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Genomic Selection for Plant Disease Resistance

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Abstract

Genomic selection (GS) is excellent method for highly polygenic complex traits with lower heritability and a complex genetic architecture that are governed by thousands of genes each with very small individual effects. GS has a greater potential to perceive minor effect loci that MAS would ignore. The main benefit of genomics-assisted disease resistance plant breeding is that it allows for very good combinations of R gene and quantitative resistance selection. The ability to select from a large number of candidates prior to advanced testing results in greater selection intensity as well as a shorter breeding cycle time. In economical point, there is no additional cost due to the use of predication model. As many disease resistances are highly heritable, phenotypic selection is difficult when using GS for disease resistance.

Keywords: Genomic selection, Disease resistance, Plant breeding, Marker assisted selection

Introduction

Any breeding programme must have an effective process for evaluating candidate genotypes for high yield, disease resistance, high agronomic performance, and improved end use attributes in order to generate improved varieties. The traditional plant breeding tactics based on phenotypic traits have shown to be less effective. There have been various successes in disease resistance breeding using traditional breeding and marker assisted selection. The majority of the research focused on major disease resistance genes, which are quite effective. The fundamental issue with major disease resistance genes is that they are extremely sensitive to breakdown when pathogenic races change rapidly even though they are quite effective. Plant breeding for disease resistance varies- depends on qualitative or quantitative resistance. Although breeding for minor gene quantitative resistance can result in more durable plant varieties, it is a complex and difficult process. Whole genome prediction models can be used to approach quantitative disease resistance. The most appropriate technique to developing improved varieties with more durable disease resistance is genomic selection (GS), rather than marker assisted selection or conventional breeding. For highly polygenic complex traits with low heritability and a complicated genetic architecture regulated by thousands of genes each with very small individual effects, genomic selection (GS) is an excellent technique (Bekele et al., 2019).

Genomic selection

Genomic selection (GS) is a method to predict the genetic value of selection candidates. It is based on the genomic estimated breeding value (GEBV) which is predicted from high-density markers distributed across the genome. Genomic selection (GS) was first proposed by Meuwissen *et al*. (2001). This technology use genome-wide molecular markers to capture total additive genetic variance and facilitates molecular breeding which is difficult quantitative traits. The GEBV, unlike marker-assisted selection, takes into account all markers, including minor and strong marker effects.

- GS is ideal for complex traits with lower heritability and a complex genetic architecture
- GS attempts to capture all additive genetic variance for the traits of interest by using all markers.
- GS is more accurate than MAS approaches that capture only a portion of the total genetic variance
- In genomic selection, a training population that contains individuals that have both phenotypic and genotypic data is used to fit a prediction model.
- The breeding value or genotypic value of individuals with only genotypic data is then predicted using that model.
- The selection process can then proceed based on these predictions.

Difference in Phenotypes between Qualitative and Quantitative Resistance

Disease resistance breeding strategies vary depending on the type of disease resistance. Mendelian ratios classify qualitative resistance traits into various categories whereas, quantitative resistance is defined as a continuous distribution of susceptible and resistant individuals (St. Clair , 2010). Qualitative resistance not have a complex genetic architecture and it is ideally suited to identifying and mapping single resistance genes with large effects. Qualitative resistance refers to a complete or high level of resistance that divide individuals into two groups: resistant and susceptible. The quantitative resistance controlled by several genes and are linked to genomic regions or QTL (quantitative trait loci) that contribute to the phenotype of pathogen resistance, each with a varying effects which provides partial resistance to the plants. It does not prevent pathogen multiplication, colonisation, or symptom severity; rather, it decreases them.

Models for Genomic Selection

In GS, a number of statistical models are employed to estimate breeding values. Among these, most commonly used models for purely quantitative traits are Genomic Best Linear Unbiased Prediction (G-BLUP) and ridge-regression BLUP (RR-BLUP). Other suitable models include Bayesian models Bayes-A, Bayes-B, Bayes-Cπ, and Bayesian LASSO.

Factors affecting the accuracy of GS

- Number of individuals in the training population
- marker density
- Heritability of the trait
- Rate of linkage equilibrium decay

Update the GS prediction model to maintain a close relationship between the training and selection candidate individuals.

Steps for combining resistance (R) genes and quantitative resistance (QR) in GS

The first step is to cross two parents, one with the R gene and one without. The selection candidates have to be genotyped with genome wide markers. For quantitative resistance, the selection candidates without R gene have to be phenotyped and it can be considered as training population for the development of prediction model. Finally select the candidates which contain high quantitative resistance along with R genes.

Role of Genomics-Assisted Breeding for Disease Resistance

- It is economically feasible as there is no additional cost due to the application of prediction model.
- More breeding candidates can be evaluated that leads to higher selection intensity.
- Decreasing breeding cycle time and increasing rates of genetic gain.

- Eliminate vertifolia effect.
- With GS, quantitative resistance can be predicted in any individual or line regardless of whether R genes are present (Poland J and Rutkoski J (2016)).

Conclusion

Genomic selection is specialized form of marker assisted selection which is ideal for complex polygenic traits with low heritability. It helps to develop improved varieties with more durable disease resistance.

References

Poland J and Rutkoski J (2016) Advances and challenges in genomic selection for disease resistance. *Annual review of phytopathology*, *54*: 79-98.

Bekele D, Tesfaye K, Fikre, A (2019) Recent developments in genomic selection for minor gene quantitative disease resistance plant breeding. *Journal of Plant Pathology & Microbiology*, *10*(478): 1-8.

Meuwissen, Hayes BJ, Goddard ME (2001) Prediction of total genetic value using genome-wide dense marker maps. *Genetics* 157:1819–29

St. Clair DA (2010) Quantitative disease resistance and quantitative resistance loci in breeding. *Annual review of phytopathology*, *48*: 247-268.