



Using Genomics to Guide Management of a Major Crop Pest, the Spotted Wing Drosophila

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Abstract

Global climate change and the steady increase in global population are currently intensifying pressure on agricultural systems. Mitigating the threat of invasive species is an important aspect in ensuring food security. *Drosophila suzukii*, also known as the Spotted Wing Drosophila (SWD) was recently introduced to California in 2008 and has since been spreading throughout North America, South America, and Europe. This vinegar fly has a serrated ovipositor that allows it to slice through the skin of fresh fruit and lay its eggs inside, where the larvae feed until maturation. Since limited biological controls are currently available to help manage the Spotted Wing Drosophila, heavy use of insecticides has been the main strategy. Unfortunately, heavy use of insecticides may lead to rapid evolution of insecticide resistance. My goal is to (1) identify insecticide resistance mechanisms in this pest and (2) determine invasion history and genetic lineages of SWD populations to help guide biological control strategies. Both objectives will be accomplished using next-generation sequencing transcriptomic analysis on SWD populations collected from various locations in the U.S., Asia, Europe, and South America. Identifying insecticide resistance markers in this species will allow for the development of genotyping assays that can help guide management strategies. Genomic approaches are often underutilized for applications in integrated pest management, but can be useful tools in evaluating insecticide resistance and insect population dynamics. Given that a close relative of SWD is a well-characterized model organism (*Drosophila melanogaster*), this invasive species provides an excellent opportunity to integrate genomic techniques into the area of pest management.

Introduction

- Global climate change and the steady rise in the Earth's population is **intensifying pressure** on agricultural systems.
- Current estimates show that insects cause **18% of losses** in global crop production [1].
- An increase in average global temperature may only **intensify the damage** caused by insects through increased overwintering survival, higher reproductive rates, and an increased number of generations [1].
- Drosophila suzukii* is an **invasive species** that threatens berries and soft-skinned fruits.
- Since its introduction to California in 2008, **significant crop losses** due to *D. suzukii* have been detected throughout the US, Canada, South America, and Europe.
- At 20% damage, an **estimated 300 million dollars** could be lost per year in California alone due to damage from *D. suzukii* [2].
- D. suzukii* has a **serrated ovipositor** that allows it to slice into the skin of fresh fruit, whereas other common *Drosophila* species prefer spoiled and unmarketable fruits.
- One important mechanism of insecticide resistance is called **target site resistance**. This is caused by mutations that change the insecticide binding site, reducing binding efficacy.



Serrated ovipositor of *D. suzukii*



Damage to a cherry caused by *D. suzukii*



D. suzukii larvae in a blackberry

Photo Courtesy: Martin Hauser

Major Goals

- Integrate genomic techniques into the field of pest management.
- Identify markers for insecticide resistance to better guide management strategies.
- Determine invasion history and genetic lineages of *Drosophila suzukii*.

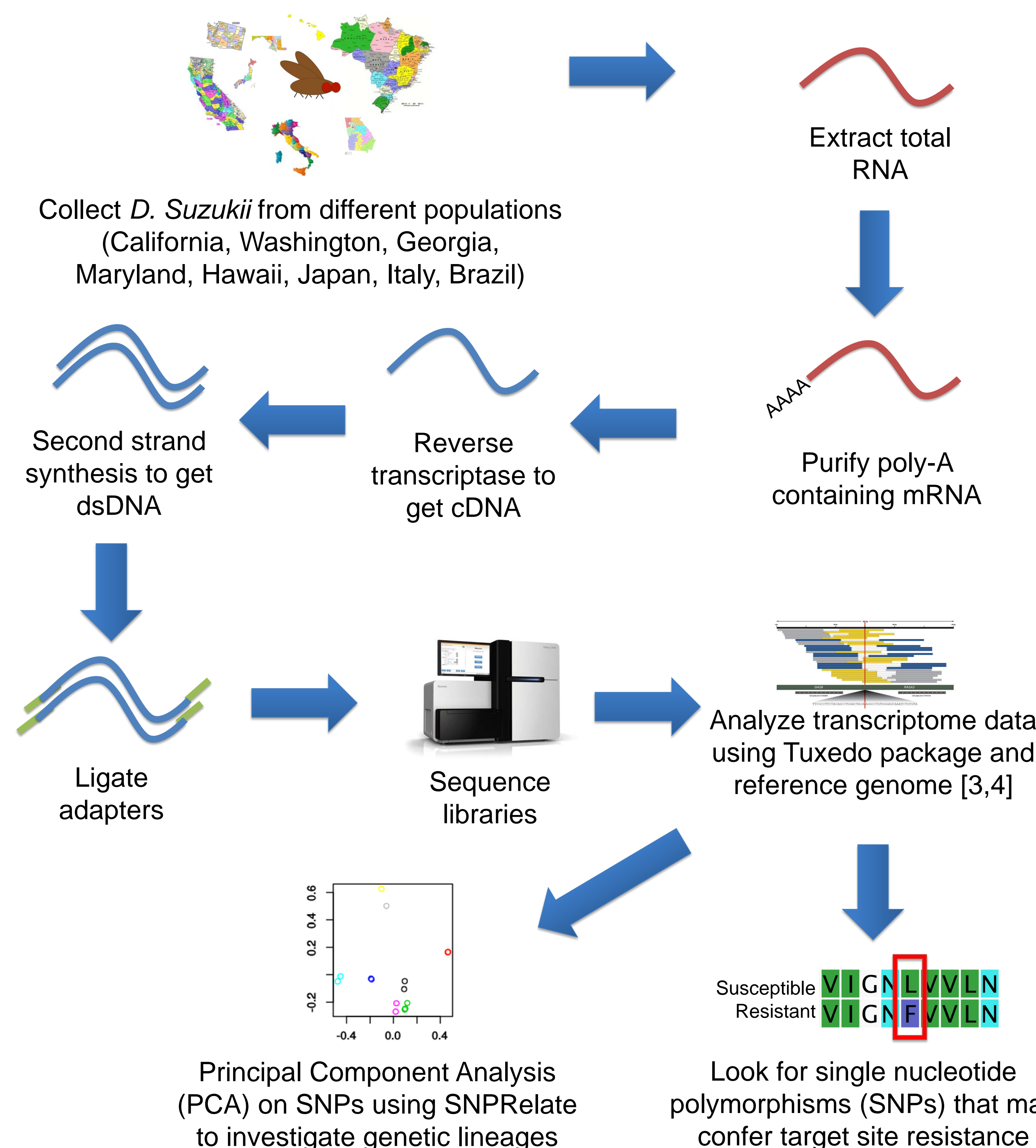


Adult male *D. suzukii*

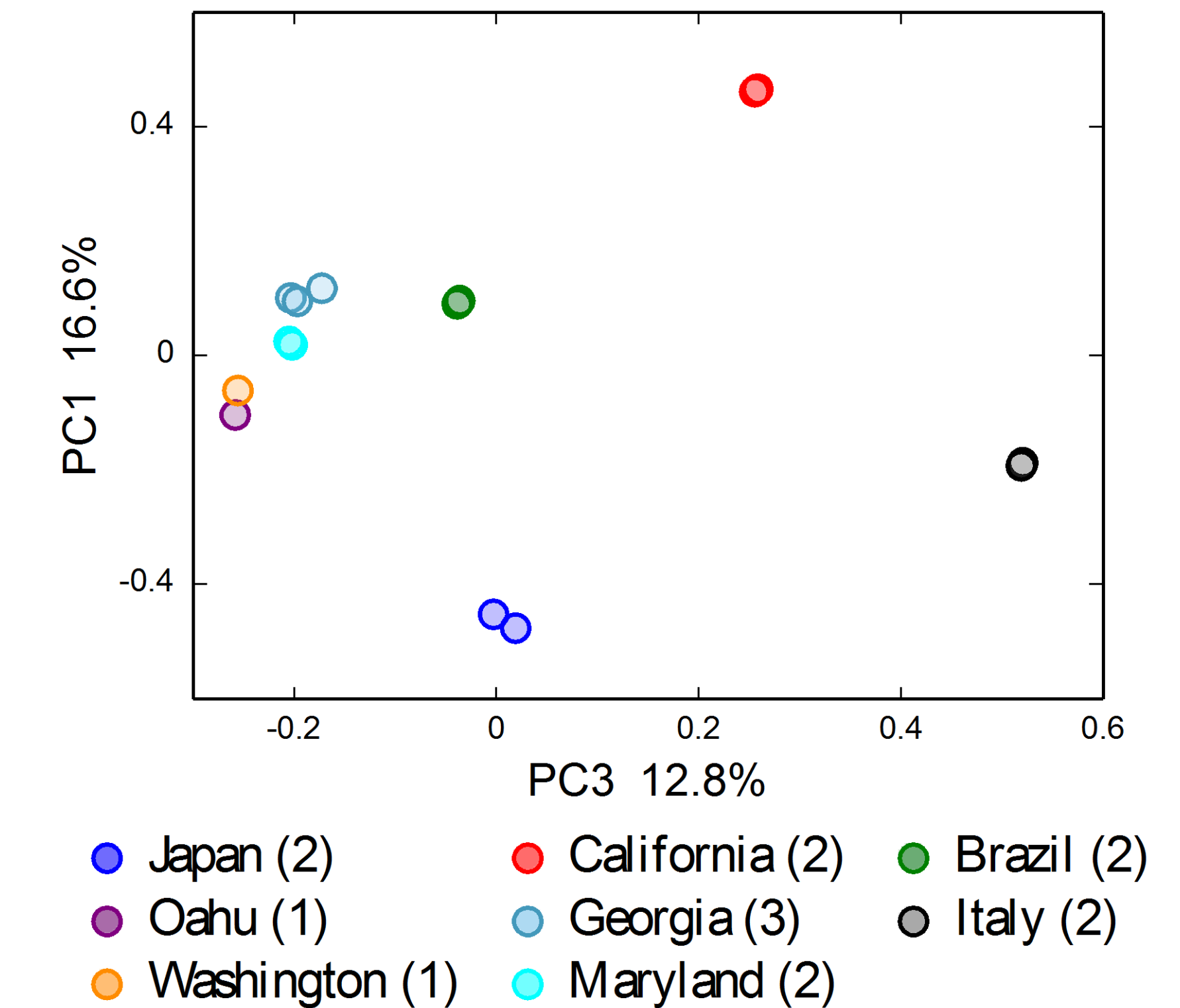


Adult female *D. suzukii*

Methods



Results



SNP genotyping reveals genetic relationships among populations of *Drosophila suzukii*. Principal Component Analysis (PCA) was performed on 317,423 SNPs using SNPRelate (<https://github.com/zhengxwen/SNPRelate>). Genetic relatedness correlates with geographic distribution, e.g. Maryland and Georgia were closely related and relatively close in geographic location. Since *D. suzukii* was first detected in California in 2008, it was hypothesized that Washington populations came from California. However, the Washington population is most closely related to the Hawaiian population, suggesting that *D. suzukii* was introduced to Washington from Hawaii, not California.

Conclusion

Key Findings

• Results show that populations of *D. suzukii* from Hawaii may have been introduced to Washington, which may have then been introduced to other places like Maryland and Georgia.

Future Directions

- Sample more individuals from each population.
- Use these results to detect local and long-distance movement of *D. suzukii* populations.
- Once insecticide resistance markers are determined, design a high-throughput assay that allows a quick assessment of insecticide resistance.
- Determine upregulation of genes involved in metabolic resistance between populations using differential expression analysis.

References

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