

Iterative QTL-seq to Discover Functional Markers of Agronomically Important Traits

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Iterative QTL-seq (iQTL-seq), as proposed here, makes the discovery of naturally-occurring, desirable genes much more tractable. To illustrate the technique's efficacy, this project aims to address white mold disease in peanut. Resistance to white mold has been sought for a century, yet it still has the highest combined cost to growers of any peanut pathogen (\$37M, 2014) with damage losses as well as expensive control measures. We describe our efforts to characterize the genes underlying superior performance using a novel modification QTL-Seq analysis, which uses classical bulk segregant analysis and next generation DNA sequencing to identify genomic intervals containing genes of interest. We have optimized iQTL using simulation of the genetic architecture expected to underlie white-mold resistance and have expanded our analysis to other traits. We also describe the software package developed for broad-scale use of the technique.