A population genetic approach to investigate effects of urbanization and habitat fragmentation on the Western black widow spider, *Latrodectus hesperus*

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ABSTRACT

Urbanization causes a sudden and drastic change to the landscape, fragmenting habitats, leading to a disruption in dispersal, potentially impacting gene flow of the organisms living in these new urban habitats. Due to the variable effects caused by urbanization, it is important to understand the genetic variation if we wish to understand why some organisms thrive in urban environments and become pest species. We test the hypothesis that urbanization and habitat fragmentation restricts gene flow in urban black widow populations and therefore may cause urban populations to exhibit patterns of genetic diversity consistent with fragmentation, isolation, and recent colonization relative to desert black widow populations. Preliminary results indicate urban populations may not only be recently derived but that isolation has been established for some time given the significant divergence between them and surrounding desert samples.

BACKGROUND

During the 20th century, human populations have grown and expanded into urban centers worldwide (United Nations Population Division 2009), transforming the natural landscapes on which we depend. Urbanization can lead to high levels of primary productivity due to the lack of seasonal variation within the urban habitat (McKinney 2002; Schocat et al. 2004). Due to the high levels of primary productivity, some species thrive in the urban environment and exhibit high levels of population growth (Faeth et al. 2005). Urbanization can have varying effects on the population genetic structure of different species and thus an understanding of historical population dynamics is critical if we wish to understand why some species thrive in urban environments.

As the fifth most populous city in the United States, Phoenix, AZ has experienced explosive growth and rapid urbanization (US Census Bureau 2009). Although researchers have found that predator diversity has decreased, there has been growth of a few urban exploiters (Faeth et al. 2005; Schocat et al. 2004).

The Western black widow spider, Latrodectus hesperus, is an urban exploiter and medically relevant pest species native to the desert Southwest, Populations of L. hesperus can be found in both highly urbanized Phoenix metropolitan areas as well as undisturbed Sonoran desert (Fig. 1). Recent surveys of both urban and desert widow populations have shown that there are clear ecologically relevant differences (Johnson, unpublished data). Although urban sites characteristically have abundant food sources (e.g. insects attracted to trash receptacles), urban spiders have significantly lower reproductive output and egg condition, perhaps due to increased competition. While it is clear that there are important ecological and behavioral characteristics of the black widow, what the impact of urbanization has on dispersal and population differentiation is unknown. This system provides a unique opportunity to assess the effects of urbanization on the population genetic structure of a historically desert species that now thrives in the urban habitat.



RESULTS

• 87 SNPs in 182 individuals

METHODS

- 182 individuals sampled across 23 sites in Phoenix (Fig. 1), with DNA extracted using DNeasy Tissue kits (QIAGEN).
- Primers designed for the mtDNA NADH dehydrogenase subunit
 (ND1) gene region (based on Griffiths et al. 2005) to amplify and sequence 600bp
- Sequences were aligned manually using the program SEQUENCHER (version 3.1.1; Gene Codes)
- Population genetic statistics computed in DnaSP (Librado and Rozas 2009), with analyses of population structure using STRUCTURE (Fig. 2; Pritchard et al. 2000) and genealogical relationships using MEGA (Fig. 3; Tamura et al. 2007)

across 600bp of ND1 resulted in θ_s = 0.025 and θ_{π} = 0.008 with a Tajima's D of -2.14 (p<0.00001) STRUCTURE analysis finds evidence for K=3 clusters, separating Peralta from urban locations (Fig. 2), consistent with our NJ tree analysis (Fig. 3) · F_{ST} pairwise comparisons among 18 locations varied from 0 - 0.18. However, between Peralta and all others $F_{ST} = 0.87$ (p< 0.001; permutation test, Hudson 2000) Figure 3. Neighbor-joining tree analysis of 182 individuals using MEGA (Tamura et al. 2007). Geographic locations are reflected by different colors.



DISCUSSION

- Samples from the desert site, Peralta, separated from all other urban sites in the F_{ST}, STRUCTURE, and NJ tree analyses, with high levels of diversity within the desert site compared to within urban sites. We are currently collecting samples during the peak of the widow breeding season from multiple surrounding desert sites to test the hypothesis that urbanization may be a potential barrier to gene flow that isolates groups.
- In spite of this structure, we also observed a significant excess of rare variants. Together with the gene genealogy, this pattern may be a signature of recent colonization/expansion within urbanized areas. This pattern may purely due to mtDNA being a single non-recombining locus of maternal ancestry, especially since female black widows are the sedentary sex. Thus, we are also conducting nuclear genome-wide analyses to evaluate demographic vs. adaptive scenarios.
- Our results, when combined with recent observations of behavioral and ecological differentiation among urban and desert black widows, have clear implications for urban planning and management. Additionally, these patterns suggest urbanization as a potential vehicle for rapid species divergence within close proximity, having implications for conservation practices..

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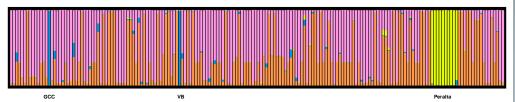


Figure 2. STRUCTURE analysis (Pritchard et al. 2000) of 182 individuals (Fig. 1). Individuals ordered by sample location. Using the Evanno et al. (2005) delta-K method, we determined K=4 clusters. Note that individuals from Peralta cluster completely from all others, as well as evidence of two rare haplotypes (GCC & VB) with high divergence even within the Phoenix city center, consistent with our NI tree analysis (Fig. 3).

References Evanno et al. (2005) Mol Ecol 14:2611-2620; Faeth et al. (2005) Bioscience 5:399-407; Griffiths et al. (2005) J Arachnol 33:776-784; Hudson (2000) Genetics 155:2011-2014; Librado and Rozas (2009) Bioinformatics 25:1451-1452; McKinney ML (2002) Bioscience 10:883-890; Pritchard et al. (2000) Genetics 155:945-959; Shochat et al. (2004) Ecol App 1: 268-280; Tamurra et al. (2007) Mol Biol Evol 24:1596-1599; US Census Bureau (2009) Census 2009;