OR291

Genetic structure of social bees in Neotropic continental islands

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Habitat destruction generates forest fragments whose ecological dynamics can be similar to those of islands. Thus evolutionary processes observed on islands can be used to predict outcomes at mainland sites. The continental islands off the south-eastern coast of Brazil are 16000 years old. We studied the genetic structure of the eusocial stingless bee *Tetragonisca angustula* and the primitively eusocial bumblebee *Bombus morio* on these islands as a predictor of the likely impact of habitat fragmentation on these species at mainland sites. We visited 11 islands that have very different sizes and distances from the mainland sampling 1003 stingless bees and 704 bumblebees. *B. morio* was found in all islands whereas *T. angustula* was found only on three islands that are both large and close to the mainland. *T. angustula* populations have low mitochondrial genetic diversity and high population structuring, which we attribute to queen philopatry. Nonetheless, microsatellites showed lower structure and moderate to high genetic diversity, indicating significant dispersal by males. The genetic diversity observed for *B. morio* for both mitochondrial and microsatellite markers was high and no population structuring was detected. For both species, island and mainland populations showed similar genetic diversity, although it was higher in *B. morio*. Geography and biological characteristics such as mating behaviour, dispersal and bee size are likely responsible for these differences in population genetic structure. We conclude that *T. angustula* and *B. morio* are unlikely to suffer extinction die to land clearing, mainly because of their capacity to survive in urban environments and their high rates of male dispersal.