Plant Communications, Volume *1*

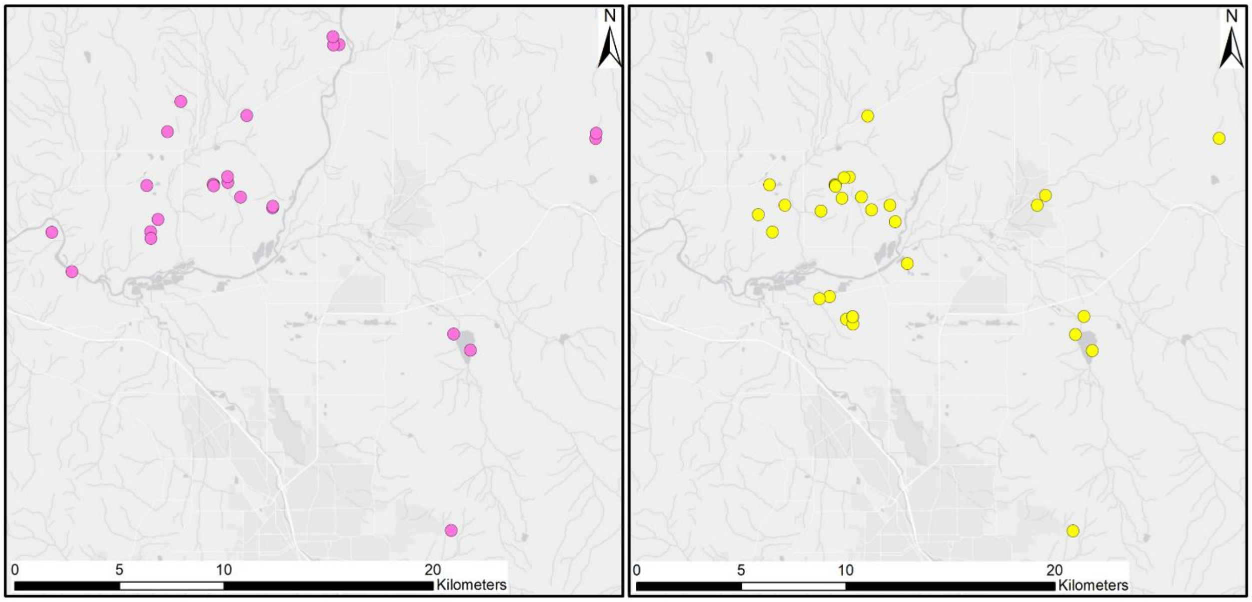
Supplemental Information

Landscape Genetics of Plants: Challenges and Opportunities

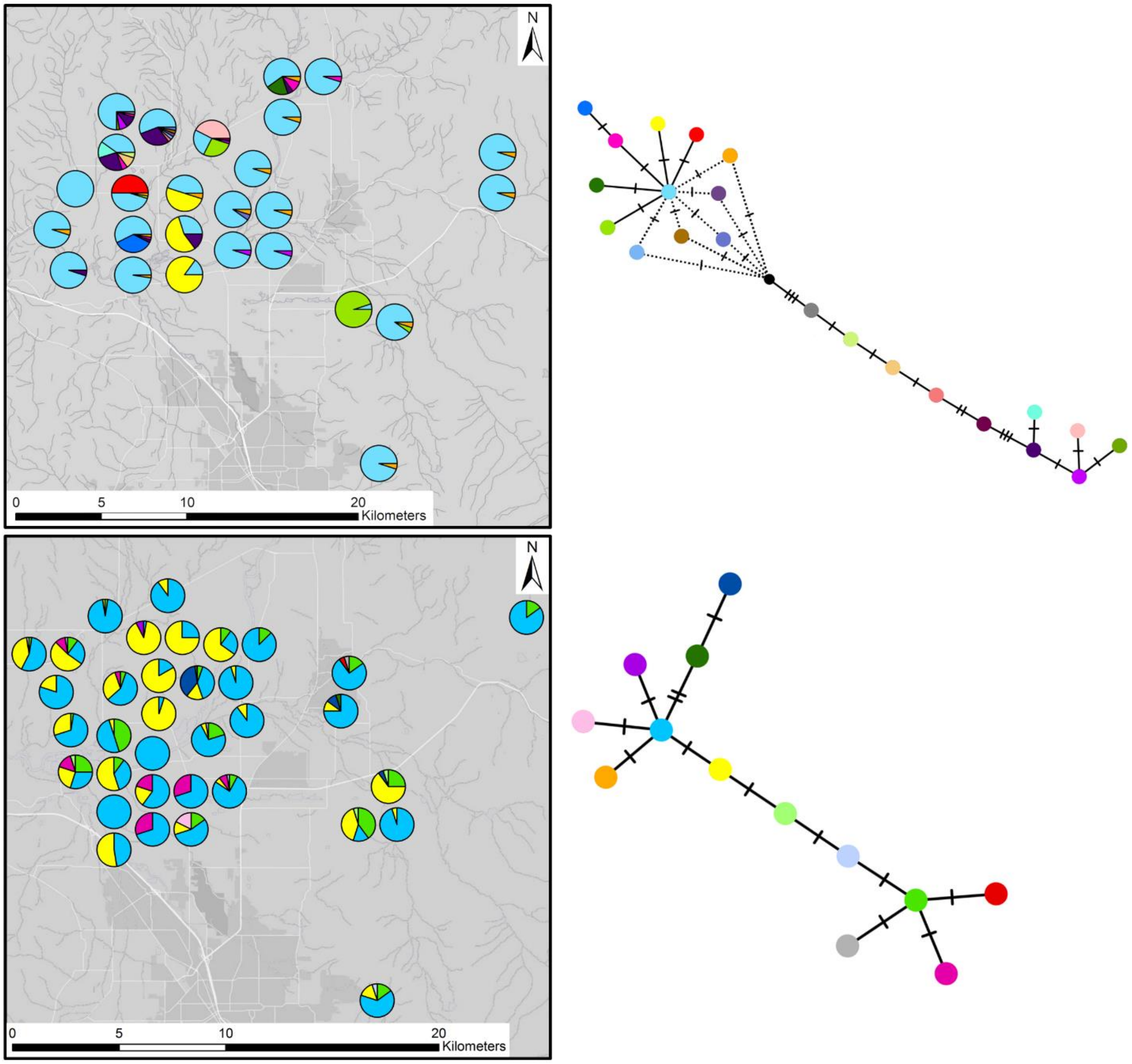
Mitchell B. Cruzan and Elizabeth C. Hendrickson

Supplemental Information.

Sampling and genetic methods for landscape genetic studies of *Plectritus congesta* and *Achyrachaena mollis*.



Supplemental Figure 1. Tissue samples were collected from 26 *Plectritis congesta* populations (left) and 35 *Achyrachaena mollis* populations (right) throughout the Medford region in southern Oregon. Approximately 20 individuals were collected at each population. Whole chloroplast genome sequencing was conducted with pooled samples following the protocol described in Kohrn et al. 2017.



Supplemental Figure 2. The top panels depict the genetic structure of *Plectritis congesta* populations, and the bottom panels depict the genetic structure of *Achyrachaena mollis* following protocols described in CallHap (Kohrn et al. 2017). Within the study region, 22 unique haplotypes were discovered for *Plectritis congesta*, and 13 unique haplotypes were discovered for *Achyrachaena mollis*. Each pie chart displays the haplotypes discovered within the population. The colors within the pie chart represent a unique haplotype identified by the pipeline, which corresponds to the haplotype network on the right. Within the haplotype network, each haplotype is assigned to a node, which are separated with novel single nucleotide polymorphisms (tick marks). Haplotypes that are centrally located within the haplotype network are considered to be older and are generally widespread. Their distribution is most likely an effect of coalescence and a shared evolutionary history, while more contemporary dispersal events can be observed in the sharing of haplotypes located on terminal nodes of the network.