**Material and Methods**

*Data analysis*

The δ13C and δ15N of earthworm samples were standardized within each site by subtracting the differences between plot-level and site-level δ13C and δ15N of soil samples at 0-5 cm depth (for site BDTR1 and BDTR2, the isotope values of soil samples at 0-5 cm depth were derived as the weighted average of the isotope values at 0-2 cm and 2-5 cm depth). To examine the isotopic niche breadth of earthworm species, we calculated Bayesian standard ellipse area (SEAB), which represents the core isotopic niche of a population, using the R SIBER package (Jackson et al. 2011). Three Markov Chain Monte Carlo (MCMC) chains were run, each with 30,000 iterations and a burn-in number of 3,000. An inverse Wishart prior was used to initiate the model. Chain convergence was assessed via trace plots and Geweke diagnostics. The 95% high density interval (HDI) was computed to quantify the uncertainty in SEAB estimates. The percentage of overlapping SEAB was also calculated to measure the degree of core niche overlap between species pairs.

To test for the differences in species’ total isotopic niches (including niche position and niche breadth), we further performed pairwise permutational analysis of variance (PERMANOVA) and permutational test for homogeneity of multivariate dispersions (PERMDISP) on the δ13C and δ15N of earthworm species using the R vegan package (Oksanen et al. 2013). PERMANOVA tests the null hypothesis of no differences in the centroid (i.e., niche position) and/or dispersion (i.e., niche breadth) of the species pairs in the isotopic space, whereas PERMDISP specifically tests the null hypothesis of no differences in the dispersion (i.e., niche breadth) of the species pairs in the isotopic space. All analyses were performed in R version 4.1.0 (R Core Team 2021).

Reference

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