

## **Resolving Genes for White Mold Resistance in Peanut Using Large-population QTL-seq Coupled with Iterative Genotyping (iQTL-seq)**

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Gene-level mapping of semi-quantitative traits, such as white mold resistance in peanut, requires substantial effort and time but has numerous benefits in the post-genomic, post-CRISPR era. QTL-Seq uses classical bulk segregant analysis and next generation DNA sequencing to identify associations between genomic loci and phenotypes. By accommodating large populations, QTL-Seq offers the possibility of achieving gene discovery in a single cross. We use extensive simulation to further explore if applying an iterative amplicon-design step (iQTL-seq), first proposed in mutation mapping, would allow more genetic resolution at a lower cost. We find that at a cost comparable or lower than 70x resequencing of the bulked pools, iQTL-seq delivers 4-fold improvement in resolution on average and locates QTLs to within ~75 kb (median) of the causal variant. Moreover, the methodology can be applied in the F2 advancement stage, suggesting gene level mapping for oligogenic traits within 1 to 2 years. We also describe the software package developed for broad-scale application of the technique.