

Leveraging single-cell genomics in QTL mapping

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Aim: Collaborative research to apply single-cell genomics in QTL (Quantitative Trait Loci) mapping of agriculturally important traits.

Approach: Integration of whole-genome sequencing (WGS) and single-nuclei RNA-seq (snRNA-seq) data to map phenotype of interest. Bulk DNA from samples representing contrasting phenotypes are sequenced to identify single nucleotide polymorphisms (SNP). snRNA-seq is used to identify cell types and cell-specific gene expression. Effect of genetic variation on cell-specific gene expression is modeled by nested linear regression.

Collaboration: A collaborative effort has been developed to leverage the proposed strategy to map single-cell QTLs that control specific economic trait including 1) brown-plant hopper and rice plant interaction, 2) gut-microbiome interaction in fruit fly, and 3) litter size in pig.

Resource: To facilitate efforts in single-cell QTL mapping, we are developing the following resources 1) computational pipeline for integrative analysis of WGS and single-cell functional genomics data, 2) community training in data analysis, 3) online hub on agricultural single-cell QTL data.

Preliminary data: We have made some progress in collecting preliminary data on gene expression of gut of *Drosophila suzukii* in response to antibiotic cleansing of microbiome. Also, pig fetal samples from small versus large litters have been collected for preliminary data analysis.

Next step: We plan to use the resources and data generated from this project to seek larger research funding from federal funding agencies including USDA.

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