

Population genetics of genomics-based crop improvement methods

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Overview

Genome-wide association studies (GWAS) and genomic selection (GS) are recently used strategies for crop improvement. These new approaches are applied using populations of unrelated individuals in order to capture substantial portion of species-wide variation or breeding-program variation.

GWAS, is a well-established methodology and widely used in human research. The motivation for doing GWAS is to identify DNA marker alleles that are associated with a quantitative trait. This association between the marker and genetic variant can lead to observable differences in the phenotype of these different marker genotype classes. In plant breeding, once associated markers are identified, they can be easily used in marker-assisted selection (MAS). MAS is a breeding strategy used to facilitate incorporation of desirable alleles using molecular markers into the breeding program.

GS is a more recent strategy than GWAS. Although it starts with the same panel of unrelated individuals which are also genotyped and phenotype, this population (also called training population) is used to build prediction models. These models will be used to predict phenotypic values on different set individuals of which only genotypic data are available. However, these individuals/lines must be closely related or somehow belongs to the same breeding program. The major motivation of GS is to dramatically reduce the time and expense in phenotyping.

Although GWAS and GS are relatively new to plant breeding, detecting quantitative trait loci (QTL) using these approaches has been more successful and less costly than in humans. GWAS in human studies has been dominated by challenges particularly the 'missing heritability' problem, which suggested to increase the population size (to many thousands) and number of markers (in millions) in order to detect more QTL. However, these challenges are somehow less relevant in other species such as domesticated animals and plants. For example, GWAS in rice on 14 traits identified SNP's which on average explained as much as ~36% of the phenotypic variation.

My presentation will focus on two classes of factors namely: (i) genetic attributes, and (ii) nature of traits and history of selection that influence the implications and application of GWAS and GS in plant breeding. I will also discuss how manipulation of some population genetic attributes, that are not applicable in humans, can increase the prospects for success of GWAS and GS.

References

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