

Genetic diversity and morphological variation in a vulnerable WV native orchid, *Corallorhiza bentleyi* Nicole Fama, Brandon Sinn, and Craig Barrett¹ *Department of Biology, West Virginia University, Morgantown, WV 26506*

Corallorhiza bentleyi, commonly known as Bentley's coralroot, is an orchid species endemic to five counties along the West Virginia/Virginia border. It was described in the 1990s, is known from only about 10 populations, and is both geographically restricted and locally rare. Patterns of genetic diversity and fungal host specificity for this orchid are poorly understood; such knowledge will be crucial to help maintain the long term stability of this species. We took a three-fold approach to quantify diversity among populations of *Corallorhiza bentleyi*. Nuclear microsatellite and inter-simple sequence repeat (ISSR) markers were developed to quantify genetic variation within *C. bentleyi*. The internal transcribed spacer region (ITS) was sequenced to assess the degree of specificity between the orchids and their ectomycorrhizal fungal hosts. Floral morphometrics and principal components analysis were used to analyze morphological diversity among all individuals sampled. Although low levels of genetic diversity were found among sequenced microsatellite regions, floral morphological measurements showed some distinction between populations at the county level. *Corallorhiza bentleyi* appears to associate with a single species of fungus, *T. fuscocinerea*, meaning that its survival is linked to that of this single species. Preliminary data from dominant ISSR banding patterns have revealed evidence of genetic variation between *C. bentleyi* populations, and among individuals within populations. The ultimate goal of this research is to obtain more information concerning genetic diversity, relationships with its fungal host, and environmental requirements in order to influence management of *C. bentleyi* populations and their habitats in southern Appalachia
