

# Arthropod community distributions are linked to *Populus trichocarpa* genes

## Background

- Genetic variation in plant species can predictably structure entire assemblages of associated organisms, such as arthropod pests and predators. To harness the breeding potential of such relationships, community genetics seeks to discover plant candidate genes and functions that underly arthropod community phenotypes. Prior studies have been unable to identify plant genes controlling community structure.

## Approach

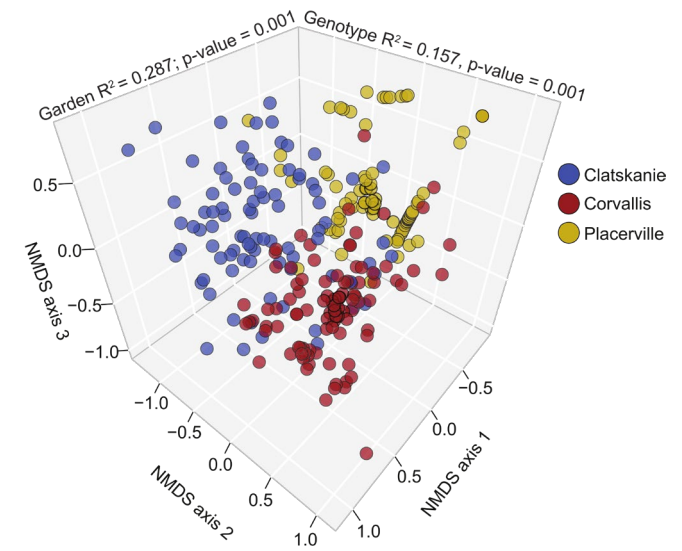
- We surveyed arthropods within three common gardens of *Populus trichocarpa* (poplar) to discover plant genes contributing to arthropod community composition. We analyzed our surveys with single-trait genome-wide association analysis (GWAS), multi-trait GWAS methods, and functional networks built from plant phenotypes—including surveyed arthropods—and six published data layers: gene co-expression, gene co-methylation, SNP correlation, metabolite GWAS, rare variant regional metabolite GWAS, and py-MBMS GWAS.

## Results

- Surveyed arthropod species were unique within each common garden; plant genotype was important in structuring the arthropod community composition in the Clatskanie and Corvallis sites.
- Several candidate poplar genes were significantly associated with arthropod traits including abundance of *Phyllonorycter* sp. (blotch miner), unique number of arthropod species (*i.e.*, richness), and composition network of the arthropod community.
- Community candidate genes had broadly applicable functions, *e.g.*, terpenoid biosynthesis or production of dsRNA binding proteins and protein kinases, that may be capable of targeting several arthropod species.

## Significance

- We have demonstrated the ability to detect, in a field environment, individual genes that are associated with the community assemblage of arthropods on a host plant and, through network analysis, gleaned information on possible gene functions that can now be targeted for validation in future studies and harnessed for positively impacting ecosystem structure.



Arthropod community plot from three gardens surveyed in 2012. Each point is the community from a single tree. The closer in spatial position of a pair of points the more similar the arthropods feeding on the trees in identity and abundance using non-metric multidimensional scaling (NMDS). The gardens were in Clatskanie, OR, Corvallis, OR and Placerville CA.

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