

Bioinformatics Workgroup Co-Chair Candidate

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Most important agronomy traits are complex traits controlled by multiple genes with genetic effects of epistasis and environment interaction. With recent advances in molecular genotyping and high-throughput technology, great opportunity is provided for revealing genetic architecture of complex traits. In recent 20 years, quantitative trait loci (QTLs) have been identified based on limited number of markers by using a linkage map derived from a mapping population. We have developed mixed model approaches for mapping QTL-QTL interaction and QTL-environment interaction. The MCIM methods and QTLNetwork software have been used for QTL mapping in cotton. As one candidate being nominated for Bioinformatics co-chair, I will continue to develop new approaches and analysis software for gene mapping based on four Omics genotypes. The new tools can be used in Genome-Wide Association Studies (GWAS) for mapping quantitative trait SNP (QTS), quantitative trait transcript (QTT), quantitative trait protein (QTP), and quantitative trait metabolite (QTM). Epistasis between genes, as well as gene-environment interaction can be estimated. We will release new software QTXNetwork using GPU parallel computation. Web-searching tool BioPubInfo will also be released soon. The new methods and tools can be used for mapping genetic architecture for complex traits in cotton.