

HM334 Genetic diversity and possible divergence of island and mainland populations of the Honduran Curlyhair Tarantula (*Brachypelma albopilosum*)

The 'tarantula' family (Theraphosidae) includes some of the most impressive spiders alive today, yet many are potentially threatened by a combination of habitat destruction, and over-collection by the exotic pet-trade. Currently, few tarantulas are known from Honduras, with only 3 described species, such as the 'Curlyhair tarantula' *Brachypelma albopilosum*. This species was originally described from distant Costa Rica, though since confirmed to range across the lush warm Caribbean lowlands of northwestern Honduras and the Bay islands. In neighboring Costa Rica, there are over 30 described tarantula species (and several more pending description), in a comparatively small geographic area, suggesting many Honduran tarantulas are waiting to be discovered. Of the 3 known Honduran species, both *B. albopilosum* and the stripeknee tarantula *Aphonopelma seemanni* have been widely collected for the exotic pet-trade. Over-collection of Mexican tarantulas previously led to protection of the genus *Brachypelma* under CITES (convention for endangered species), and trade in Mexican tarantulas has since been tightly monitored by wildlife agencies. But, trade in Honduran tarantulas cannot be easily regulated yet due to poor scientific understanding of endemic species. It is therefore especially valuable to study the vulnerability of these tarantula populations against the pressures from pet-trade collection and habitat destruction. This topic could be developed into multiple research questions to better understand island tarantula populations versus the mainland. Islands are extremely useful to biologists to testing questions about origin and persistence of species when population size is reduced and closely related individuals are forced to interbreed. The Bay Islands including Útila and Cayos Cochinos provide an ideal testing ground for studying the vulnerability of tarantula populations and the importance of genetic variability. Projects would exploit a non-lethal DNA sampling technique to collect tissue samples from Bay Island populations, and conduct molecular genetic analyses in field laboratory facilities at the forest base-camp of Cusuco National Park to understand genetic variation in island tarantulas as compared to mainland samples from the northern coast of Honduras.

The tarantula family (Araneae, Theraphosidae) includes some of the most impressive spiders alive today, and many are consequently in demand by the exotic pet-trade. In particular, the genus *Brachypelma* includes some of the most conspicuous members of the Central American spider fauna, and alongside threats from habitat destruction, several species are also threatened by pet-trade over-collection. These factors led to the blanket protection of the entire genus *Brachypelma* under CITES (Convention on International Trade in Endangered Species) in the 1990's. Subsequently, with greater protected status, knowledge on the Mexican species continues to grow, but few specific studies have been conducted on *Brachypelma* from other Central American countries. Only Costa Rica is relatively well studied, where the number of described tarantula species is far greater than other larger neighboring countries like Honduras where almost no research has been made on endemic spiders. Only three species of tarantula are formally described from Honduras. Of these species, the curlyhair tarantula *Brachypelma albopilosum* has been commonly collected for the exotic pet trade. The docile nature and long-life span of the species means that continued pet trade collections have been

made in Honduras, though consequences on natural populations of such pressures is unknown. Further studies on the diversity, ecology and behavior of Honduran tarantulas will be vital to understand how these species may cope with continued human impacts on their wild populations.

Conservation efforts to protect threatened taxa can be most effectively focused with clarification of the genetic affinities among individuals. Studies of relatedness and genetic diversity have proved especially valuable to understanding the vulnerability of organisms of island systems, such as providing insights on the effects of isolating mechanisms on small populations. Curlyhair tarantulas (*B. albopilosum*) are found the Bay Islands (Islas de la Bahias), namely Útila at 18 miles (29 km) off the Honduran coast, and the closer islets of Cayos Cochinos. The Bay Islands were formed from the exposed volcanic peaks of the Bonacca undersea ridge that makes up the south end of the Mesoamerican Barrier Reef System, the second-largest in the world. This whole area is protected by the Bay Islands Conservation Association (BICA). On the mainland, the species appears restricted to the lush coastal lowlands, around San Pedro Sula and the coastal city of La Ceiba. Unlike other *Brachypelma* species with narrow geographic ranges, the curlyhair tarantula appears unusually widespread, ranging from northern Costa Rica, through Nicaragua to the Caribbean coast of Honduras. Due to its large range, the species provides a useful low-risk species with which to evaluate the effects of distance on genetic variation, effects of isolation on islands, and compare against other species with much smaller ranges and likely higher vulnerability.

Recent developments in molecular techniques to discriminate animal populations now allow biologists to conduct genetic analyses in the field with minimal equipment. An increasingly popular technique is using Inter Simple Sequence Repeats (ISSR). This method target simple repetitive regions of DNA using simple primers to screen a large part of the genome without prior knowledge of the sequences. This provides highly reproducible results, generates abundant polymorphisms, and can be done at relatively low cost. In other techniques like microsatellite analysis or targeted gene sequencing some prior knowledge of target genome is important to effect successful amplifications. However, with ISSR, it can also be useful to conduct an initial survey of suitable simple primers, as genomes vary in the types and abundances of repetitive sequences. Such studies of primer efficacy have already been conducted on *Brachypelma* tarantulas, using a species from Belize and Mexico that is very closely related to the Honduran Curlyhair.

This topic could be developed into a series of different research questions focused on understanding the genetic variation in island populations of curlyhair tarantulas, which could be related to mainland variation. The major goals of such a project would be to examine the levels of genetic variability of island populations, to provide insights on age of origin, source population, and current vulnerability. Knowledge of genetic variability is critical to make informed decisions about populations, especially when fragmented or involving island systems. The loss of genetic diversity and increased inbreeding after isolation can lead to the extinction of populations or species, but this is not necessarily the case. Isolation also may have no effect or even positive consequences on populations, such as facilitating spread of adaptive alleles through small residual population. Using such genetic data on tarantulas, we can ask whether island populations would be able to cope with human exploitation for the pet-trade, and if local-captive breeding for pet-trade export could be a useful source of revenue. If island forms are

genetically unique, it will be important to determine whether further specific protection may be required.

Burkey, TV (1989) Extinction in nature reserves: the effect of fragmentation and the importance of migration between fragments. *Oikos* 55:75-81

Falush, D., Stephens, M., & Pritchard J.K. (2007) Inference of population structure using multilocus genotype data: dominant markers and null alleles. *Molecular Ecology Notes* 7: 574-578

Joyce, D.A. & Pullin, A.S. (2003). Conservation implications of the distribution of genetic diversity at different scales: a case study using the marsh fritillary butterfly (*Euphydryas aurinia*). *Biological Conservation* 114:453–461.

Kothera, L., Richards, C.M. & Carney, S.E.. (2007). Genetic diversity and structure in the rare Colorado endemic plant *Pisaria bellii* (Brassicaceae). *Conservation Genetics* 8:1043–1050.

Locht, A., Yanez, M. & Vazquez, I. (1999) Distribution and natural history of Mexican species of *Brachypelma* and *Brachypelmides* (Theraphosidae, Theraphosinae) with morphological evidence for their synonymy. *Journal of Arachnology*, **27**, 196-200.

Longhorn, S.J., Nicholas M., Chuter J. & Volger A.P. (2007) The utility of molecular markers from non-lethal DNA samples of the CITES II protected “tarantula” *Brachypelma vagans* (Araneae, Theraphosidae). *Journal of Arachnology* 35:278-292

M'Rabet, S. M., Henaut, Y., Rojo, R. & Calme, S. (2005) A not so natural history of the tarantula *Brachypelma vagans*: Interaction with human activity. *Journal of Natural History*, **39**, 2515-2523.

Machkour-M'Rabet, S., Hénaut Y, Charruau P, Gevrey M, Legal L (2009) Extinction risk of the American Crocodile in the Mexican Caribbean revealed by ISSR-PCR method: Implication for Conservation. *Marine Biology* 156:1321-1333

Machkour-M'Rabet, S., Hénaut Y, Charruau P, Gevrey M, Legal L (2009) Extinction risk of the American Crocodile in the Mexican Caribbean revealed by ISSR-PCR method: Implication for Conservation. *Marine Biology* 156:1321-1333

Machkour-M'Rabet, S., Y. Henaut, S. Calme, and L. Legal. In Press. When landscape modification is advantageous for endangered species. The case of a synanthropic tarantula, *Brachypelma vagans*. *Journal of Insect Conservation*.

Petersen, S.D., Mason, T., Akber, S., West, R., White, B., and Wilson, P. (2007) Species identification of tarantulas using exuviae for international wildlife law enforcement. *Conservation Genetics* 8:497-502

Roux, O., Gevrey, M., Arvanitakis, L., Gers, C., Bordat, D. & Legal, L. (2007) ISSR-PCR: Tool for discrimination and genetic structure analysis of *Plutella xylostella* populations native to different geographical areas. *Molecular Phylogenetics & Evolution* 43:240-250