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Genetic diversity of *Drosophila suzukii* in San Diego.

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The introduction of the fruit fly *Drosophila suzukii* has caused major problems in California's soft fruit industries (Cline 2009). The species is native to Asia and has been spotted on crops in Japan since 1916 (Kanzawa 1936). *Drosophila suzukii* was first introduced to Hawaii in the 1980's (Kaneshiro 1983), and it was spotted in 2008 in central California. Since 2008 it has spread throughout the western coast of the United States and to areas of Florida (Walsh *et. al*., 2010). Unlike other species of *Drosophila*, female *D. suzukii* have very large ovipositors that are capable of inserting eggs into unripe fruit. The puncture at the oviposition site is then susceptible to secondary microbial infections, ruining the commercial value of several thin-skinned summer fruits including cherries, pears, grapes, peaches, and blueberries (Walsh *et al*., 2010). The extent of the economic loss caused by these flies is not known.

Eight male *D. suzukii* were collected in a La Jolla, California residential yard during the summer of 2010. The DNA from these flies was extracted using DNeasy kits (Qiagen) following the manufacturer's protocol. A 631 bp fragment of the mitochondrial Cytochrome Oxidase I gene of each fly was sequenced to estimate the genetic diversity of the population. These sequences were then compared to sequences from a stock of flies from Hachijo Island, Tokyo, Japan caught in 1978 (UCSD Drosophila Stock Center) and to sequences on GenBank from flies collected in Washington, California, and Spain in 2009 (GenBank: HM803273.1 - HM803279.1 and HM636439.1, respectively). Sequences from this study can be found on GenBank under accession numbers: HQ646995-HQ646999.

The sequences from the La Jolla *D. suzukii* show an extremely high genetic diversity at the CO1 locus (Table 1), with five distinct haplotypes in only eight flies. As a comparison, well-established populations of *D. emarginata* and *D. sturtevanti* in Panama had haplotype diversity values of 0.205 and 0.406, respectively (Schumacher and Hooton, 2011). Such high levels of genetic diversity were unexpected in the La Jolla *D. suzukii* population, because it was reportedly introduced to the western United States only two years ago (Walsh *et al*., 2010). Moreover, a bottleneck or founder effect significantly decreases genetic diversity (England *et al*., 2003). Thus, *D. suzukii* either has been established in the western United States for a significant period of time, has been introduced multiple times, or was introduced only once but with enough individuals to maintain a genetically diverse pool.

Table 1. Genetic diversity and neutrality test of the *D. suzukii* from La Jolla.

Gene	N	Haplotypes	Bp	Polymorphic sites	Haplotype diversity (±SD)	Π (±SD)	Tajima's D
COI	8	5	631	9	0.873±0.005	0.005±.000	-.387 NS

Table 2. Relative abundance of *D. suzukii* COI haplotypes in La Jolla.

Haplotype Name	Number of individuals sequenced
1	3
2	1
3	1
4	2
5	1

It is interesting to note the negative neutrality test values. Negative values for a Tajima's D test indicate growth in the sampled population (Tajima, 1989). A negative neutrality value is expected, because this population is thought to have recently arrived in California. The test results were not significant, because the sample size was too small.

The origin of *D. suzukii* in western North America is not clear. The flies sequenced from Japan shared a haplotype with the California populations, consistent with the theoretical Japanese origin. In order to assess if the observed haplotypes originated in Japan, flies from additional populations from Japan should be sequenced. The GenBank sequence from Washington differed from Japanese and California flies but overlapped with those of *D. suzukii* recently found in Spain (Calabria *et al*., 2010).

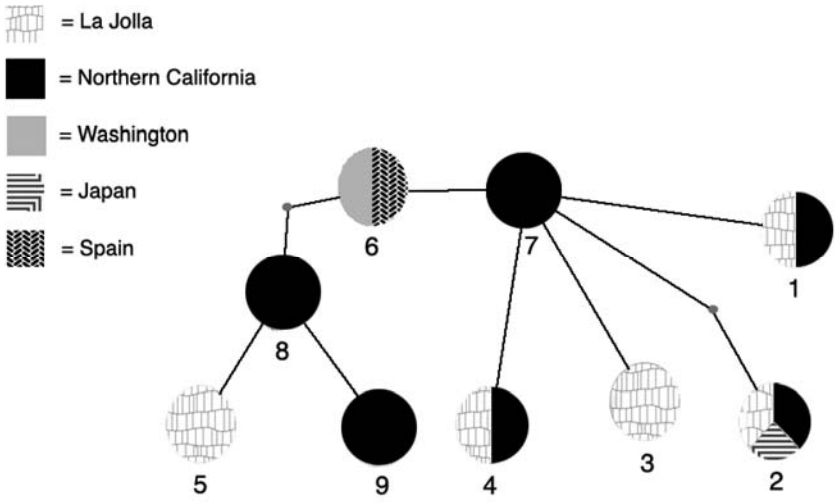

Figure 1. CO1 Haplotype Network of the sequences of flies from this study and sequences from GenBank. The numbers under the circles are the name of each haplotype and correspond to the names in Table 2. The relative abundance of each haplotype is not represented in this figure.

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