

Genetic Diversity for Novel Freezing Tolerance in Winter Wheat Landraces Summary:

- Single Nucleotide polymorphism (SNP): The change in a nucleotide at a specific location within a genome
- Cold tolerance is a complex quantitative trait
- Genome Wide Association Study (GWAS) or Association Study (AS) is a powerful method in discovering QTL's and does so by statistically associating a SNP with the phenotype being studied
- AS provides information about a study populations genetic diversity, ancestry and stratification
- AS has issues with detecting rare variants in a study population and must have population structure addressed to avoid confounding of the data
- Necessities in setting up an AS: a clear phenotype must be established, type of study must be decided and samples selected accordingly, genotyping must be performed, analysis is done with a software package that will typically use a GLM or MLM for statistical analysis
- Analysis provides the researcher any SNPs that are statistically associated with the phenotype in question
- Two types of SNPs are discovered in an AS: causal and non-causal. Most SNPs found will be non-causal and are associated with the phenotype due to it being in high linkage disequilibrium. The lucky researcher discovers causal SNPs which are directly responsible for the variance in the phenotype being studied
- Results suggested the alleles on chromosome 6A were essentially fixed for this QTL
- This fixation of alleles could be explained by human migration from the Fertile Crescent to the North

References:

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