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The Genetics and Biological Control of *Hyalopterus pruni*, an Invasive Aphid Pest in California

1. Abstract

• The mealy plum aphid, *Hyalopterus pruni*, is an invasive pest on prune in California. The genus *Hyalopterus* originates from the Mediterranean, and is currently believed to be comprised of two indistinguishable species that feed on multiple hosts in the genus *Prunus.*

• Biological control using *Aphidius transcaspicus,* a parasitoid from *H. pruni*'s ancestral home, is a potential way to mediate the effect of this pest.

• Using molecular genetics and ecological experiments I will characterize the population structure of these two species and their interactions to aid the design of an effective biocontrol program for mealy aphid in California.

2. The Problem

• Pesticide use in CA is under increasingly strict regulation due to better awareness of negative effects on human and environmental health.

• The mealy plum aphid is a key barrier to reducing pesticide application on prune in CA and is an ideal candidate for biological control—control achieved through the introduction of a natural enemy from a pest's region of origin.

• A biocontrol program could be improved by a better understanding of the taxonomy, sub-specific population structure, and the strength of ecological interactions for *Hyalopterus* and its natural enemies in CA and their native Mediterranean home.

3. Research Approaches

A. Molecular Methods

1) Examine the population structure of *H. pruni* and *A. transcaspicus* in the Mediterranean and clarify issues surrounding their taxonomy.

• I will use DNA sequences for the mitochondrial (mtDNA) COI gene to look for deeper level differences within the two taxa, such as biotypes, host races, or even cryptic species.

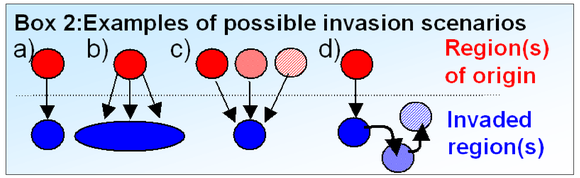
• I will develop microsatellite DNA libraries for both aphids and parasitoids to examine fine scale structuring not revealed by mtDNA.

2) Examine the invasion history of *H. pruni* in California.

• Parameters associated with invasion are crucial for a pest's success in a new environment and understanding such variables can aid the design of effective management strategies. Invasion parameters can include:

- Geographic origin(s) of the pest
- Number and size of invasion events
- Patterns of spread in the invaded region

• The combination of microsatellite data and population genetics statistical methods will help trace the invasion history for mealy plum aphid and distinguish between possible invasion scenarios (Box 2).



B. Virulence Experiments

• Virulence is a parasitoid's ability to overcome its host's defenses and successfully reproduce.

• I will expose multiple geographic populations of *A. transcaspicus* to Californian *H. pruni* in cages to examine reproductive success and determine the relative virulence of each parasitoid strain.

• In correlation with genetic data, this will provide valuable information on the structure of mealy aphid-parasitoid interactions and help identify the most virulent parasitoid strain for introduction.

4. Initial Findings

• mtDNA sequences for aphids from Spain, Greece, Italy, Tunisia, China, and CA show 3 main groups (haplotypes) within *Hyalopterus* (Fig. 1, left).

• These groups are largely determined by the host plant from which the sample was taken, though Haplotype 1 aphids are found on all 4 host plants—Plum, Almond, Peach, and Apricot (Fig. 1, left & right).

• Aphids collected on prune in CA's Central Valley belong to Haplotype 1. This indicates some possibility for mealy aphid in CA to feed on multiple *Prunus* hosts, and thus have the potential to threaten other stone fruit crops.

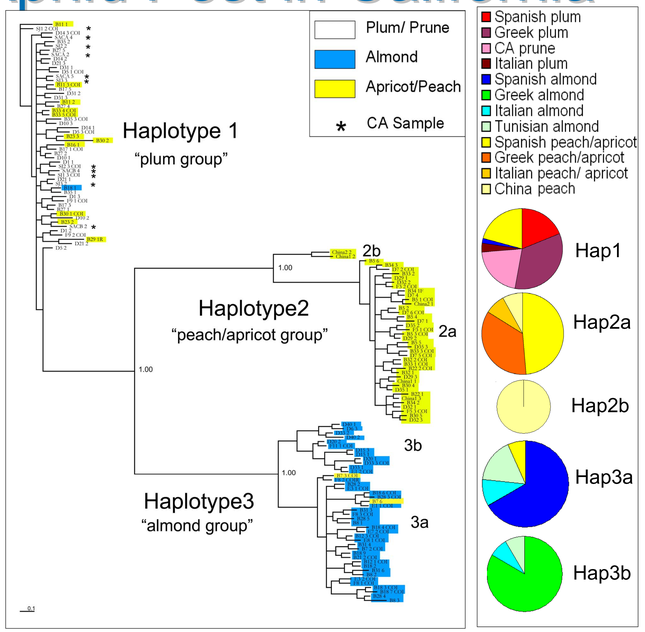


Fig. 1: COI phylogeny for *Hyalopterus* (left) and the occurrence of geographic/ host plant composition of each haplotype (right)

5. Impact

• Will increase understanding of the biology of *Hyalopterus* and its parasitoid in CA and the Mediterranean and allow proper identification of morphologically indistinguishable types.

• Will aid in the discovery of the most effective agent for biological control of mealy plum aphid.

• Will examine how a combination of genetic and ecological techniques can be used to study invasive species and biological control in general.

• Such information will be of great value in the study of a variety of other systems.

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