

Mapping Genes for Categorical Traits in Cotton

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Cotton breeders and geneticists have strong interest in identifying genes that underlie traits such as leaf shape and nectary presence. The classical genetics techniques like linkage mapping often have low resolution but high power. On the other hand, genome wide association studies (GWAS) have high resolution but suffer from high false positive rates due to the correlation between the phenotype and the underlying population structure. In this study, we show a proof of concept study design that combines the power of linkage mapping with the resolution of genome wide association to identify genes controlling categorical traits. We tested the method by re-mapping the known causal genes for four categorical traits important to cotton breeders. A case-control GWAS was conducted in a cotton diversity panel, revealing dozens of loci associated with each categorical trait. By constraining the case-control results to genome regions (eg, chromosome arms) suggested by linkage mapping, in three of four traits a narrow region corresponding to the known underlying gene was identified. We show that even with highly imbalanced group sizes (trait classes), genes for binary traits can be mapped with this technique, as long as the general physical position of the gene is known from linkage mapping and the same gene underlies the trait in both the mapping population and diversity panel. Our study supports the continued use of linkage mapping for the mapping of genes in cotton, and highlights the importance of integrating evidence from single populations as well as broader diversity panels.