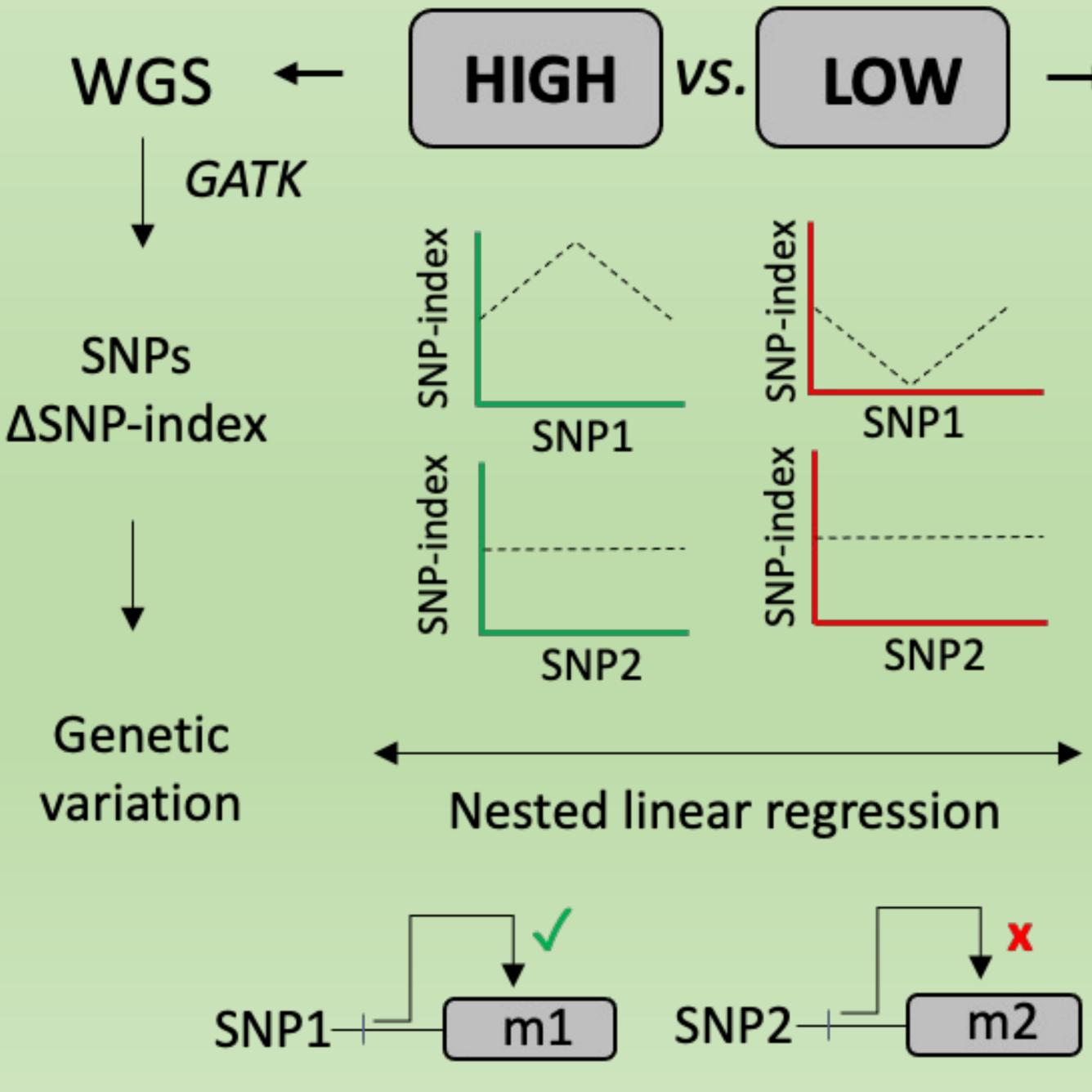
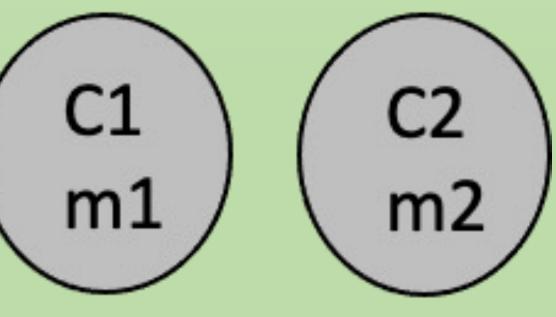
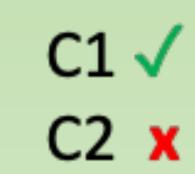
Leveraging single-cell genomics in QTL mapping Susanta K. Behura, Division of Animal Sciences, University of Missouri, Columbia MO

Collaboration: A collaborative effort has been Aim: Collaborative research to apply single-cell genomics in QTL (Quantitative Trait Loci) mapping of developed to leverage the proposed strategy to map single-cell QTLs that control specific economic agriculturally important traits. trait including 1) brown-plant hopper and rice plant Approach: Integration of whole-genome interaction, 2) gut-microbiome interaction in fruit sequencing (WGS) and single-nuclei RNA-seq fly, and 3) litter size in pig. (snRNA-seq) data to map phenotype of interest. Bulk DNA from samples representing contrasting **Resource:** To facilitate efforts in single-cell QTL mapping, we are developing the following resources phenotypes are sequenced to identify single 1) computational pipeline for integrative analysis of nucleotide polymorphisms (SNP). snRNA-seq is used to identify cell types and cell-specific gene WGS and singe-cell functional genomics data, 2) expression. Effect of genetic variation on cellcommunity training in data analysis, 3) online hub specific gene expression is modeled by nested linear on agricultural single-cell QTL data. regression. **Preliminary data:** We have made some progress in snRNA-seq collecting preliminary data on gene expression of LOW HIGH VS. \rightarrow WGS 🔶 gut of Drosophila suzukii in response to antibiotic Seurat GATK cleansing of microbiome. Also, pig fetal samples Cell types (C) from small versus large litters have been collected Marker genes (m) SNPs SNF **S** for preliminary data analysis. Δ SNP-index SNP1





Cell-specific expression variation



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.

Funding: This project was funded by AG2PI and USDA NIFA.