Dietary analysis of green lacewing using shotgun metagenomics to evaluate its potential as a biocontrol for almonds

Christine A. Tabuloc[1], Sara Gooder[2], Brad Higbee[2], and Joanna C. Chiu[1]

[1] Department of Entomology and Nematology, College of Agricultural and Environmental Sciences, University of California, Davis, CA 95616, USA
[2] Wonderful Orchards in Kern County, Shafter, CA 93263, USA

Introduction

Green lacewings (GLW) (*Chrysopa* and *Chrysoperla* spp) are ubiquitous in almonds in the San Joaquin Valley. Typically known as aphid predators, the ecosystem services provided by these widespread generalist predators are still not fully understood. Lacewings have been shown to prey on shallot aphids that are found in strawberry crops[1], fennel aphids, a major pest of fennel[2], the horticultural pest azalea lace bugs[3], and the cotton aphids[4], to name a few examples. Identifying the prey species make-up and benefit provided by these natural predators will assist the almond industry by demonstrating environmental stewardship, and coupled with other information being developed on pesticide impacts to GLW, will help inform management decisions that may impact conservation of these natural biocontrol agents.

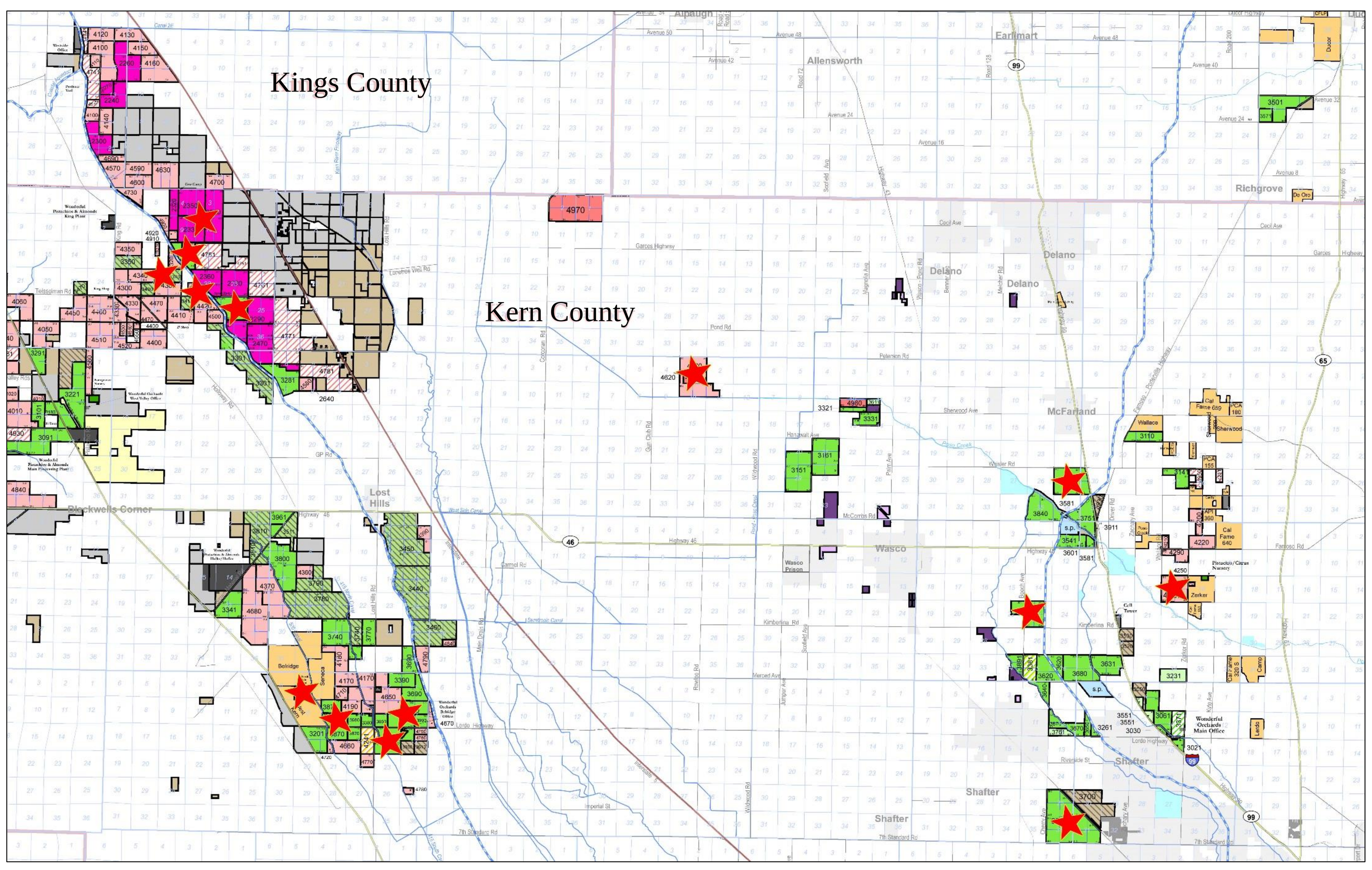
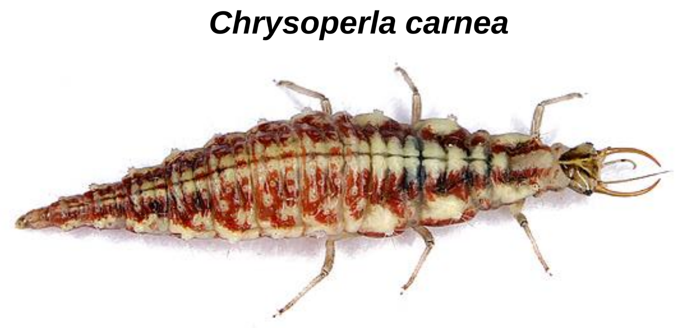


Figure 1. **Distribution of GLW in Kern County.** In a two year trapping survey using known attractants (Herbivore Induced Plant Volatiles or HIPVs) tuned specifically to GLW (Wonderful Orchards in Kern County; B. Higbee), *Chrysoperla carnea* and *Chrysoperla commanche* were by far the most abundant species. The stars above indicate GLW collection sites.

Hypothesis

Chrysoperla carnea



Spider mite

Common pests of almonds make up a large part of the GLW diet, making GLW a good biological control agent.

Methods

We will perform gut content analysis on GLW larvae using shotgun metagenomics via high-throughput sequencing[5], which is much more reliable, sensitive, and quantitative than conventional approaches, e.g. visual examinations and first-generation PCR-based molecular analysis[6,7,8].

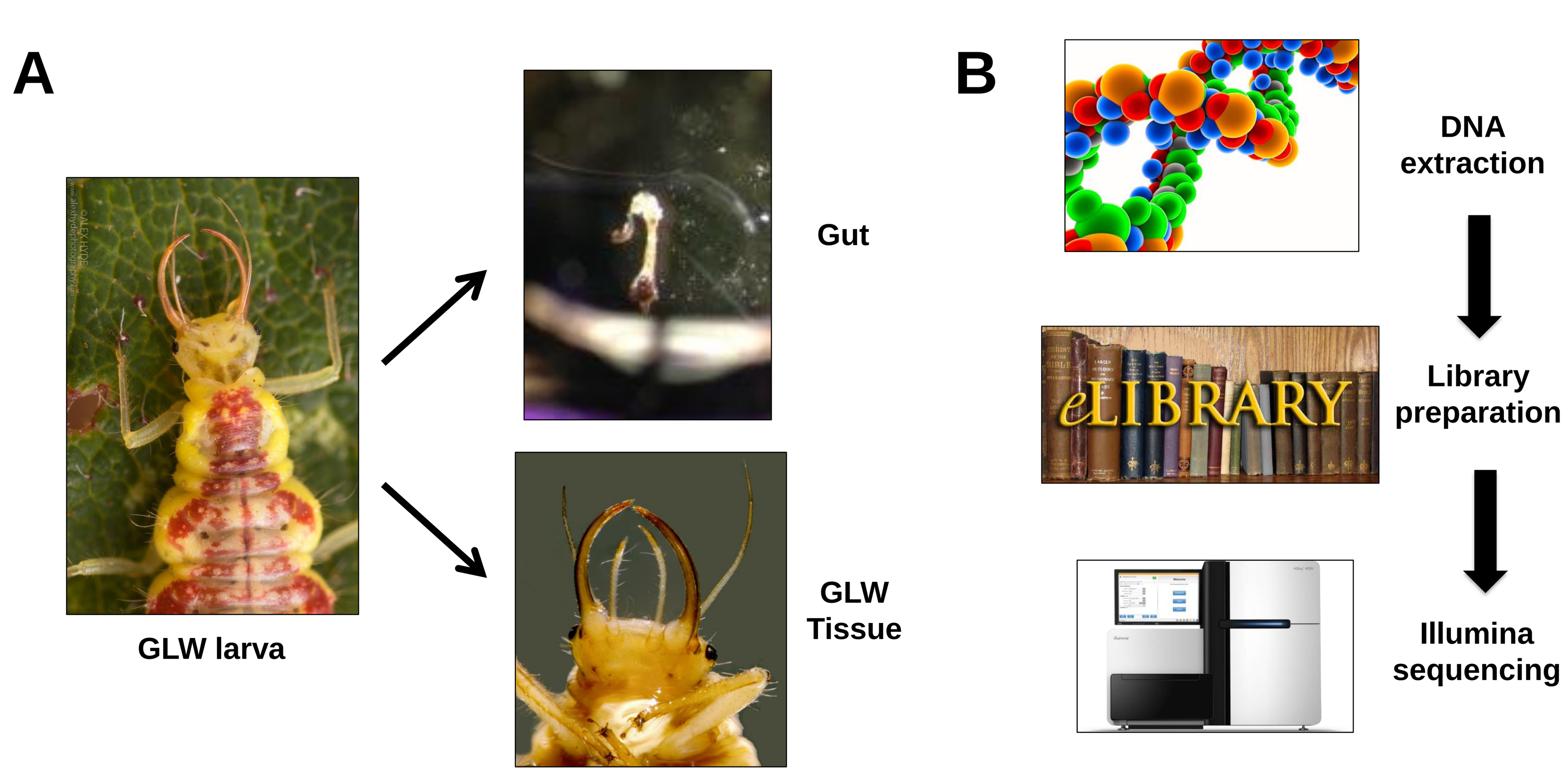
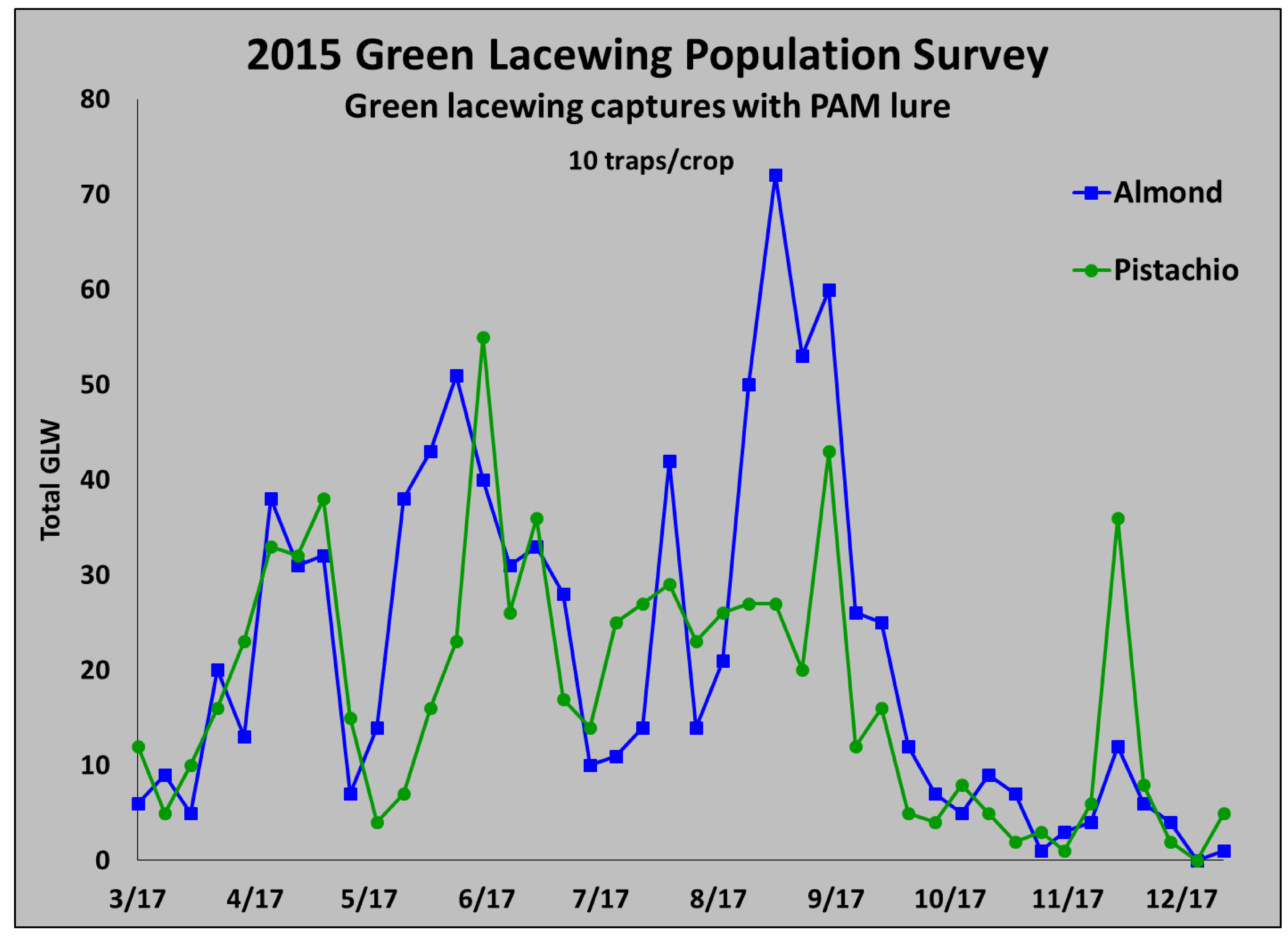


Figure 2. Overview of the experimental plan to examine dietary composition of GLW larvae. (A) Because in the Chrysoperla genera, larvae are predacious, GLW guts will be dissected from 10 larvae collected from almond orchards. GLW tissue will also be sequenced in order to differentiate between predator and prey DNA. **(B)** Genomic DNA will be extracted from these tissues using a conventional CTAB method. Libraries will be generated using the Qiagen QIAseq FX DNA Library Kit, subjected to quality control using the Agilent Bioanalyzer, and sequenced at the UC Davis Genome Center, using PE150 reads on the HiSeq 4000 platform.

Results



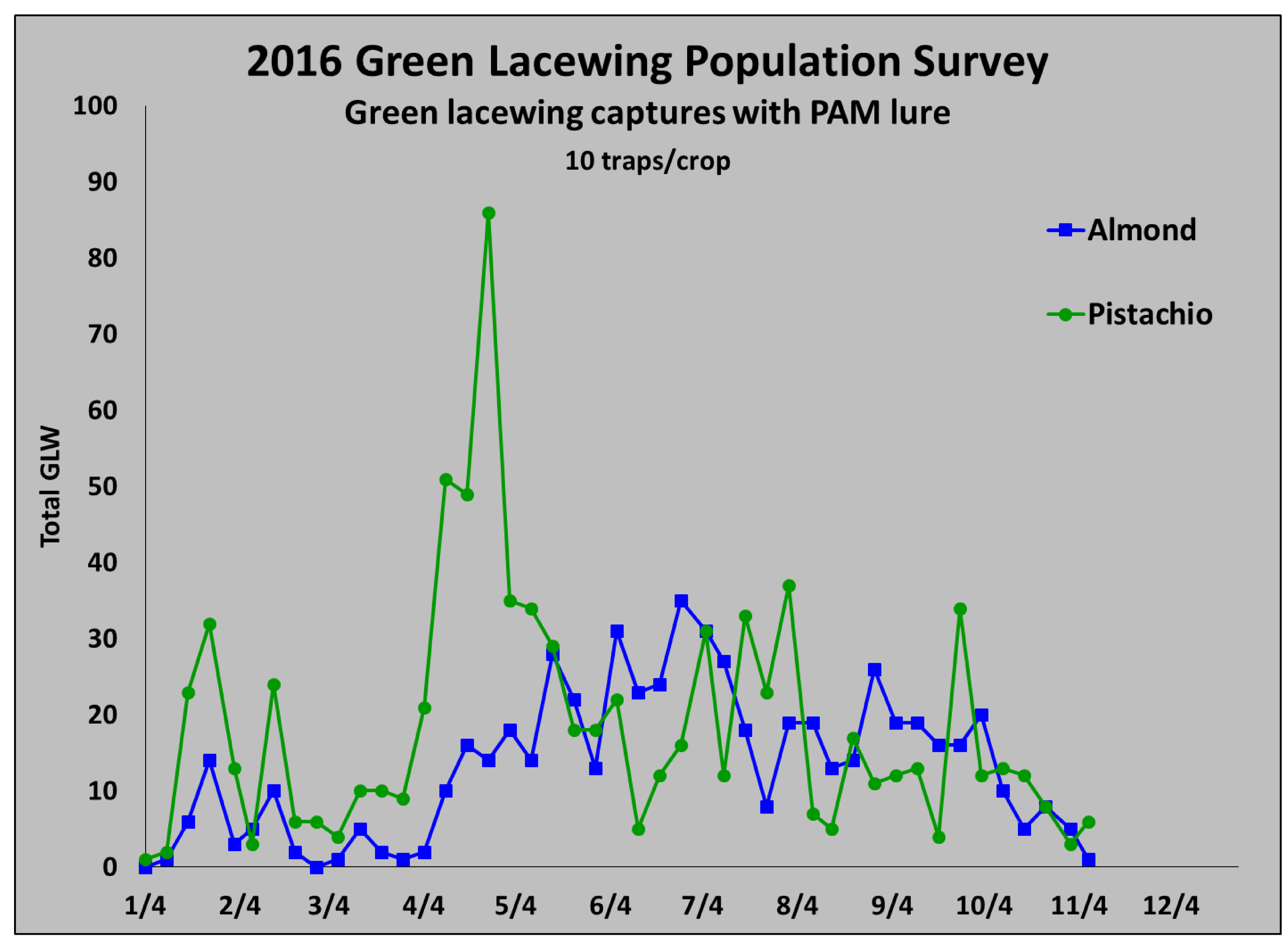


Figure 3. GLW larvae population survey in Kern County. Ten widely separated sites (Wonderful Orchards) were monitored throughout the season using an HIPV lure developed by Vince Jones at Washington State University. A delta trap loaded with a lure was placed at each site. The traps were checked weekly and lures were replaced every 4 weeks. Trapped GLW were brought to the Wonderful Entomology Laboratory (B. Higbee) for identification and tabulation. The larvae were then placed in 95% ethanol and transported to the Chiu Lab for gut content analysis. Because GLW larvae have a closed digestive system, all dietary components remain in the gut and can thus be studied.

Future Directions

- Identify prey of GLW larvae found in the San Joaquin Valley through gut content analysis by shotgun metagenomics
- Determine whether mites and other almond pests make up a large portion of the diet of GLW
- Evaluate the value of GLW as a sustainable management tool for almond crops

Acknowledgements

We thank the Almond Board of California for providing funding support. We acknowledge Josef Dvořák for the *Chrysoperla carnea* photo, Jack Kelly Clark for the spider mite photo, Alex Hyde for the GLW larva photo, and Duke University for the GLW tissue photo.

References

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