Does coevolution with toxic milkvetches drive diversification in seed-feeding beetles?

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Introduction

Plant-insect relationships are among the most common organismal relationships observed in biology. As these two organisms closely interact with one another, profound effects on adaptation and interaction can be observed. The genus Astragalus (milkvetches) is the most rapidly speciating plant lineage known, and it has an astounding array of fruit morphology and defensive chemistry. One possible explanation is that rapid diversification is driven (at least in part) by specialist seed beetles in the genus Acanthoscelides. While there are 450 species of Astragalus in western North America alone, there are only seven species of seed beetles that feed on them. Because of the phenotypic diversity of the plants that seems related to defense against insects, the anticipated paradigm of this interaction is that only specialists would utilize each species as a host. Instead, one species of seed beetles is able to utilize many Astragalus species, exemplified by the species Acanthoscelides pullus feeding on over 25 Astragalus species, including multiple species in California alone. This relationship poses a challenge for understanding the nature of specialization and speciation in these seed beetles. There are three alternative scenarios that offer the most plausible explanations: Ac. pullus is a generalist species, a genetically structured species, or an ecologically structured cryptic species. The goal of my project is to determine which scenario best describes the relationship between different populations of Ac. pullus on their respective host plants.

Methods

Specimens were collected from host-plants at 13 locations across Southern California. DNA was extracted from beetles using full body destructive preps. The mitochondrial CO1 (cytochrome oxidase 1) gene was amplified using PCR and then sequenced. The Genious v9 was used to align sequences. A phylogeny was reconstructed using Bayesian analysis in the MrBayes v3.2 software program (Fig. 3 and 4).

Results and Discussion

While some diversification into separate clades is noted in Figure 3, diversification does not seem to be fully correlated to host plant (Figure 4). Bayesian analysis resulted in clades composed of individuals from multiple populations. However, no population was restricted to just one clade (Figure 5). Each population was composed of members belonging to at least two clades with no evidence of relationship between which the number of individuals of a population, host plant, and clade. This implies that there is still a substantial amount of gene flow that occurs between populations. Based on these data alone, it is possible that there is some genetic structuring between populations of Ac. pullus, but that generalist qualities remain within this species.

Future Directions

While examining one gene allows us to gain insight into potential patterns of divergence within Ac. pullus, further investigation is needed to fully understand the relationships between host plant and beetle. Currently, I am working on analyzing sequences from the nuclear EF1 gene from the same set of specimens. Additionally, I am performing a genomic study using the RAD-sequencing protocol to gain genome-wide data of diversity within and between populations of Ac. pullus.

References

4 Johnson, Clarence D. “Biosystematics of the Arizona, California, and Oregon species of the seed beetle genus Acanthoscelides Schilsky (Coleoptera: Bruchidae).” Biosystematics of the Arizona, California, and Oregon species of the seed beetle genus Acanthoscelides Schilsky (Coleoptera: Bruchidae).” 59 (1970).