

WORMS WITHOUT BORDERS: POPULATION GENETIC TRENDS IN SOUTH AMERICAN *OTOTYPHLONEMERTES* (DIESING, 1863)

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Disentangling the relative role of the evolutionary processes underlying the demographic history and genetic variation in natural populations remains a challenge, especially in groups where the natural history is poorly known. This is particularly true for interstitial organisms, with populations distributed discontinuously due to ecological factors that might impose limit range. In this study, we evaluated the genetic variation and populational history of three species of *Ototyphlonemertes* (Hoploneuridae): (1) *O. lactea* and (2) *O. erneba*, along eight locations at the Brazilian coast; (3) and the *Lactea* morph *Ototyphlonemertes* sp. collected in eight locations between regions V and XV from the Chilean coast. To assess the genetic variation we analyzed the mitochondrial region cytochrome c oxidase 3 for the Brazilian samples and the cytochrome c oxidase 1 and 3 regions for the Chilean samples. Our data showed that the level of differentiation between populations within each species is moderate to high (F_{ST} = 0.059, 0.582 and 0.098, respectively for *O. erneba*, *O. lactea* and *Ototyphlonemertes* sp.), there are shared haplotypes among locations, and most of the variation is found within populations, except for *O. lactea*. The demographic history analysis showed that most populations from the three species may be in expansion, and that the populations of the Chilean *Ototyphlonemertes* sp. have more variation in the population divergence time (τ varies between 0.32 and 107, with an average of 34.1) than the Brazilian species (τ averages for *O. erneba* and *O. lactea* are 4.24 and 24, respectively). These results suggest that Brazilian populations have a more recent establishment compared to the Chilean species. Both Brazilian and Chilean populations showed signs of populational expansion with high diversity of haplotypes and asymmetrical gene flow among populations. These results seem to contradict the expected low variation due to the ecological constriction and habitat discontinuity faced by these organisms, which reinforces the need of further studies in order to obtain a comprehensive evolutionary picture of interstitial organisms.

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