

A mapping framework of competition-cooperation QTLs that drive community dynamics

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Genes have been thought to affect community ecology and evolution, but their identification at the whole-genome level is challenging. Here, we develop a conceptual framework for the genome-wide mapping of quantitative trait loci (QTLs) that govern interspecific competition and cooperation. This framework integrates the community ecology theory into systems mapping, a statistical model for mapping complex traits as a dynamic system. It can characterize not only how QTLs of one species affect its own phenotype directly, but also how QTLs from this species affect the phenotype of its interacting species indirectly and how QTLs from different species interact epistatically to shape community behavior. We validated the utility of the new mapping framework experimentally by culturing and comparing two bacterial species, *Escherichia coli* and *Staphylococcus aureus*, in socialized and socially isolated environments, identifying several QTLs from each species that may act as key drivers of microbial community structure and function.

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