

Understanding Native Bee Decline

Shalene Jha – University of Texas at Austin. sjha@austin.utexas.edu

December 2012

Introduction

More than 60% of earth's terrestrial surface is managed by humans as agriculture or urban areas, (Scialabba and Williamson 2004), yet little is known about how ecological processes in human-altered landscapes compare with natural landscapes. In particular, pollination is a critical ecosystem service that is responsible for the increased quantity, quality, and stability of over 60% of world crops (reviewed in Klein et al. 2007) and innumerable wild plant species (Potts et al. 2010). Despite the undoubted importance of pollinators as ecosystem service providers, a number of native pollinator communities are exhibiting pronounced declines across the globe. Though community level studies have revealed a few species-specific declines in human-altered areas (Larsen et al. 2005), very little is known about population processes and what population mechanisms may be most affected by land-alteration, often associated with natural habitat destruction (e.g., Kearns et al. 1998, Biesmeijer et al. 2006, Winfree et al. 2009). While there has been increasing concern about the status of native pollinator communities, virtually nothing is known about basic pollinator population dynamics and movement patterns across natural and human-altered landscapes.

The proposed research examines how fragmentation of native pollinator habitat impacts the population viability, colony health, and dispersal patterns of native Texas bee species. In the proposed research, we will compare foraging movement, colonization, and survivorship patterns of the collected species in natural landscapes and urban landscapes to identify what natural and human-induced dispersal barriers exist between bee populations across Texas. We utilized Balcones Canyonlands National Wildlife Refuge as a representative of natural landscape within the area. Thus, the significance of the research is to provide greater knowledge about the maintenance of genetic diversity within native bee populations across natural and human-altered landscapes. The findings will reveal insight into the optimal land management techniques needed to support essential gene flow processes for native pollinators on the islands and across species ranges.

Materials and Methods

Field Methods

In order to examine what habitat attributes are most important for colony densities in each site, we sampled all native pollinator species across a 1km transect within each study site, including Balcones Canyonlands National Wildlife Refuge. At Balcones, the transect was placed near FM1174, going from just south of the Doeskin Ranch Visitor area and stretching 1km north, primarily following the road. We visited the site three times in 2012 (May, June, and July of 2012). Other sites around Austin sampled for this project include Barton Creek Habitat Preserve, Milton Reimers Ranch Park, Wildflower Center, and Water Quality Protection Lands. We also sampled at Fort Worth Nature Center & Refuge, Cedar Hill State Park, and 3 Nature Conservancy sites; Clymer Meadow Preserve, Smiley-Woodfin Native Prairie Grassland, and Matthews Prairie.

Across each transect, we collected bees via a combination of netting and use of pan traps (no reproductive queens were sampled) and we stored these specimens in 95% ethanol or frozen until they could be mounted on pins and identified. Specimens will be used later for molecular analysis. After identification and analysis, the samples will be placed with the UT Austin Entomological Collection.

While in the field, we also conducted vegetation surveys (observation-based) and we will use GIS images to investigate the relationship between native bee nest densities and land management at varying spatial scales. Pollen was collected from single flowers for use as a reference for identification of bee pollen balls. We will visit for a second round of sampling in 2013.

Laboratory Methods

Pollen identification:

Pollen loads from worker bees will be identified to the species level whenever possible. Pollen will undergo acetolysis, which breaks open the pollen grains allowing for more specific identification, and matched to a pollen reference collection for identification.

DNA analysis:

Using molecular markers (e.g., Stolle et al. 2009), we will screen DNA from select species to examine colony density patterns across all sites, including Balcones Canyonlands National Wildlife Preserve (as in Jha and Kremen *in review*). For social species, colony-mates are sisters and can be identified as colony-mates with genetic clustering statistics (i.e., Relatedness®, Goodnight and Queller 1999), revealing the relative number of colonies and colony sizes across the landscape. For non-social species, genotypes will be used to examine relatedness and shared ancestry.

As an indicator of colony health, we will measure inbreeding using F-statistics and will conduct genetic structure analyses to determine deme distribution and reveal distinctions in and between each Balcones colonization patterns vs. agricultural and urbanized landscape colonization patterns.

Results

On average, we caught 37 bees per observation period across all of our sites. At Balcones, we caught 545 bees total during our three visits. We caught 34 bees with nets. The remaining bees were caught via pan traps. We also collected data on flowering plants and vegetation cover. The data is currently being processed and will be analyzed this winter.

Discussion

The first component of this research tests the hypothesis that native bee population densities are limited by the area of natural habitat available (e.g. area of suitable nesting habitat within the island and within agriculturally-fragmented sites). Floral resource cover has often been considered to be the most predictive variable for native bee abundance (Westphal et al. 2003). However, without using molecular tools, it has been impossible to tell for social species whether increased native bee abundance was due to greater colony densities (number of colonies/area) or greater numbers of workers visiting from a small number of colonies.

Additional studies have indicated that proximity to natural habitat is more important for bees than the availability of flowering plants because natural habitat provides access to more consistent floral resources across the entire season (e.g., Jha and Vandermeer 2009, Goulson et al. 2010, Jha and Kremen *in review*). Past research utilized molecular tools to show that the area of oak-woodland and chaparral was the most important factor for predicting bumble bee colony density (not abundance) within agriculturally-fragmented landscapes in the Central Valley (Jha and Kremen *in review*).

The second component of this research project examines bee colony health by measuring inbreeding. Microsatellite markers are powerful tools to detect population bottlenecks, breeding patterns, and regional limitations to gene flow across natural and human-altered landscapes (e.g., Jha and Dick 2009). These analyses will also reveal distinctions in historic and contemporary gene flow patterns and will provide insight into the distinct dispersal barriers confronting each species.

The third component of this research project examines native bee foraging patterns. While mechanisms driving bee foraging patterns are dependent on both floral resource availability and habitat composition, the impacts of these factors on bee foraging are rarely simultaneously analyzed. Past research in agriculturally-fragmented landscapes has indicated that the foraging patterns of native bees depend critically on both floral resource level and nest-site availability (Jha and Vandermeer 2009a). However, it is completely unknown how foraging patterns for native bees may differ between natural habitat islands vs. human-fragmented 'islands'. Using the same DNA collected in the previous sections, we will calculate colony foraging ranges based on the relative distances between collected colony-mates (Chapman et al. 2003, Jha and Kremen *in review*). We hypothesize that native bees on the Balcones Canyonlands National Wildlife Refuge will exhibit shorter foraging ranges than those within urbanized landscapes, given the greater floral resource availability in the Refuge.

Conclusions

The research integrates molecular and field-based tools to provide a robust and innovative approach to understanding pollinator ecology and population genetics. The project will yield some of the first analyses comparing native bee population genetics across natural and urban landscapes, revealing potential barriers to population gene flow and colony success. As managers of our landscapes, humans are critically dependent on the health of our native pollinators for crop and native plant reproduction. Findings from this research will provide biologists, conservationists, and agriculturalists with greater knowledge about the maintenance of genetic diversity and the habitat requirements of essential native pollinators.

Literature cited

- Biesmeijer, J. C., S. P. M. Roberts, M. Reemer, R. Ohlemuller, M. Edwards, T. Peeters, A. P. Schaffers, S. G. Potts, R. Kleukers, C. D. Thomas, J. Settele, and W. E. Kunin. 2006. Parallel declines in pollinators and insect-pollinated plants in Britain and the Netherlands. *Science* **313**:351-354.
- Chapman, R. E., J. Wang, and A. F. G. Bourke. 2003. Genetic analysis of spatial foraging patterns and resource sharing in bumble bee pollinators. *Molecular Ecology* **12**:2801-2808.
- Darvill, B., J. S. Ellis, G. C. Lye, and D. Goulson. 2006. Population structure and inbreeding in a rare and declining bumblebee, *Bombus muscorum* (Hymenoptera : Apidae). *Molecular Ecology* **15**:601-611.
- Goodnight, K. F. and D. C. Queller. 1999. Computer software for performing likelihood tests of pedigree relationship using genetic markers. *Molecular Ecology* **8**:1231-1234.

- Goulson, D., O. Lepais, S. O'Connor, J. L. Osborne, R. A. Sanderson, J. Cussans, L. Goffe, and B. Darvill. 2010. Effects of land use at a landscape scale on bumblebee nest density and survival. *Journal of Applied Ecology* **47**:1207-1215.
- Jha, S. and C. W. Dick. 2009. Isolation and characterization of nine microsatellite loci for the tropical understory tree *Miconia affinis* Wurdack (Melastomataceae). *Molecular Ecology Resources* **9** 344-345.
- Jha, S. and C. Kremen. *in review*. Bumble bee populations genetics reveal long-distance foraging and high colony density in agricultural landscapes.
- Jha, S. and J. Vandermeer. 2009. Contrasting bee foraging in response to resource scale and local habitat management. *Oikos* **118**:1174 -1180.
- Kearns, C. A., D. W. Inouye, and N. M. Waser. 1998. Endangered mutualisms: The conservation of plant-pollinator interactions. *Annual Review of Ecology and Systematics* **29**:83-112.
- Klein, A. M., B. E. Vaissiere, J. H. Cane, I. Steffan-Dewenter, S. A. Cunningham, C. Kremen, and T. Tscharntke. 2007. Importance of pollinators in changing landscapes for world crops. *Proceedings of the Royal Society B-Biological Sciences* **274**:303-313.
- Larsen, T. H., N. Williams, and C. Kremen. 2005. Extinction order and altered community structure rapidly disrupt ecosystem functioning. *Ecology Letters* **8**:538-547.
- Potts, S. G., J. C. Biesmeijer, C. Kremen, P. Neumann, O. Schweiger, and W. E. Kunin. 2010. Global pollinator declines: trends, impacts and drivers. *Trends in Ecology & Evolution* **25**:345-353.
- Scialabba, N. E. and D. Williamson. 2004. The scope of organic agriculture, sustainable forest management and ecoforestry in protected area management. Working Paper No. 18. *in* Food and Agriculture Organization of the United Nations, Rome, Italy.
- Stolle, E., M. Rohde, D. Vautrin, M. Solignac, P. Schmid-Hempel, R. Schmid-Hempel, and R. F. A. Moritz. 2009. Novel microsatellite DNA loci for *Bombus terrestris* (Linnaeus, 1758). *Molecular Ecology Resources* **9**:1345-1352.
- Westphal, C., I. Steffan-Dewenter, and T. Tscharntke. 2003. Mass flowering crops enhance pollinator densities at a landscape scale. *Ecology Letters* **6**:961-965.
- Winfree, R., R. Aguilar, D. P. Vazquez, G. LeBuhn, and M. A. Aizen. 2009. A meta-analysis of bees' responses to anthropogenic disturbance. *Ecology* **90**:2068-2076.