. DNA markers linked to QTLs for drought resistance can enhance tolerance in hybrids. A study identified a QTL for grain yield under drought stress on chromosome 4AL, associated with grain filling, spike density, yield, drought sensitivity, and biomass production. Genetic diversity in rice is high, but abiotic stresses, especially salinity, cause significant yield losses. Resistance to salinity is genetically complex, and various stress-related

QTLs have been identified in rice. Detection of QTLs for salinity resistance in rice using contiguous DNA markers can complement conventional breeding methods. In rice, 20 QTLs for salinity resistance were found on chromosomes 1, 2, 4, 6, 8, 9, and 12, with unique QTLs qSESF12.1 and qSESI12.1 offering potential for improving salt resistance. [13]. In peas, drought tolerance is a key challenge. A study identified 10 QTLs linked to drought resistance, which can aid in breeding for drought tolerance. For cold tolerance, a study on pea populations identified 161 QTLs for frost resistance, seed quality, and productivity, suggesting potential for breeding cold-resistant varieties [14].

Table 2. Application of DNA markers for QTL mapping in agronomic crops.

Crop	DNA Marker	No. of QTLs	No. of Chromosomes with QTLs Loci	Objective	Reference
Cotton	Simple sequence repeats (SSR); Single-strand conformation polymorphic (SSCP)	14	11	Salt resistance trait identification Mapping strength assessment for QTL detection	Saeed et al 2014 [15]
Maize	Single nucleotide polymorphism (SNP)	29	1, 3 and 5	Accessing salt resistance at the seedling stage using unconditional and conditional QTLs	Cui et al 2015[16]
Sorghum	Restriction fragment length polymorphism (RFLP)	7	1 and 2	To estimate the genetic difference of Asian barley for salt resistance • To identify and screen out salt resistance traits in accessions	Kebdee et al 2001[17]

6. Marker-Assisted Selection by SNP Marker

Association mapping identifies more alleles in large populations than linkage analysis and is useful for detecting genes linked to complex traits like drought resistance. However, it struggles with rare alleles and is more expensive due to the need for extensive genotyping. Fixed multiplex SNP chips are a cost-effective, time-saving alternative for genome-wide mapping,

providing high-quality, and precise genotyping data. SNPs, abundant and diverse, are ideal for identifying functional genes and genetic differences, making them preferable over traditional markers like SSRs. For example, 27 SNPs linked to drought tolerance were identified in maize by Hao et al., 2011[18].

7. Conclusions

Abiotic stress management is essential for improving crop quality and yield. Molecular genetics offers DNA markers that help explore genetic modifications, stress tolerance, and resistance to abiotic stresses. Early marker technologies provided basic stress resistance data, while current advancements can identify specific genes linked to tolerance. Combining DNA markers with QTL mapping helps pinpoint stress-tolerance genes on specific chromosomes. Ongoing advancements in marker technology will enable more detailed stress tolerance analysis, especially with climate change.

8. Conflicts of interest

The author declares no conflicts of interest

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