

**Association Mapping in crop plants**Shiv Om<sup>1</sup> and Dr. Aakash Gaurav Singh<sup>2</sup>**Introduction:**

An effective and well-respected method for examining the genetic foundation of intricate quantitative traits in both plants and animals is quantitative trait locus (QTL) mapping (Yan et al., 2011). A potent gene tagging tool for crops in the plant genomics era of the twenty-first century is demonstrated by the recent developments in the creation of unbiased association mapping methodologies and their effective applications in the dissection of a variety of simple to complex features in many crops.

**Association mapping:**

Association Charting The dissection of complicated genetic features can be greatly aided by the highresolution method of association mapping, which maps quantitative trait loci based on the notion of linkage disequilibrium (Buckler, 2002). It is an extremely useful tool for deciphering intricate agronomic features and locating alleles that may help improve a desired trait. The size of the experimental population, the strength of the target allele effect, the density of markers used, the rate of LD decay between the marker

and the target allele, errors in the phenotyping and genotyping data, and the intended level of statistical significance all influence the power of association studies.

The Association Mapping Process in General The population composition and the study design selected will determine the specifics of the process (Singh and Singh 2016). This is a brief summary of the standard protocol for genome-wide association mapping in plants, based on Abdurakhmonov and Abdukarimov (2008).

**General procedure of association mapping:**

Population Mapping by Association For association mapping, a sizable random sample from a natural population, a set of breeding lines that includes cultivars, or a population formed from multiparent crossings of the relevant species are used. As much genetic variety as is practically possible from the population collection should be included in the sample. The association mapping population, association mapping panel, or association panel is made up of this sample.

**Using phenotypes:**

Phenotyping is the process of growing

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a chosen sample in the field and evaluating the many features of interest morphologically. To reduce the impacts of the environment, phenotyping should ideally be based on duplicated trials carried out over a period of time and locations. A suitable experimental design, such as a randomised block design, enhanced design, nested design, etc., should be used for the trials. An accurate and trustworthy phenotyping is essential to every mapping project.

### **Utilising Genotyping to Analyse Population Structure:**

The sample is next subjected to genotyping, which involves testing it using a collection of molecular markers that are uniformly distributed throughout the species' whole genome (ideally SSR markers). These markers ought to be unlinked, meaning they should be spread out across the genome by more than 40 cM (Pritchard et al., 2000a,

b). Analysis of Kinship and Structure Next, using the STRUCTURE programme to identify and estimate the sample's population structure, and the TASSEL programme to determine the degree of kinship among sample members, the marker data are analysed.

### **LD Analysis via Genotyping:**

In order to discover LD between markers and the loci of interest, the sample was also genotyped using a sufficiently high number of molecular markers that cover the

complete genome as densely as is practical. The number of markers needed for sufficient coverage of the entire genome would depend on the pattern of LD in the relevant genomic regions of the species and the degree of LD seen across various populations of the species. The most popular marker systems for this are SSR and SNP.

### **AM and LD Evaluations:**

A model-based study of the degree of relatedness between the genotype and phenotypic data used to identify and measure the level of linkage (LD) between the markers and the genes/QTLs controlling the desired attributes. To reduce erroneous connections between the markers and the genes/QTLs of interest, the model uses estimates of population structure and kinship as variables. Because these studies need a lot of work, appropriate computer programmes are used to carry them out.

### **Statistical Approaches Uses For Association Mapping:**

These days, a number of programmes are used to evaluate the relationship between characteristics and marker loci. Among the most widely utilised statistics is logistic regression, which allows for organised associations. A multiple regression model coupled with the estimates for the false Discovery rate proposed by Kraakman et al. (2006), a unified mixed-model approach

described by Yu et al. (2006) and implemented in TASSEL Mixed Linear Model (Yu and Buckler, 2006, TASSEL),

### **Linkage Disequilibrium:**

Alleles between genetic loci that are not randomly associated are referred to as being in linkage disequilibrium (LD). The population of alleles that share a chromosome was the subject of the term's initial definition. Despite the fact that LD is a population-based phenomena, it is typically seen that alleles that are placed closer together tend to have higher LD. Therefore, linkage may lessen the random association between alleles, resulting in the so-called disequilibrium.

The structure of LD is influenced by a wide range of genetic and non-genetic processes, including as admixture, mating pattern, drift, selection, and recombination. The LD between physically related markers and functional loci is crucial to the process of association mapping. Linkage disequilibrium is therefore a crucial component of association mapping. The degree of LD can be estimated using a number of statistical factors, most notably  $r^2$ , which calculates the correlation between the allelic states of two given polymorphic loci (Hedrick, 1987). The estimation of linkage disequilibrium can be significantly overestimated when sample sizes less than fifty people are used.

### **Application of Association Mapping:**

There are several uses for linkage disequilibrium in crop plant genomics research. Studying the relationship between a characteristic and its marker, then using marker-assisted selection (MAS), is one of the main applications of LD in plants. Its usage in agricultural development initiatives, research of population genetics, and genetic diversity in wild populations and germplasm collections is another significant application. In agricultural plants, marker-trait relationship is typically investigated by linkage analysis using techniques such as QTL interval mapping, t-test, and simple regression analysis (Hackett, 2002).

LD-based association mapping, which may be used to elite germplasm, synthetic populations, and germplasm bank collections, has essentially addressed the restrictions of the linkage analysis approach imposed by the availability of mapping populations (Mackay 2001; Hackett 2002). A technique known as "genetic association mapping," or "linkage disequilibrium mapping," uses linkage disequilibrium to examine the connection between genetic variations and phenotypic variation.

### **Conclusion:**

The potential for association mapping to promote crop genetic improvement is substantial.

This is reinforced by the application of high throughput and reasonably priced next generation sequencing techniques, which will make GWA investigations a common and standard procedure. As an alternative to linkage mapping and other methods for gene identification and validation, association mapping is still complementary. Furthermore, a barrier to our current understanding of the genetic architecture of complex characteristics is the disparity between the enormous number of variants with minor effects found by GWA research and the small number of genomic areas with big impacts found by linkage mapping.

However, the combination of the association mapping and linkage mapping methodologies gives a significant potential to address the unique limitations of each approach while maximising their distinct strengths in practical applications. Population structure continues to be a major barrier to association studies, necessitating the development of sophisticated statistical techniques as well as careful germplasm selection.

#### References:

1. Singh, B.D., A.K. Singh Marker assisted Plant Breeding, Principles and practices, Springer
2. Kushwaha U.K.S.,Mangal, V., Bairwa, A.K., Aadhikari, S., Ahmed, T., Bhat,

p.,...and Singh, N.K Association mapping, principles and techniques J.Biol.Environ. Eng,2 (1), 1-9

