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Population genetic structure of the predatory, social wasp Vespula pensylvanica in its native and invasive range

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Authors
Chau, LM
Hanna, C
Jenkins, LT
et al.

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Population genetic structure of the predatory, social wasp *Vespula pensylvanica* in its native and invasive range

Linh M. Chau¹, Cause Hanna², Laurel T. Jenkins¹, Rachel E. Kutner¹, Elizabeth A. Burns¹, Claire Kremen³ & Michael A. D. Goodisman¹

¹School of Biology, Georgia Institute of Technology, Atlanta, Georgia 30332
²Environmental Science and Resource Management, California State University, Camarillo, California 93012
³Environmental Science, Policy and Management, University of California, Berkeley, California 94720

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Correspondence
Michael A. D. Goodisman, School of Biology, Georgia Institute of Technology, Atlanta, GA.
Tel: (404) 385 6311;
Fax: (404) 894 0519;
E-mail: michael.goodisman@biology.gatech.edu

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Abstract
Invasive species cause extensive damage to their introduced ranges. Ocean archipelagos are particularly vulnerable to invasive taxa. In this study, we used polymorphic microsatellite markers to investigate the genetic structure of the social wasp *Vespula pensylvanica* in its native range of North America and its introduced range in the archipelago of Hawaii. Our goal was to gain a better understanding of the invasion dynamics of social species and the processes affecting biological invasions. We found that *V. pensylvanica* showed no significant genetic isolation by distance and little genetic structure over a span of 2000 km in its native range. This result suggests that *V. pensylvanica* can successfully disperse across large distances either through natural- or human-mediated mechanisms. In contrast to the genetic patterns observed in the native range, we found substantial genetic structure in the invasive *V. pensylvanica* range in Hawaii. The strong patterns of genetic differentiation within and between the Hawaiian Islands may reflect the effects of geographic barriers and invasion history on gene flow. We also found some evidence for gene flow between the different islands of Hawaii which was likely mediated through human activity. Overall, this study provides insight on how geographic barriers, invasion history, and human activity can shape population genetic structure of invasive species.

Introduction
Invasive species are recognized as one of the top threats to the environment (Sakai et al. 2001; Pejchar and Mooney 2009; Kirk et al. 2013; Simberloff et al. 2013). Introduced species can displace native taxa, alter habitats, act as vectors for foreign diseases, and reduce levels of biodiversity (Sakai et al. 2001; Kenis et al. 2009; Brockerhoff et al. 2010; Beggs et al. 2011). Invasive species are often transported to new locations through human-mediated methods (Sakai et al. 2001). Consequently, the growing rate of globalization has increased the risk of non-native species being introduced to new regions (Pejchar and Mooney 2009).

Many social insects are highly successful invasive species (Moller 1996; Tsutsui et al. 2000; Chapman and Bourke 2001; Tsutsui and Suarez 2003; Beggs et al. 2011; Husseneder et al. 2012; Evans et al. 2013; Kirk et al. 2013; Gotzek et al. 2015). Introductions of invasive termites, ants, social bees, and social wasps have caused substantial damage to local ecosystems and economies (Holway et al. 2002; Suarez and Case 2002; Beggs et al. 2011; Evans et al. 2013). The success of social insects as invasive species is likely associated with their social structure, in addition to other factors such as their occupation of broad niches, high dispersal power, and effective predator defense (Moller 1996). These traits allow invasive social insects to work efficiently and rapidly increase in density in new environments, raising the likelihood of invasion success (Moller 1996; Smith et al. 2008).

*Vespula* wasps are particularly notorious invasive social insects. *Vespula* wasps are native to various regions throughout the northern hemisphere but have been introduced to many locations, such as Australia, South America, Hawaii, and New Zealand (Akre et al. 1981; Brockerhoff et al. 2010; Beggs et al. 2011; Monceau et al. 2017).
We collected 1364 V. pensylvanica workers from their native range in the western part of the United States and their invasive range in Hawaii in 2008 (Table S1, Supporting information). Native samples were collected from 170 traps within the states of California, Colorado, Oregon, Wyoming, and New Mexico. Invasive samples were collected from 178 traps from the Hawaiian Islands of Kauai, Oahu, Molokai, Lanai, Maui, and Hawaii (Fig. 1). Specimens were collected by deploying 5–15 Seabright Yellow Jacket and Wasp Traps	extsuperscript{®}, separated by $\geq325$ m, for 24–48 h. The traps were baited with n-heptyl butyrate emitted from controlled-release dispensers (Landolt et al. 2003). Wasps collected in traps were placed in 95% ethanol for subsequent genetic analysis.

Sampling was conducted in a hierarchical manner consisting of four levels: traps, transects, regions, and ranges. Multiple traps were set along more or less linear transects, which spanned up to 14.5 km. Several transects were found within regions, defined as either the focal state in the native habitat or island in the invasive habitat. Regions were then grouped into two distinct ranges; the native range consisted of all states in the mainland of the United States and the invasive range consisted of the Hawaiian Islands (Table 1).
DNA extraction and genotyping

We assayed the multilocus genotype of 1364 *V. pensylvanica* workers at the following 15 microsatellite markers: VMA6, LIST2002, LIST2003, LIST2004, LIST2007, LIST2008, LIST2010, LIST2014, LIST2015, LIST2017, LIST2019, LIST2020, RUFA3, RUFA5, and RUFA19 (Thorén et al. 1995; Daly et al. 2002; Hasegawa and Takahashi 2002). DNA was extracted from the legs of *V. pensylvanica* workers using a modified Chelex protocol (Goodisman et al. 2001). Loci were PCR-amplified with fluorescently labeled primers (Hoffman et al. 2008). The resulting PCR fragments were subsequently run on an ABI 3100 Genetic Analyzer. Alleles were scored using GeneMarker v 4 (SoftGenetics).

Genetic data analysis

Genetic diversity measures, including number of alleles, effective number of alleles, observed heterozygosity (*H₀*), and expected heterozygosity (*Hₑ*), were calculated with GenAlEx v 6.5 (Peakall and Smouse 2012). We used GENEPOP v 4.3 to test for deviations of genotype frequencies from Hardy–Weinberg equilibrium within each transect (Rousset 2008). The Bonferroni correction was used to adjust for multiple testing.

Our initial analysis detected significant deviations from Hardy–Weinberg equilibrium in 32 transects. We found that most departures were caused by an excess of homozygosity at the locus LIST2002. Microchecker v 2.2 was thus used to detect the presence of null alleles by identifying heterozygote deficiencies at each locus (van Oosterhout et al. 2006). We confirmed that LIST2002 displayed significant evidence of null alleles in 26 of 44 transects. Due to the deviation from Hardy–Weinberg equilibrium and the putative presence of null alleles, we eliminated LIST2002 from our analyses. All subsequent statistical tests were thus performed without LIST2002.

We screened for linkage disequilibrium between loci within transects using GENEPOP v 4.3 (Rousset 2008). Default parameters were used for all tests. Allele number and sample size corrected allelic richness were calculated with FSTAT v 2.9.3 (Goudet 1995). Wilcoxon signed-rank tests were used to compare allelic richness between the native and invasive ranges, and also among regions within ranges. We used Friedman tests to compare levels of allelic richness among the Hawaiian Islands in the invasive range.

We estimated Weir and Cockerham’s *θ* using Genetic Data Analysis (GDA) v 1.1 in order to assess levels of genetic differentiation (Weir and Cockerham 1984; Weir 1996; Holsinger and Weir 2009). Estimates of population structure were obtained at multiple levels, including individuals within traps, traps within transects, transects within regions, and regions within ranges. GDA was also used to calculate 95% confidence intervals (based on 1000 bootstraps) around estimates of *θ*. Traps, transects, and regions with less than two samples were excluded from the analyses.
Pairwise measures of $F_{ST}$ were calculated between all traps using GENEPOP. These measures of genetic distance were then compared to geographic distance to determine whether *V. pensylvanica* displayed evidence of genetic isolation by distance (Wright 1943; Rousset 2008). The significance of the correlation between geographic and genetic distance was assessed with Mantel tests. These tests were performed with 1000 permutations in the R package vegan v 2.0 (Dixon 2003).

Individuals were assigned to putative populations using Bayesian clustering as implemented by STRUCTURE v 2.2 (Pritchard et al. 2000). To estimate the number of populations ($K$) present in the native range and invasive range, we performed different simulations, each under the assumption of a different $K$ value (1 to 44), representing the total number of transects. For each simulation, we used an admixture model with uncorrelated allele frequencies to account for wasps with mixed ancestry and the LOCPRIOR model to use sampling location to inform clustering. Each simulation was run 10 times with 10,000 steps of burn-in and 50,000 Markov chain Monte Carlo (MCMC) repetitions. The most likely number for $K$ was selected based on log likelihood and the $\Delta K$ statistic developed by Evanno et al. (2005) as implemented in STRUCTURE HARVESTER (Pritchard et al. 2000; Evanno et al. 2005; Earl and Vonholdt 2012). For a given set of simulations for each $K$, CLUMPP v 1.1.2 was used to align the 10 replicate runs (Jakobsson and Rosenberg 2007). Distruct v 1.1 was then used to visualize the results of the clustering process (Rosenberg 2004).

We used the program GeneClass2 to determine the origin of individuals from the invasive range (Piry et al. 2004). We first used assignment tests to determine the likelihood that an individual *V. pensylvanica* wasp in the invasive range was from an identified reference population in native range. For the assignment tests, we used the Bayesian criteria developed by Rannala and Mountain (1997) with an assignment threshold of 0.05. We also used GeneClass2 to exclude native regions as source populations for invasive *V. pensylvanica*. To exclude individuals, we used the Bayesian criteria from Rannala and Mountain (1997) along with the resampling algorithm from Paetkau et al. (2004). We calculated the exclusion probability for each introduced individual with 1000 MCMC simulations and an alpha level of 0.01.

We used the program DIYABC 2.0 (Cornuet et al. 2014) to further understand the invasion process and detect possible source populations of invasive *V. pensylvanica*. DIYABC 2.0 uses approximate Bayesian computation (ABC) which is a Bayesian approach that compares the posterior probabilities of a large number of simulated

### Table 1. Total numbers of traps and individual *Vespula pensylvanica* wasps collected from each transect in the different sampled ranges and regions.

<table>
<thead>
<tr>
<th>Range</th>
<th>Region</th>
<th>Transect</th>
<th>Traps</th>
<th>Individuals</th>
</tr>
</thead>
<tbody>
<tr>
<td>Native</td>
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<td>Atascadero</td>
<td>8</td>
<td>38</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Balboa Park</td>
<td>5</td>
<td>21</td>
</tr>
<tr>
<td></td>
<td></td>
<td>BR</td>
<td>8</td>
<td>29</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Corning</td>
<td>3</td>
<td>8</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Diablo</td>
<td>10</td>
<td>43</td>
</tr>
<tr>
<td></td>
<td></td>
<td>La Jolla</td>
<td>2</td>
<td>9</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Lake Shasta</td>
<td>7</td>
<td>27</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Los Padres</td>
<td>9</td>
<td>43</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Morgan Hill</td>
<td>4</td>
<td>20</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Portrero Road</td>
<td>7</td>
<td>23</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ramona</td>
<td>11</td>
<td>43</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Santa Maria</td>
<td>8</td>
<td>31</td>
</tr>
<tr>
<td></td>
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<td>Tilden Park</td>
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<td>59</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Tres Pinos</td>
<td>8</td>
<td>29</td>
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<tr>
<td>Colorado</td>
<td></td>
<td>Loveland</td>
<td>2</td>
<td>10</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Outside Fort</td>
<td>4</td>
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<tr>
<td></td>
<td></td>
<td>Outside Larimer County</td>
<td>1</td>
<td>5</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Within Fort Collins</td>
<td>8</td>
<td>35</td>
</tr>
<tr>
<td>New Mexico</td>
<td></td>
<td>Chimayo</td>
<td>1</td>
<td>5</td>
</tr>
<tr>
<td>Oregon</td>
<td></td>
<td>Chemult</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Columbia River</td>
<td>3</td>
<td>7</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Gorge</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Klamath Falls</td>
<td>1</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Mill City</td>
<td>4</td>
<td>8</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Salem Area</td>
<td>37</td>
<td>131</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sisters</td>
<td>3</td>
<td>5</td>
</tr>
<tr>
<td>Wyoming</td>
<td></td>
<td>Chugadul Caspar</td>
<td>2</td>
<td>5</td>
</tr>
<tr>
<td>Invasive</td>
<td>Hawaii</td>
<td>Kahuku</td>
<td>11</td>
<td>45</td>
</tr>
<tr>
<td></td>
<td></td>
<td>SRA</td>
<td>7</td>
<td>22</td>
</tr>
<tr>
<td></td>
<td>Kauai</td>
<td>Highway-552</td>
<td>11</td>
<td>35</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Makaha Ridge</td>
<td>9</td>
<td>40</td>
</tr>
<tr>
<td></td>
<td>Lanai</td>
<td>Garden of the Gods</td>
<td>1</td>
<td>5</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Monroe Trail</td>
<td>23</td>
<td>101</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Shipwreck</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Maui</td>
<td></td>
<td>Hosmer Grove</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Haleakala</td>
<td>7</td>
<td>25</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Maui Iao Valley</td>
<td>10</td>
<td>45</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Olinda Road</td>
<td>13</td>
<td>62</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Waiehe Ridge</td>
<td>14</td>
<td>64</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Trail</td>
<td></td>
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<tr>
<td></td>
<td></td>
<td>Waipoli Road</td>
<td>9</td>
<td>30</td>
</tr>
<tr>
<td>Molokai</td>
<td></td>
<td>Forest Reserve</td>
<td>27</td>
<td>122</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Road</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Molokai</td>
<td>2</td>
<td>8</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Kalaupapa 23</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Oahu</td>
<td></td>
<td>Manana</td>
<td>9</td>
<td>33</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Satellite Road</td>
<td>11</td>
<td>39</td>
</tr>
<tr>
<td></td>
<td></td>
<td>WV</td>
<td>9</td>
<td>23</td>
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<tr>
<td>Total</td>
<td></td>
<td></td>
<td>348</td>
<td>1364</td>
</tr>
</tbody>
</table>
datasets under given models to those calculated from observed data (Beaumont 2010). For each test, we compared scenarios to find potential source populations of an invasive population and to check for the presence of low effective population size after introduction (bottleneck). We compared four scenarios: (1) the focal invasive population was sourced from the native western regions (CA/OR), (2) the focal invasive population was sourced from the native central regions (WY/CO/NM), (3) the focal invasive population was sourced from the native western regions and underwent a bottleneck, and (4) the focal invasive population was sourced from the native central regions and underwent a bottleneck. The models included uniform priors with the following constraints: $t_2 > t_1$, $db < t_2$, and $N_{lb} < N_1$. A generalized stepwise mutation model was used for all analyses. Each test generated reference tables with $4 \times 10^5$ simulated datasets. Posterior probabilities were estimated for each scenario using polychotomous logistic regression.

Poptree2 was used to generate neighbor-joining (NJ) trees for individuals within transects and regions (Takezaki et al. 2010). Each tree was constructed using Nei’s $D_A$ distance. Node confidence was assessed using 1000 bootstraps (Nei et al. 1983).

Finally, the program Bottleneck was used to identify populations that may have recently undergone a decrease in population size (Luikart et al. 1998; Piry et al. 1999). This program exploits the principle that allele number is reduced faster than heterozygosity in populations that have recently experienced a reduction in effective population size. We used the Wilcoxon test with the two-phase mutation model (TPM), which is recommended for microsatellite datasets with small sample sizes per population and low numbers of polymorphic loci, to determine whether populations showed significant evidence of having passed through a recent bottleneck.

**Results**

**Genetic diversity**

We investigated whether levels of genetic diversity differed between native and invasive *V. pensylvanica*. We found that wasps from the native range had significantly higher allelic richness (Wilcoxon Sign-Rank Test; $P < 0.001$) and effective number of alleles ($P = 0.001$) than wasps from the invasive range (Table 2). We also found that number of private alleles in the native range (30 total) differed significantly ($P = 0.0219$) from the number of private alleles in the invasive range (8 total). Finally, the native range had a significantly higher level of expected heterozygosity ($P = 0.001$) and observed heterozygosity ($P = 0.023$) when compared to the invasive range. Overall, these results suggest that there is a slightly, but significantly, higher level of genetic diversity in the native range than the invasive range of *V. pensylvanica*.

We next investigated differences in genetic diversity between different islands in the invasive Hawaiian range (Table S2, Supporting information). There were significant differences in observed heterozygosity (Friedman test; $P = 0.0023$), expected heterozygosity ($P < 0.001$), effective number of alleles ($P < 0.001$), and number of private alleles ($P < 0.001$) among the islands. Interestingly, the island of Hawaii had the highest effective number of alleles, observed heterozygosity, expected heterozygosity, and allelic richness. Maui had highest number of private alleles. In contrast, Kauai had the lowest observed heterozygosity, expected heterozygosity, allelic richness, effective number of alleles, and number of private alleles.

Recently bottlenecked populations may display an excess of heterozygosity compared to expected heterozygosity calculated from observed allele number (Cornuet and Luikart 1996; Luikart et al. 1998). We found significant excesses of heterozygosity in Maui ($P = 0.034$) and New Mexico ($P < 0.001$). Additionally, there were marginally significant excesses of heterozygosity present in the islands of Hawaii ($P = 0.052$), Lanai ($P = 0.052$), and Molokai ($P = 0.086$). In contrast, Oahu ($P = 0.852$) and Kauai ($P = 0.380$) displayed no signs of bottlenecks. Overall, there is some evidence for population bottlenecks in the eastern islands of Hawaii but not the western islands.

**Genetic differentiation**

We measured genetic differentiation among hierarchically structured traps, transects, regions, and ranges of *V. pensylvanica*. We first considered measures of genetic structure for all individuals, combining data from both the native and invasive ranges. The metric $f$, which measures true inbreeding within populations, was relatively low, albeit significant (Table 3). We also uncovered significant differentiation at higher levels of sampling structure. Differentiation between transects within regions, as well as regions within ranges, was moderate. In spite of these results, we found no significant genetic differentiation between the native and invasive ranges (Table 3).

We next assessed the level of genetic differentiation between different hierarchical levels within the native and invasive ranges separately. We found significant genetic differentiation at most hierarchical levels in both ranges, although there were substantial differences in the magnitudes of differentiation in the native and invasive habitats. In the native range, measures of $\Theta$ were relatively low (Table 3). In contrast, all measures of $\Theta$ for the invasive range were high and strongly significant (Table 3).
Overall, there was substantially more genetic differentiation across hierarchical levels in the invasive range than the native range.

Pairwise $F_{ST}$ values were calculated between all regions (Table 4). Values of $F_{ST}$ were often less than 0.01 for comparisons within the native region, indicating relatively low levels of differentiation. In contrast, values of $F_{ST}$ in the invasive range were substantially higher, with many estimates exceeding 0.1. In addition, all pairwise comparisons involving Kauai had $F_{ST}$ values greater than 0.2, suggesting that Kauai may be the most genetically distinct island in the invasive range.

We tested for the presence of genetic isolation by distance. Our analysis revealed no significant correlation between genetic distance ($F_{ST}$) and geographic distance (km) for individuals sampled from different traps in the native range ($r = 0.042, P = 0.102$) (Fig. 2A).

In contrast, there was a strong and significant isolation-by-distance relationship between individuals sampled from different traps within the invasive region ($r = 0.569$, $P < 0.001$).
We found no evidence for isolation by distance within the individual Hawaiian Islands of Kauai ($r = 0.011, P = 0.546$), Oahu ($r = 0.062, P = 0.181$), Molokai ($r = 0.028, P = 0.665$), or Lanai ($r = 0.120, P = 0.157$). However, we did find significant isolation-by-distance relationships in Hawaii ($r = 0.163, P = 0.005$) and Maui ($r = 0.063, P = 0.002$).

**Table 4.** Pairwise estimates of $F_{ST}$ for all regions.

<table>
<thead>
<tr>
<th>Region</th>
<th>California</th>
<th>Colorado</th>
<th>Oregon</th>
<th>Wyoming</th>
<th>New Mexico</th>
<th>Molokai</th>
<th>Hawaii</th>
<th>Kauai</th>
<th>Lanai</th>
<th>Maui</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colorado</td>
<td>0.009*</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Oregon</td>
<td>0.005*</td>
<td>0.008*</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Wyoming</td>
<td>0.019*</td>
<td>0.005</td>
<td>0.014</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>New Mexico</td>
<td>0.029*</td>
<td>0.026*</td>
<td>0.034*</td>
<td>0.031*</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Molokai</td>
<td>0.083*</td>
<td>0.095*</td>
<td>0.081*</td>
<td>0.111*</td>
<td>0.107*</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hawaii</td>
<td>0.033*</td>
<td>0.046*</td>
<td>0.034*</td>
<td>0.054*</td>
<td>0.072*</td>
<td>0.124*</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Kauai</td>
<td>0.171*</td>
<td>0.197*</td>
<td>0.168*</td>
<td>0.244*</td>
<td>0.277*</td>
<td>0.244*</td>
<td>0.222*</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Lanai</td>
<td>0.091*</td>
<td>0.101*</td>
<td>0.095*</td>
<td>0.122*</td>
<td>0.101*</td>
<td>0.095*</td>
<td>0.118*</td>
<td>0.279*</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Maui</td>
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<td>0.059*</td>
<td>0.053*</td>
<td>0.076*</td>
<td>0.074*</td>
<td>0.119*</td>
<td>0.084*</td>
<td>0.230*</td>
<td>0.067*</td>
<td></td>
</tr>
<tr>
<td>Oahu</td>
<td>0.064*</td>
<td>0.084*</td>
<td>0.066*</td>
<td>0.108*</td>
<td>0.109*</td>
<td>0.096*</td>
<td>0.108*</td>
<td>0.218*</td>
<td>0.135*</td>
<td>0.111*</td>
</tr>
</tbody>
</table>

*P < 0.05.

**Figure 2.** Relationship between genetic distance ($F_{ST}$) and geographic distance (km) in the (A) native mainland (Mantel test $r = 0.042, P = 0.102$) and (B) invasive Hawaiian range ($r = 0.569, P < 0.001$) of *Vespula pensylvanica*. 

$P < 0.001$) (Fig. 2B). We found no evidence for isolation by distance within the individual Hawaiian Islands of Kauai ($r = -0.011, P = 0.546$), Oahu ($r = 0.062, P = 0.181$), Molokai ($r = -0.028, P = 0.665$), or Lanai ($r = 0.120, P = 0.157$). However, we did find significant isolation-by-distance relationships in Hawaii ($r = 0.163, P = 0.005$) and Maui ($r = 0.063, P = 0.002$).

**Genetic clustering**

*Vespula pensylvanica* wasps from the native and invasive ranges were both clustered into putative populations based on their multilocus genotypes. This analysis grouped individuals into two genetically distinct populations (Fig. 3A). All of the individuals from the native range formed a single population. Individuals from the islands of Hawaii, Kauai, and Oahu in the invasive regions clustered into this single population. Conversely, individuals from Molokai, Lanai, and Maui formed another distinct population separate from the other island and the mainland regions. Most individuals were assigned to a single cluster, suggesting a lack of admixture.

We performed the clustering analysis considering only individuals from the native range. In this case, it was difficult to assign the most likely number of populations ($K$), as the $\Delta K$ metric was similar for $K = 2$ and 3. Nevertheless, $K = 3$ had the highest $\Delta K$. Interestingly, almost all individuals in the native range were partially assigned to all three putative populations (Fig. 3B). Individuals sampled from Balboa Park transect in California were a slight exception and tended to form a more distinct group than individuals sampled from other transects. However, the overall analysis indicated a general lack of genetic structure within the native range of *V. pensylvanica*.

We next clustered individuals within the invasive range only. The $\Delta K$ metric produced a clear peak, in contrast to the analysis of the native range samples, suggesting the most likely number of populations was seven (Fig. 3C). Individuals within islands tended to form distinct clusters. Specifically, *V. pensylvanica* within Molokai, Kauai, and Lanai each formed separate and distinct populations. Samples from Oahu were separated into two clusters, where individuals were either part of a cluster that also consisted of samples from Hawaii or part of a cluster that
consisted solely of samples from Oahu (Fig. 3C). All of the Oahu individuals that clustered with Hawaiian samples were collected from a single transect, Satellite Road, and showed no signs of admixture. In contrast, individuals from Maui displayed signs of admixture. Most individuals from Maui were partially assigned to two clusters; however, the fractional memberships of individuals varied by transect. Individuals from the transects of Hosmer Grove, Haleakala, Olinda Road, and Waipoli Road had a higher probability of being assigned to one cluster (Fig. 3C) while individuals from Maui Iao Valley and Waihee Ridge Trail had a higher probability of being assigned to the other Maui cluster (Fig. 3C). Regardless, the overall analysis of samples from the invasive range showed substantial evidence for population genetic structure both within and between islands.

We assigned individuals from the invasive range to regions in the native range to determine the potential origins of invasive *V. pensylvanica* in Hawaii. We found that 80% of the individuals from the invasive range had the highest score of being assigned to the western regions of the native range (Table S3A, Supporting information). Overall, the mean assignment scores for the western regions were higher than those found for the central regions (Table 5a). This suggested that the western part of the native range was the most probable source of the invasive population. Notably, however, exclusion probabilities were generally high for all individuals (*P* > 0.05), suggesting that we cannot exclude either the western or the central regions as the source population for invasive *V. pensylvanica* (Table S3B, Supporting information).

In contrast to the assignment tests, approximate Bayesian computation suggested that the central regions of the native range were the most likely source of the invasive populations (Table 5b). Specifically, the scenario where individuals from the invasive range were derived from the central part of the native range without a bottleneck had the highest probability among different tested scenarios (Posterior Probability = 0.655; 95% C.I. of 0.603 to 0.708).

We visualized the relationships between individuals sampled from different transects with neighbor-joining trees. Transects from the native regions formed a starlike structure, indicating a lack of strong genetic relationships in the native range (Fig. 4A). In contrast, transects in the invasive range from the same island clustered together, reflecting the genetic differences between islands (Fig. 4B). We also produced a neighbor-joining tree of all regions in both the native and invasive ranges and found that samples from Maui, Lanai, and Molokai formed a single group while samples from Hawaii, Oahu, and Kauai grouped with mainland regions (Fig. 4C).

**Discussion**

**Small reduction in genetic diversity in the invasive range of *V. pensylvanica***

Introduced species tend to experience drops in genetic diversity due to population bottlenecks derived from founder events (Luikart et al. 1998; Goodisman et al. 2001; Sakai et al. 2001; Dlugosch and Parker 2008). Reduced genetic diversity could have negative effects on invasion success because it can affect a population’s
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**Table 5.** Assignment of invasive *Vespula pensylvanica* populations to the western regions (California and Oregon) or central regions (Wyoming, Colorado, and New Mexico) of the native range. (a) Assignment scores of individuals from invasive regions to combined reference regions. (b) Relative posterior probability (with 95% C.I. in parentheses) for demographic scenarios where invasive regions were derived from either the western or central regions with or without associated bottlenecks.

<table>
<thead>
<tr>
<th>Island</th>
<th>a. Scores</th>
<th>b. Relative posterior probability</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>West</td>
<td>Central</td>
</tr>
<tr>
<td>Kauai</td>
<td>90.2</td>
<td>9.8</td>
</tr>
<tr>
<td>Molokai</td>
<td>67.5</td>
<td>32.5</td>
</tr>
<tr>
<td>Maui</td>
<td>76.2</td>
<td>23.8</td>
</tr>
<tr>
<td>Lanai</td>
<td>70.2</td>
<td>29.8</td>
</tr>
<tr>
<td>Hawaii</td>
<td>87.6</td>
<td>12.4</td>
</tr>
<tr>
<td>Oahu</td>
<td>90.9</td>
<td>9.1</td>
</tr>
<tr>
<td>All Islands</td>
<td>78.2</td>
<td>21.8</td>
</tr>
</tbody>
</table>

growth and ability to adapt to changing selection pressures (Sakai et al. 2001). However, a lack of genetic diversity does not necessarily preclude population growth or adaptation (Dlugosch and Parker 2008; Moran and Alexander 2014). Thus, there is considerable interest in understanding whether invasive species experience losses of genetic diversity and whether such losses are associated with invasion success (Dlugosch and Parker 2008; Purcell et al. 2012; Moran and Alexander 2014).

We compared levels of genetic diversity found within the native and invasive ranges of *V. pensylvanica*. Overall, greater levels of genetic diversity were observed in the native range than those in the invasive range. This is attributed to a lack of genetic structure in the native range (Table 2). However, the differences in variation between the two ranges were modest. *Vespula pensylvanica* from the invasive range had 97% of the expected heterozygosity and 64% of the allelic richness found in the native range. The overall drop in expected heterozygosity is quite small compared to the drop in allelic richness, which is a characteristic of a brief population bottleneck (Luikart et al. 1998). In this case, some rare alleles are lost, although observed heterozygosity, which is more strongly influenced by common alleles, is not severely reduced (Luikart et al. 1998).

The allelic richness lost by invasive *V. pensylvanica* is similar to that lost by other invasive social insects, such as the Formosan subterranean termite, *Coptotermes formosanus*, and the paper wasp, *Polistes chinensis arenalis*, in their invasive ranges (Husseneder et al. 2012; Tsuchida et al. 2014). In contrast, the Argentine ant, *Linepithema humile*, the Eastern Subterranean termite, *Reticulitermes flavipes*, and the Buff-tailed bumblebee, *Bombus terrestris*, experienced drops in allelic richness of 50% or more in their invasive ranges (Tsutsui et al. 2000; Vargo 2003; Schmid-Hempel et al. 2007).

In addition to a reduction of genetic diversity in the invasive range, we detected some evidence of genetic bottlenecks in the eastern islands of Molokai, Maui, Hawaii, and Lanai. Interestingly, there was no significant evidence for bottlenecks in Kauai and Oahu. The populations on both of these islands were introduced in the early 1900s (Nakahara 1980), so it is possible that allelic diversity and heterozygosity may have reached equilibrium, making it difficult to detect bottlenecks (Cornuet and Luikart 1996; Luikart et al. 1998). In contrast, populations on Molokai, Maui, Hawaii, and Lanai were established more recently and may not have reached equilibrium with respect to allelic heterozygosity.

In other invasive social insects, losses of genetic diversity have been implicated in the development of supercolonies, which are large, multiqueen colonies that consist of multiple nests and lack substantial boundaries (Holway et al. 2002; Tsutsui and Suarez 2003; Suarez and Tsutsui 2008; Helanterä et al. 2009). Hanna et al. (2014a) showed that workers from native colonies of *V. pensylvanica* were always produced by a single queen, whereas colonies in the invasive range often contained workers produced by multiple queens (Goodisman et al. 2001; Hanna et al. 2014a). It is possible that the reduction of genetic diversity found in invasive *V. pensylvanica* is associated with this change in social structure and invasion success. However, the magnitude of genetic diversity in the invasive range is still high compared to other introduced species that produce supercolonies (Helanterä et al. 2009). In addition, perennial *V. pensylvanica* colonies can be found in parts of the native range, suggesting that phenotypic plasticity, rather than changes in genetic diversity, might be involved in the formation of multiqueen, perennial *Vespula* nests (Gambino 1991; Visscher and Vetter 2003).

**Lack of genetic structure in the native range of *V. pensylvanica***

*Vespula pensylvanica* showed a remarkable lack of genetic structure in its native range in the United States, which stands contrary to our original prediction (Table 3). There was little evidence for genetic differentiation among
hierarchically sampled locations and no significant evidence of genetic isolation by distance, suggesting a high level of gene flow across the entire native range (Fig. 2A and Table 3). This is particularly notable because our sampling scheme spanned over 2000 km of western North America. The lack of genetic structure in the native range of *V. pensylvanica* could have resulted from human-mediated dispersal, which may have led to high rates of gene flow across the native range (Moller 1996). Alternatively, the dispersal distances of *Vespula* queens may be sufficient to develop genetic homogeneity over long, evolutionary timescales.

Our finding that native *V. pensylvanica* lacks genetic structure parallels results found in other native *Vespula* species over smaller ranges. For example, Hoffman et al. (2008) failed to detect genetic structure in *Vespula maculifrons* and *Vespula squamosa* along a span of approximately 130 km in its native range of North America (Hoffman et al. 2008). The sampling range for *V. maculifrons* and *V. squamosa* was more than an order of mag-

Figure 4. Unrooted neighbor-joining trees for (A) native transects only (B) invasive transects only, and (C) all regions. Bootstrap support for nodes is represented by color.
The invasion history of *V. pensylvanica* in Hawaii

We attempted to identify potential source populations of invasive *V. pensylvanica* in Hawaii. Given historical records, we expected that Oregon would be the source of invasive populations (Nakahara 1980). In accord with this prediction, we found that a majority of introduced individuals were assigned to the western part of the native range using one particular assignment test (Table 5A). However, a different assignment procedure suggested that the central area of the native range was the most likely source of invasive *V. pensylvanica* (Table 5B). These contrasting results may reflect the general lack of genetic differentiation among native *V. pensylvanica* populations, which may make the determination of the source of invasive populations difficult to ascertain. In addition, our limited sampling from the central regions of native *V. pensylvanica* may preclude our ability to assign source populations with high confidence (Muirhead et al. 2008).

*Vespula pensylvanica* displayed substantial levels of genetic differentiation both between and within Hawaiian Islands, in contrast to our expectations that genetic differentiation would be limited. For example, we found that the relationship between genetic and geographic distance in the invasive range was nonlinear and displayed gaps at certain spans of geographic distance (Fig. 2B). This trend mostly reflected strong genetic differences between islands combined with modest genetic structure within islands. The difference in patterns of isolation by distance between the native and invasive ranges was particularly notable given the great difference in geographic distance in the ranges. The native range stretches across 2000 km of western United States, while the invasive range spans approximately 600 km. Yet the invasive range showed substantially greater levels of genetic structure and isolation by distance. These trends could result, in part, from the expanses of ocean between the Hawaiian Islands (Pierce et al. 2014). The differences between native and introduced species may also reflect nonequilibrium conditions found in the introduced range (Akre et al. 1981). A similar, significant isolation-by-distance relationship, spanning approximately 225 km, was found for *V. germanica* in its invasive region of Australia (Goodisman et al. 2001).

We also found significant differences in the levels of genetic diversity among the Hawaiian Islands. Out of all the islands, Kauai had the lowest levels of all diversity metrics (Table 2). A survey conducted by the Hawaii Department of Agriculture suggests that *V. pensylvanica* was introduced multiple times to Kauai (Nakahara 1980). Multiple introductions are generally expected to result in greater genetic variation in an invasive habitat (Sakai et al. 2001; Kolbe et al. 2004). Therefore, it was somewhat unexpected that Kauai would have low levels of genetic variation. Kauai was also the most genetically distinct population when compared to other islands in the invasive range.

The *V. pensylvanica* population on Oahu was also thought to have been founded by multiple introductions (Nakahara 1980). Levels of genetic diversity in Oahu were relatively high and individuals within Oahu formed two distinct populations (Fig. 3A). These results suggest that *V. pensylvanica* may have been introduced multiple times to Oahu. This island contains a large percent of the Hawaiian Island’s human population, so it is possible that such putative introductions were facilitated by human-mediated shipments from the mainland (Nakahara 1980).

The existence of a discrete genetic population consisting of all individuals from Hawaii and a few individuals from Oahu was surprising as Oahu and Hawaii are separated by the islands of Molokai, Lanai, and Maui (Figs. 1, 3C). It thus seems unlikely that Oahu individuals directly seeded the Hawaiian population, or vice versa, through natural dispersal. However, human-mediated dispersal could account for this pattern. Regardless, all of the aberrant Oahu individuals originated from a single transect that was the most western of all the Oahu transects. As these individuals were confined to the western section of the island, physical barriers, such as the volcanoes Waialae or Ko'olau, may have prevented gene flow and the homogenization of allele frequencies across Oahu (Roderick and Gillespie 1998).

The islands of Molokai and Lanai also each formed a separate, genetically distinct population from all of the other islands (Fig. 3C). This is consistent with the idea that Molokai and Lanai were colonized through single, separate introductions in the late 1970s (Nakahara 1980). Even though both islands formed a distinct population, Molokai and Lanai cluster together in the NJ tree (Fig. 4B). The populations on both islands may have been seeded by genetically similar source populations. Substantial genetic drift may have occurred during population formation, creating genetically distinct populations on each island.
Finally, we uncovered an unusual pattern of genetic structure in Maui. Individuals from transects on the eastern part of Maui tended to form a somewhat differentiated population from those on the western part of the island (Fig. 3C). This suggests low levels of gene flow between western and eastern *V. pensylvanica* in Maui, possibly due to physical isolation (Roderick and Gillespie 1998). Such a result also raises the possibility that there may have been at least two introductions of *V. pensylvanica* to this island.

**Conclusions**

We examined the population genetic structure of *Vespula pensylvanica*, a wasp introduced to the archipelago of Hawaii from its native range in North America (Nakahara 1980; Gambino and Loope 1992). Remarkably, we found that invasive populations displayed substantially higher levels of genetic structure than native populations. Thus, *V. pensylvanica* is capable of high levels of dispersal and gene flow, likely through human-mediated transportation. However, such gene flow is apparently constrained in the invasive habitats of Hawaii, which consists of islands separated by wide expanses of water. The presence of genetic structure in invasive populations reflects the influence of geographic barriers, invasion dynamics, and a nonequilibrium state of population structure. Continued study of this taxon over the coming decades may be particularly useful for understanding how invasive species come to be established in their introduced habitats. Overall, study of the invasion of *V. pensylvanica* in Hawaii may provide further insight on the process of biological invasions on archipelagos, which could help in the development of policy that can prevent and curb invasions to vulnerable regions.

**Acknowledgments**

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**Data accessibility**

Sampling information and microsatellite genotypes can be found in Table S1 and S4, respectively.

**Conflict of Interest**

None declared.

**References**


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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Table S1. Locations and total numbers of V. pensylvanica wasps collected from traps in the sampled transects, ranges, and regions (NA = location not determined).

Table S2. Measures of genetic diversity at microsatellite loci for V. pensylvanica from invasive regions, including number of samples (N), number of alleles (Nₑ), effective number of alleles (Nₑₑ), observed heterozygosity (Hₒₒ),
expected heterozygosity ($H_e$), allelic richness ($A$), and number of private alleles ($N_p$).

**Table S3.** Assignment and Exclusion test of invasive Hawaiian populations to mainland populations in the United States.

**Table S4.** Locations of, total numbers of, and genotypes of *V. pensylvanica* wasps collected from, each trap in the sampled transects, ranges, and regions (NA = location not determined) at 15 loci.