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Response to Comment on “Global distribution of earthworm diversity”

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Abstract (60 words)

James et al. claim that there are areas of concern in (1). We believe that James et al. may have misunderstood the methods behind our paper (1) and that differences in scale have been overlooked. Once those misunderstandings have been resolved, their remaining criticisms are either not sustained or agree with our statements (1). To advance the field, we recommend additional sampling using comparable methodologies in underrepresented areas.

Main Text

Criticisms in James et al. (2) can be broken into three main areas: i) criticisms of the conclusions, ii) criticisms of the data used, and iii) criticisms of including anthropogenic habitats.

The Authors (2) incorrectly claim that (1) “concludes that tropical earthworm communities are less diverse and abundant than temperate communities”. In fact, we conclude that “it is likely that the tropics harbor more species overall”. However, we would also draw attention to other global distribution studies that found lower local soil biodiversity in tropical soils compared with temperate or arctic regions (e.g. microbes (3), nematodes (4)). (2) also claims that using local/site-level estimates of diversity to understand global patterns is not appropriate. This is not true, as different scales of diversity can be used to test ecological principles, such as the latitudinal diversity gradient (5). These modelled outputs provide a general pattern, and discrepancies are expected to occur if it were to be ground-truthed.

We applied transparent inclusion criteria (see page 3 of Supplementary Materials, ‘Literature search’) (1) for papers screened, which is a required method in synthesis studies (6), and is necessary when different methodologies have been applied. This resulted in removal of 92.3% of papers which is not an exceptional amount. For example, a highly-cited ecological meta-analysis (7) removed 90.6% of papers during their screening process. However, we

need to stress that it was not mandatory for datasets to include species-level identification as was stated in (2).

In (2), a list of publications was provided which appear to contradict our results. These papers are highly informative in terms of earthworm inventories, but their results are not directly comparable to our study. The majority of the papers listed in (2) do not give adequate alpha-level (local level) estimates of earthworm diversity to allow a quantitative analysis, such as ours, to be carried out. In (1), we defined “local” in terms of site-level data, where “site” was defined as “a location of one or more samples that adequately captured the earthworm community”. In a number of the listed papers, such as (8) (their reference (5) - note: the values reported in (2) do not match the actual values in this publication), the values given are totals of several sampling sites (using our definition), and hence not alpha-diversity, but rather overall diversity within a larger region. Importantly, the literature presented does not contradict our conclusion, but instead reinforces it on the high levels of beta-diversity of earthworms in the tropics.

(2) also discusses the sampling curves of earthworm species within temperate and tropical biomes. Unfortunately, as no citation was provided, we are unable to establish the foundation of these claims. However, given our findings in Figure 2 (high regional diversity, implying high-beta diversity when local diversity is low), we would not argue against this point.

In (2), the spatial biases in our data was also discussed. However, we had already highlighted in (1) that we need more sampling in the tropics and other underrepresented areas. Figure 2 in (1) was not intended to show where future sampling should occur (as longitude should also be taken into account for such recommendations), but rather to account for less sampling across certain broad latitudinal zones. Thus, we reiterate our call, adding to comments in (2), for more sampling not only in the tropics but also in many other places, such as underrepresented temperate zones like Russia (see Figure 1a in (1)).

The taxonomic expertise of our data contributors was also called into question. We had already highlighted the high percentage of unidentified species in the tropics in our text as well as in Table S4 (1). However, we do disagree with James et al. regarding identification expertise needed for the temperate realm, as there are also many species in temperate regions that cannot be identified by external features alone. In addition, the taxonomy presented in (1) was checked by multiple earthworm taxonomists (see Author Contributions/Materials and Methods), and thus we stand by its reliability. But we wholeheartedly agree that more taxonomists are needed globally to help improve current knowledge of earthworm geographic patterns.

Throughout (2), additional ways of sampling earthworm communities were suggested. Although we agree with these methods, we stress they are only suitable in certain instances. Qualitative methods (e.g., a free search for earthworms at a site) are often used for species inventories, and we agree with (2) that this would give higher numbers of earthworm species in an area. However, due to lack of a standardised sampling effort and area, qualitative methods are not comparable across studies. Conversely, quantitative approaches (e.g., hand-sorting through soil within a 50 cm x 50 cm quadrat) typically use standardized methods that are comparable across studies but are unlikely to detect every species that could be present at a particular habitat or site (in particular those associated with certain microhabitats or microsites, such as dead logs, or compost piles). In (1) we needed comparable results to allow us to analyse a large set of standardised quantitative data, and to decrease the total variation associated with the collated data sets. Thus, typically taxonomic literature (e.g. reporting species presence/absence using qualitative approaches) was excluded, and as a result, there will be a bias towards less rare species. While DNA barcoding would be useful for future global synthesis studies, there is not enough data for

such studies yet. Furthermore, several studies (e.g. (9)) have reported the existence of cryptic species in the temperate realm, so diversity is also expected to increase outside the tropics using molecular methods.

In a world undisturbed by anthropogenic activities, we would only predict large-scale biogeographic patterns using data from natural habitats. However, as human impacts are causing unprecedented amounts of land use change (10), and there are relatively few areas of natural habitats in certain parts of the world (e.g. Europe), anthropogenic habitats need to be considered in biodiversity studies. To present the most realistic view possible of the current earthworm communities, we included a global layer on habitat cover within our models (see Figure S5 and S6 in (1)). If these habitats contain only a few species, we felt it was important to show the impact this had across a global-scale, rather than excluding these expanding systems (e.g. agriculture covers 37% of the Earth's land (11)) from our analysis. The distribution of each category of habitat cover was relatively even across temperate and tropical regions in (1), although some disparity existed (e.g., 22.2% of sites in the tropics were identified as 'cropland', but only 14.9% in the temperate region).

Finally, we would like to highlight again, that with more data the reliability of conclusions can only be improved, and we welcome any additional sampling using comparable methodologies in underrepresented areas. However, it is crucial that this data is made freely available, either in original publications or in online repositories.

This response has been submitted on behalf of all co-authors of (1), with their knowledge.

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