



Association Mapping for Abiotic Stress Tolerance in Plants: Prospects and Limitations

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Abstract

Abiotic stress is one of the major challenges faced by plants, which negatively affects their development, growth, and production. The use of association mapping in plants is a highly effective technique for pinpointing specific areas of the genome that are linked to increased tolerance to abiotic stress. Association mapping (AM) is a technique that utilizes thousands of genetic variations to identify the effects of quantitative trait loci (QTL) on traits. It is a powerful tool for discovering new genes and alleles, as well as for breaking down complex traits. Compared to linkage analysis, AM is advantageous because it relies on the structure of linkage disequilibrium (LD) to provide high resolution. However, several factors must be considered when using AM, including marker density, population structure, sample size, and germplasm selection. This article discusses the prospects and limitations of association mapping for abiotic stress resilience in plants.

Keywords: Abiotic stress, Genome-wide association mapping (GWAS), Linkage disequilibrium (LD), Marker-trait associations

Introduction

Plants face multiple types of abiotic stress that can impede their growth, development, and overall productivity, including factors like high or low temperatures, drought, salinity, and even exposure to heavy metals that can be toxic to them. Abiotic stress has a significant impact on agricultural output and quality, which poses a danger to world food security. Identifying particular genes and markers associated with stress tolerance is essential for developing crops that can better endure abiotic stress. Association mapping is a potent technique that can help us pinpoint specific regions of a plant's genome that are linked to complex traits, such as abiotic stress tolerance. In association mapping, the focus is on identifying specific genetic markers that are linked to a particular trait of interest, like the ability to withstand abiotic stress. These markers can be single nucleotide polymorphisms (SNPs), insertion-deletions (InDels), or simple sequence repeats (SSRs), located in the genome of the plant species being studied. The genetic markers are genotyped in a diverse panel of individuals, such as accessions or lines that vary in

their phenotypic response to abiotic stress. The association between the genotypes and the phenotype is then analyzed statistically to identify significant marker-trait associations (MTAs). Association mapping offers several benefits for identifying genetic factors associated with resistance to abiotic stress in plants. One of the key advantages is that it is a cost-effective approach, as it eliminates the need for developing mapping populations, which can be a time-consuming and expensive process. Secondly, association mapping can identify genetic factors that are responsible for natural variations in abiotic stress tolerance, which can be useful for breeding purposes. Thirdly, association mapping can detect marker-trait associations (MTAs) that are linked to multiple traits, including abiotic stress tolerance, making it possible to develop crops with multiple stress tolerances.

Principles of Association Mapping

Association mapping is a method that relies on the naturally occurring differences in DNA sequences to help us identify specific regions of the genome that are linked to complex traits of interest. The principle of association mapping is based on the fact that natural variations in

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DNA sequences are associated with phenotypic variations. Association mapping can be performed using two types of markers: genotyping-by-sequencing (GBS) markers and single nucleotide polymorphisms (SNPs). GBS markers are generated by sequencing a smaller, representative portion of the genome, while SNPs are variations in single nucleotides found in DNA sequences. In association mapping, genetic data is analysed to find patterns of connection between markers and phenotypes using various statistical models, including the general linear model (GLM), mixed linear model (MLM), and compressed mixed linear model (CMLM). The choice of model depends on factors such as the structure of the population being studied, the number of markers being used, and the level of relatedness among individuals in the population. Each model has its strengths and limitations, and selecting the appropriate one is critical for obtaining accurate results.

Common Abiotic Stress Tolerance Traits in Plants

When it comes to abiotic stress tolerance in plants, there are two main categories of traits: stress avoidance and stress tolerance. Stress avoidance traits are those that allow plants to prevent stress from occurring by reducing water loss, increasing their water-use efficiency, or maintaining turgor pressure. Stress tolerance traits are those that enable plants to survive and grow under stress conditions by maintaining cellular homeostasis, scavenging reactive oxygen species, or accumulating compatible solutes. Some examples of abiotic stress tolerance traits are root length, root density, water use efficiency, chlorophyll content, proline content, and ion homeostasis.

Strategies Used in Association Mapping

There are various methods for conducting association mapping, including genome-wide association mapping (GWAS), candidate gene association mapping, and multi-locus association mapping. GWAS is a strategy that involves scanning the entire genome for associations between markers and traits, while candidate gene association mapping involves selecting a set of candidate genes based on their known function or expression and testing their association with traits. Multi-locus association mapping involves identifying multiple loci associated with traits using statistical models that consider the effects of multiple loci simultaneously.

Major Findings

Association mapping has become a widely-used and effective technique for discovering regions of a plant's genome that are linked to its ability to tolerate abiotic stresses such as drought and salinity. Nayyeripasand *et al.* (2021) identified 151 trait-marker associations under salt stress conditions that were dispersed across 10 chromosomes of rice, organized into 29 genomic regions.

Javid *et al.* (2022) conducted a GWAS analysis on 298 Iranian bread wheat accessions at the seedling stage to identify candidate genes associated with salt tolerance; and as a result, they detected 29 functional marker-trait associations (MTAs) that were linked to salinity stress.

Luo *et al.* (2021) investigated the genetic basis of seedling salt tolerance in 348 maize inbred lines by analyzing 557,894 polymorphic SNPs, ultimately identifying 13 candidate genes associated with seedling salt tolerance through GWAS. Zheng *et al.* (2021) analyzed 149 cotton genotypes using 18,430 polymorphic SNPs and discovered six seedling salt tolerance genes associated with various processes such as cell amplification, auxin response, and osmotic pressure balance. Thabet *et al.* (2021) assessed seedling salt tolerance in 121 barley accessions using 9K SNPs and identified around 1500 candidate genes, which encode potassium channels mapped on Ch.1H.

Limitations of Association Mapping for Abiotic Stress Tolerance

Despite its potential, association mapping has some limitations that must be considered. One of the main limitations is the high rate of false positives due to population structure, which can result in spurious MTAs. Another limitation is the relatively low resolution of association mapping, as it is based on linkage disequilibrium (LD), which can extend over long distances in plant genomes. It's important to note that the MTAs identified through association mapping may not necessarily have a direct role in abiotic stress tolerance, but could potentially be linked to other traits that indirectly contribute to stress tolerance.

Conclusion

Association mapping is a useful technique for finding out which genes are related to stress tolerance in plants caused by environmental factors. However, it has its own set of limitations that must be considered. To overcome these limitations, several approaches have been proposed, including the use of multi-parental populations and the integration of association mapping with other omics data. The use of association mapping enables us to uncover valuable information about the genetic mechanisms that drive plant stress tolerance. Armed with this knowledge, we can design breeding strategies that result in crops with enhanced resilience to abiotic stress.

References

- Javid, S., Bihamta, M.R., Omid, M., Abbasi, A.R., Alipour, H., Ingvarsson, P.K., 2022. Genome-wide association study (GWAS) and genome prediction of seedling salt tolerance in bread wheat (*Triticum aestivum* L.). *BMC Plant Biology* 22, 581. DOI: <https://doi.org/10.1186/s12870-022-03936-8>.
- Luo, M., Zhang, Y., Li, J., Zhang, P., Chen, K., Song, W., Wang, X., Yang, J., Lu, X., Lu, B., Zhao, Y., Zhao, J., 2021. Molecular dissection of maize seedling salt tolerance using a genome-wide association analysis method. *Plant Biotechnology Journal* 19(10), 1937-1951. DOI: <https://doi.org/10.1111/pbi.13607>.
- Nayyeripasand, L., Garoosi, G.A., Ahmadihah, A., 2021. Genome-wide association study (GWAS) to identify salt-tolerance QTLs carrying novel candidate genes in rice during early vegetative stage. *Rice* 14, 9. DOI: <https://doi.org/10.1186/s12284-020-00433-0>.

- Thabet, S.G., Moursi, Y.S., Sallam, A., Karam, M.A., Alqudah, A.M., 2021. Genetic associations uncover candidate SNP markers and genes associated with salt tolerance during seedling developmental phase in barley. *Environmental and Experimental Botany* 188, 104499. DOI: <https://doi.org/10.1016/j.envexpbot.2021.104499>.
- Zheng, J., Zhang, Z., Gong, Z., Liang, Y., Sang, Z., Xu, Y., Li, X., Wang, J., 2021. Genome-wide association analysis of salt-tolerant traits in terrestrial cotton at seedling stage. *Plants* 11(1), 97. DOI: <https://doi.org/10.3390/plants11010097>.