Genetic distance not correlated with geographical distance: possible evidence for speciation in *Corallorhiza maculata*

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Introduction

•*Corallorhiza maculata* is a parasitic plant that preys on fungi. It is non-photosynthetic and gathers nutrients by extracting carbon and nitrogen from the hyphe of mushrooms that enter its roots. Currently it is believed that there are six varieties of *C. macuata,* each of which associates with a different group of fungi.

•We are interested in the potential speciation of *C. maculata*.

•We made a phylogenetic tree by comparing the DNA sequence of the plant tissues taken from different populations found around the United States. These populations were in: Arizona, Colarado, Utah, New Mexico, and Wyoming.

•We chose specific regions of the DNA to compare. We amplified the internal transcribed spacer region and a chloroplast locus. Both of these regions were chosen because they are non-coding and highly variable.

•This project provides valuable insight into the evolutionary concepts of plants through association with their nutrient sources

Methods

•Using the DNEasy extraction kit, we extracted DNA from fifteen tissue samples from the same species of Orchids, *C. maculata,* collected from different areas of the United States.

•We used PCR to amplify the internal transcribed spacer region in the DNA sequence using primers ITSIP with ITS4. We also amplified a chloroplast locus using the primers trnL with rpl32.

•We cleaned up my PCR reactions by removing unused PCR ingredients using ExoSAP. We then sent the DNA off to be sequenced by McLab in San Francisco California.

•Sequences were manually cleaned and aligned by eye using Bioedit software program.

•We built two maximum parsimony trees, one for each locus using the program MEGA 4.

Results

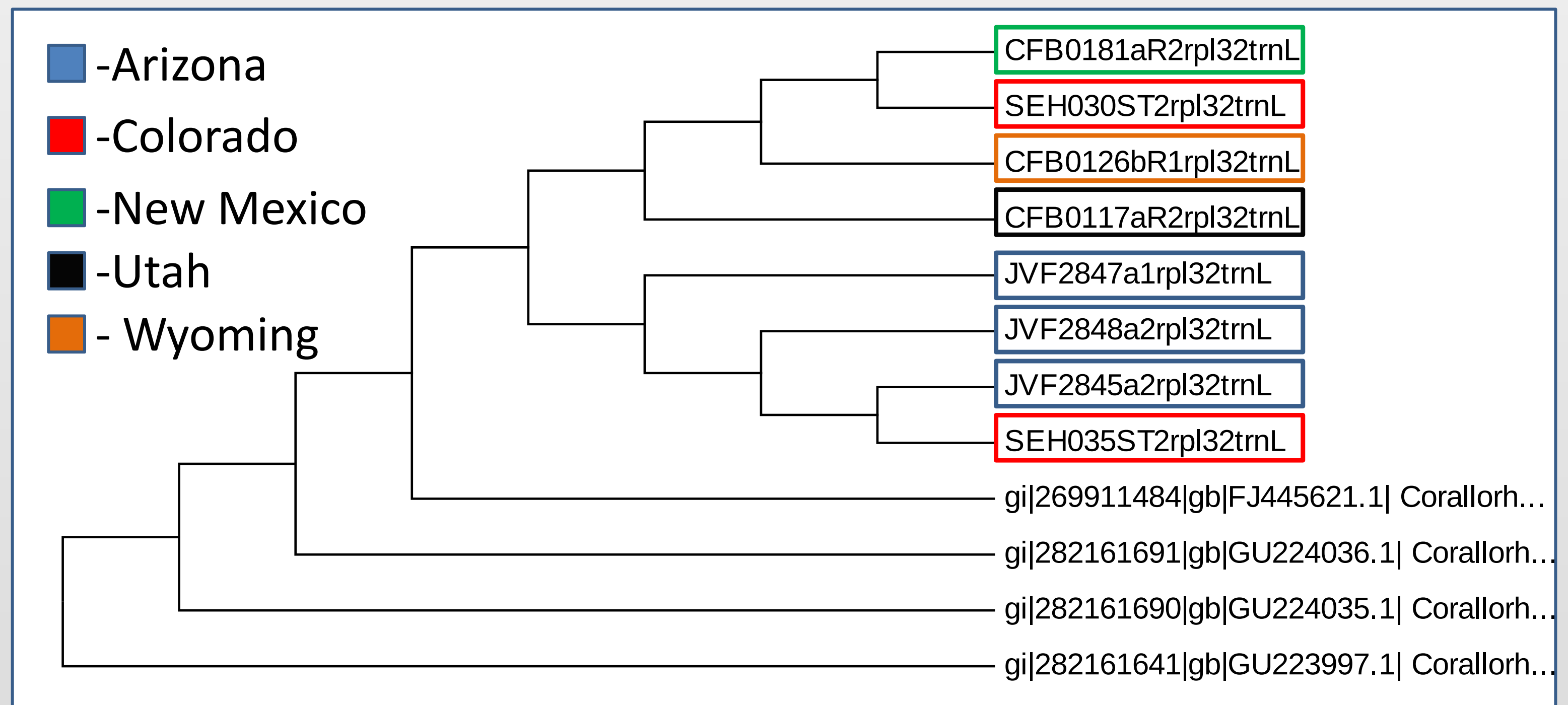

Figure 1. Maximum parsimony tree of chloroplast region

•By looking at the two phylogenetic trees, we were able to determine that several plants were genetically more related to plants in a different state, than to plants growing alongside them.

•In Figure 1. we saw a clade consisting of plants from Colorado and New Mexico, and another clade consisting of plants from Colorado and Arizona.

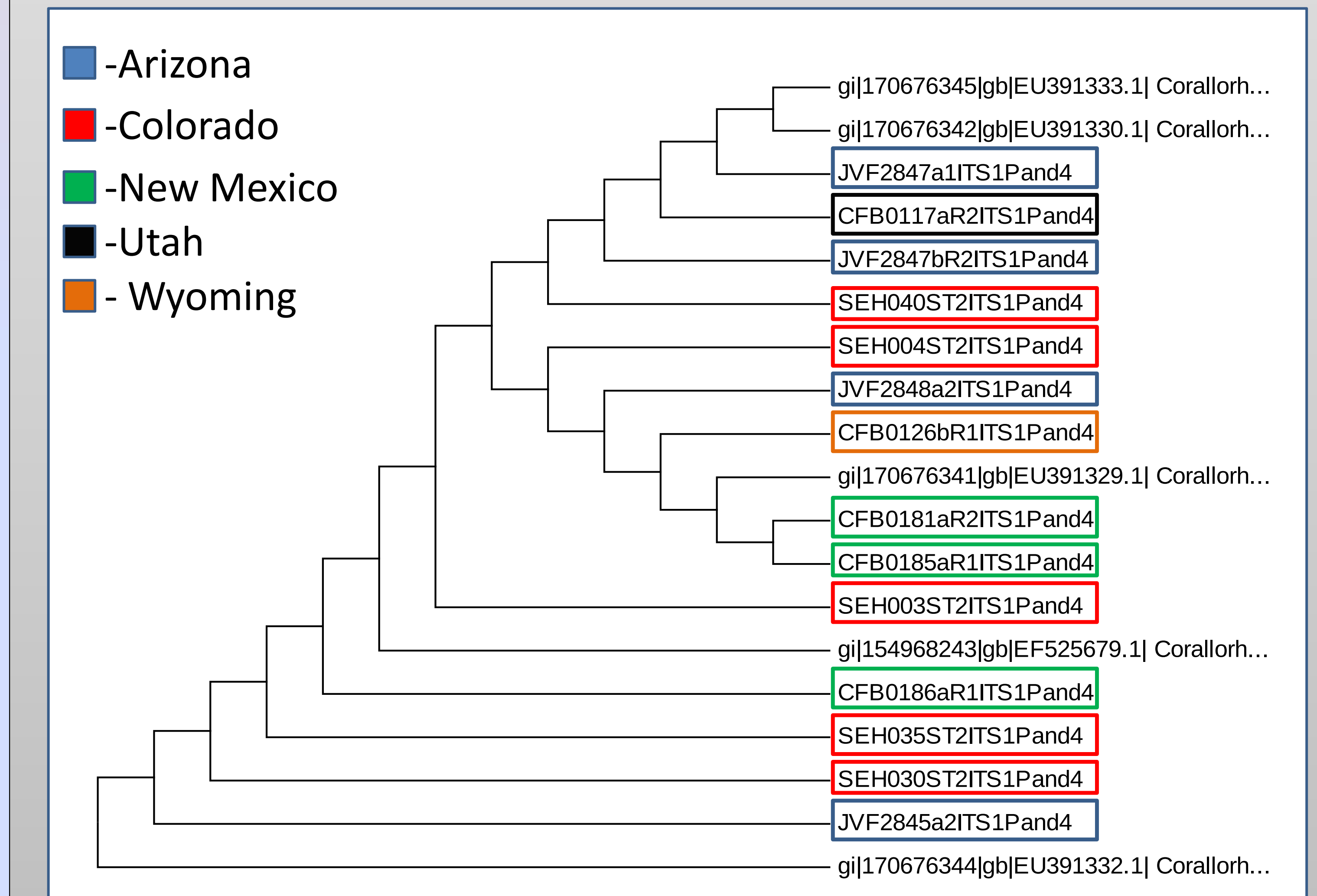

Figure 2. Maximum parsimony tree of internal transcribed spacer region

•In Figure 2. an individual from Arizona was closer in genetic makeup to another individual from Utah than to a different individual in Arizona

Acknowledgements

•RAHI 2, Alaska BioPREP, Alaska INBRE, and the University of Alaska Fairbanks helped fund this project, making it possible.
•I would also like to thank the Taylor lab for hosting me during this project and special thanks to Sarah Hopkins for being my mentor throughout every step of this project.
•Special thanks to Scott McArthur, Kent Bovee, Robert Parsons, Andrea Price, and Keiko Herrick for teaching me concepts that I have applied to this project.
•"The project described was supported by Award Numbers P20RR016466 and R25RR024282 from the National Center for Research Resources, a part of the National Institutes of Health. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Center for Research Resources or the National Institutes of Health."

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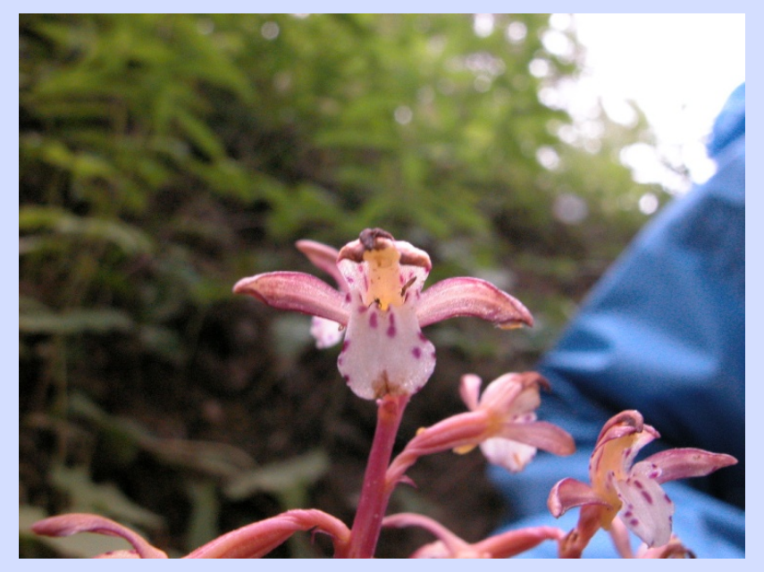

Conclusion

•After viewing our results, we believe that we are seeing some speciation in *C. maculata*.
•Many plants in a population are more closely related to others in a different state than their own population.
•This could be correlated to the specialization of the individuals to their fungal nutrient source.
•We could determine this by examining the fungal partners for individual plants in these locations.
•This project shows that there is significant structure within these populations which could imply that speciation is occurring.