



A molecular approach to understand the riddle of the invasive success of the tarantula, *Brachypelma vagans*, on Cozumel Island, Mexico



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ABSTRACT

Invasive populations typically demonstrate genetic isolation which results in a loss of genetic diversity and a reduction in invasion success. This study focused on the genetic population of a successful invasive species of tarantula. Individuals were sampled in two mainland localities of the Yucatan Peninsula (Zoh-Laguna and Raudales), in addition to two island localities (El Cedral and Rancho Guadalupe on Cozumel Island). All populations present high genetic diversity (mean: $H_e = 0.23$, $P = 99\%$), with significant differences between the Raudales and Rancho Guadalupe localities. The AMOVA analysis revealed a significant population structure (14.5% variation among populations), consistent with the gene differentiation coefficient ($G_{ST} = 0.21$), and spatial analysis of population structure. Our results suggested that the original introduced population did not suffer a loss of genetic diversity during establishment on the island, possibly a result of different biological conditions. Population structure analysis leads us to suggest that one island population is similar to the original genetic profile, whereas the genotypic profile of the other island population reflects recent introductions from the mainland. We identified a potential risk of extinction for one local mainland population, suggesting that this species may be a successful invader in a new environment but endangered in some parts of its natural area.

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1. Introduction

A well-known characteristic of many invasive populations is their genetic isolation from native-range source populations (Allendorf and Lundquist, 2003). Isolation generally reduces the number of initial colonists, leading to a founder effect characterized by a loss of genetic diversity and restricted gene flow (Frankham et al., 2005). These genetic consequences of

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isolation usually limit the success of invasive species (Crawford and Whitney, 2010). However, the literature describes numerous cases of invasive species which present a high degree of success (Tsutsui et al., 2000). Recent evidence shows that introduced populations present similar (Lee et al., 2004) or higher genetic variation than populations in their native range (Kolbe et al., 2004, 2007), which could explain the high success rate of some invasive species. Several theories have been proposed to explain this apparent paradox (Frankham, 2005), including a rapid population expansion at the time of establishment (Zenger et al., 2003), the hybridization process among differentiated populations (Ellstrand and Schierenbeck, 2000), the admixture of multiple native-range sources (Kolbe et al., 2007; Krehenwinkel and Tautz, 2013), or multiple introductions (Kolbe et al., 2004).

Brachypelma vagans Ausserer, 1875 (Mygalomorphae: Theraphosidae), the Mexican redrump tarantula, which has the widest distribution of its genus (Fig. S1), provides a specific case of an invasive species. To the best of our knowledge, it is the only known invasive species of tarantula, and is protected under CITES (appendix II). *Brachypelma vagans* demonstrates invasive potential, and has been reported in two invasive events, the first, taking place in Florida (Edwards and Hibbard, 1999). According to the authors, the establishment of this spider in Florida was successful due to similarities in the soil, vegetation and climate between central Florida and the Yucatan Peninsula in southeast Mexico, a region within the original distribution range of *B. vagans*. The second invasion event occurred on Cozumel Island in the Mexican Caribbean, as first reported by Machkour-M'Rabet et al. (2012). The introduction of specimens to Cozumel Island occurred during the filming of a movie in 1971, dating the invasion event to 42 years ago. According to local inhabitants, tarantulas, boa constrictors and peccaries, all absent from the island prior to making the movie, were used during filming and subsequently released at two sites (Fig. S2): near to the village of El Cedral in Southwest Cozumel and, on a beach in the north-east of the island (Martínez-Morales and Cuarón, 1999). In a first study, we demonstrated that the insular population of the El Cedral locality presented lower genetic diversity than mainland populations, possibly due to a very recent founder effect. However, as overall genetic diversity remained high, we hypothesized that this island population experienced rapid expansion, reducing the effect of genetic drift and maintaining a high level of polymorphism. New field expeditions in the more conserved part of the island, enabled the discovery of another population near to the second release point of individuals in 1971. This second population gave us the opportunity to gain a better understanding of the genetic structure of the insular populations of *B. vagans*, and thus understand the factors that played a role in their successful invasion.

The aim of this study is based on the following questions: 1) Do the island populations of *B. vagans* present signs of a founder effect? 2) Do some populations show significant variation of genetic diversity over five-year intervals? and 3) Does population structure demonstrate a clear separation between mainland and island populations, and are both local island populations part of a larger single population?

2. Methods

2.1. Tarantula samples

All individuals were collected from four rural communities in the Yucatan Peninsula: Raudales and Zoh-Laguna comprised the mainland localities while Rancho Guadalupe and El Cedral were selected as the island localities (Fig. S2). Details of sampling are given in Table 1. Sampling was carried out at the same localities in 2007 and 2012, considering a similar sample size and the same sampling methodology criteria to ensure that sampling biases did not affect the results. Sampling at the Rancho Guadalupe site only occurred during 2012.

The mainland villages were selected due to the high density of *B. vagans* found in previous studies (Machkour-M'Rabet et al., 2005, 2009), in addition to possessing distinct genetic profiles: the Zoh-Laguna_{M1} (the small letter -M1- indicates that the site is located on the mainland and presents high genetic diversity) population presents a mixed genetic profile reflecting a highly connected population, while the Raudales_{M2} (the small letter -M2- indicates that the site is on the mainland with low genetic diversity) population presents a genetic profile characteristic of an isolated population (Machkour-M'Rabet et al., 2012). For the present study, the island sites (El Cedral_{I1} and Rancho Guadalupe_{I2}, the small letter -I1 and I2- indicates that sites are on the island with high and low polymorphism respectively) were selected because of their proximity to locations where individuals of *B. vagans* were released 42 years ago.

At each site, we collected 30 individuals of *B. vagans*, consisting of only females and juveniles. Since *B. vagans* is a protected species, samples were collected using a non-lethal technique that consists of inducing limb autotomy (Machkour-M'Rabet et al., 2009). Once a sample was obtained for genetic analysis, each spider was released in front of its burrow entrance. Samples were preserved in 96% ethanol at 4 °C until processed.

2.2. DNA extraction, PCR conditions and genotyping

For DNA analysis, only a small section of the limb was used and DNA extraction was carried out following the protocol described by Roux et al. (2007). Inter Simple Sequence Repeat (ISSR) analysis was performed using four different primers: (ACA)₅BDB, BDB(ACA)₅, (GACA)₄WB, WB(GACA)₄. Details of primers, and the technique used for PCR amplification and electrophoresis, are fully explained in Machkour-M'Rabet et al. (2009).

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