Biological evolution is argued to occur in the context of complex networks of interacting species; however, the genetic basis to ecological network structure has largely been unexplored. Using both a long-term experimental garden and a naturally established forest, we found that genotypic variation in the foundation tree species, *Populus angustifolia*, contributes to the interaction network structure of a model community of epiphytic lichens. These results demonstrate strong support for a genetic basis to ecological network structure, resulting from the strong asymmetry of interactions resulting from foundation species. This work sets the stage for studies that address greater complexity in the evolution of biological systems and provides a framework for the discovery of evolutionarily dynamic compartments in ecosystems.