The jury's in the details

Yuan-Ye Zhang[1]

[1]Key Laboratory of the Ministry of Education for Coastal and Wetland Ecosystems, Xiamen University

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Abstract

Sánchez-Tójar et al. (2020, Ecol Lett) question the methodology, transparency and conclusion of our study (Yin et al. 2019, Ecol Lett, 22, 1976). I feel that these arguments ignore critical assumptions and are based on a misunderstanding of our peer-review process. General does not mean always; the jury is in deciding when and where a transgenerational effect is beneficial, which enlightens future research.

Sánchez-Tójar et al. (2020) suggest that the conclusion of our meta-analysis is not robust and methods have limitations, which would have been avoided by transparency at the peer-review stage. I will address these concerns below.

How robust are the results?

A major criticism from Sánchez-Tójar et al. is that Yin et al. did not fully account for non-independence in the data. As only accounting for phylogenetic non-independence changes the results (Supplementary information 5 in Sánchez-Tójar et al. and Fig. S1), the discussion will focus on this point. First, as we have briefly addressed in Yin et al., ignoring phylogenetic structure is not because it is unimportant or non-exiting, but because such non-independence due to a shared common ancestor probably very weak and extremely difficult, if not impossible, to estimate with our data. The data include both plants and animals that are so remotely related, that too many events such as independent selection get involved in the evolution of these organisms, thus substantially weakening the constraints imposed by the common ancestor. Furthermore, our data include various nonhomologous traits measured for different species. The common ancestor of these traits, if any, is difficult to be approximated with the phylogenetic relatedness of species.

Even if such approximation was properly, the approach of the comment still has issues. First, the authors employ the Brownian motion model (Felsenstein 1985) to estimate the variance-covariance matrix (Fig. 1), which assumes evolutionary change to be gradual with time and the absence of selection that could change the rate of evolution. While such a neutral assumption may hold for short evolutionary time or small phylogenies, it is hardly applicable to our data including plants and animals. Second, the Brownian motion model requires using coalescence time to estimate branch lengths, but the authors use the number of leaves of subtrees (Grafen 1989) instead. Such estimation is biased by the sample size along each branch; e.g., underestimation of the branch length of gymnosperm (Supplementary information 3.1 in Sánchez-Tójar et al. and Fig. S2). Ignoring these assumptions and blindly employing phylogenetic structure can dramatically reduce statistical power, leading to overly conservative results. This approach appears to reduce the independent sample size to three referring to three major clades of plants, invertebrates and vertebrates, with high variance-covariance coefficients (>0.6) within each clade (Fig. 2). Although alternative evolutionary models can generate significant results (Fig. S1), I do not consider these models to be reasonable, as critical assumptions have been violated before adopting them.

Where is the jury?

Although the general patterns prove robust, I disagree with the comment that the "jury" lies in the "generality" nor the previous meta-analysis "challenges" this generality. Both Radersma et al. (2018) and Uller et al. (2013) revealed an overall positive (albeit non-significant) effect, and a pattern of generality is thus anticipated. We may find nothing more than they anticipated, but the significance of our study, the "jury", is to obtain the most detailed picture to show when and for which taxa such an effect is beneficial. Instead of always being beneficial, this picture shows transgenerational effects are disadvantageous for some taxa in some environments, consistent to the high heterogeneity revealed by Sánchez-Tójar et al.

The comment also suggests focusing on F2 and F3 generations and excluding the effect of parental condition transfer (Engqvist & Reinhold 2016). While these concerns are important for experimental studies, I wonder whether it is feasible to the evidence-demanding meta-analysis, given the difficulty of conducting multi-generation experiments and separating parental "cues" and "conditions" (Engqvist & Reinhold 2016). Furthermore, whether condition transfer should be considered adaptive is still controversial (Bonduriansky & Crean 2018; Engqvist & Reinhold 2018). Our study thus represents a first feasible step, which draws a picture compatible with these concerns.

How transparent is our study?

While I agree that our meta-analysis has limited coverage, I do not accept the criticisms relating to publication bias and, in particular, transparency at the peer-review stage. The conclusion is also based on all alternative assessments showing no evidence for publication bias, and both the raw data and code are submitted for revision. Owing to such transparency, most issues raised in the comment have been carefully evaluated by reviewers, who (i) repeated the literature search stepwise, (ii) evaluated the influence of missing words, (iii) suggested to dig into the data for a diet effect, and (iv) assessed the effects of combining fully factorial with non-fully factorial experiments. They have identified the limitations, but are enthusiastic about the detailed picture provided and the opportunity to weigh empirical evidence with theories (please refer to the point-to-point reply of Yin et al. (2019) in the supplementary files).

With many thanks to Sánchez-Tójar et al., I hope these discussions will promote open science practices, methodological development and maturation of meta-analysis research, which bridges empirical evidence with theories and enlightens future explorations.

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Figures Legends

Figure 1 Phylogenetic meta-analysis. The blue arrow shows the basic principle of phylogenetic meta-analysis in which effect sizes are not independent owning to their shared evolutionary history/common origin/common ancestor. The dashed box indicates how this non-independence is generally modeled in a meta-analysis approach. The solid box shows how it is specifically modeled in Sánchez-Tójar et al. (2020). The open arrows provide alternative modelling approaches for phylogenetic non-independence.

Figure 2 Heatmap (a) and histogram (b) of the variance-covariance matrix calculated following Sánchez-Tójar et al. (2012) as illustrated in Fig. 1. A detailed heatmap with species names is shown in Fig. S2.
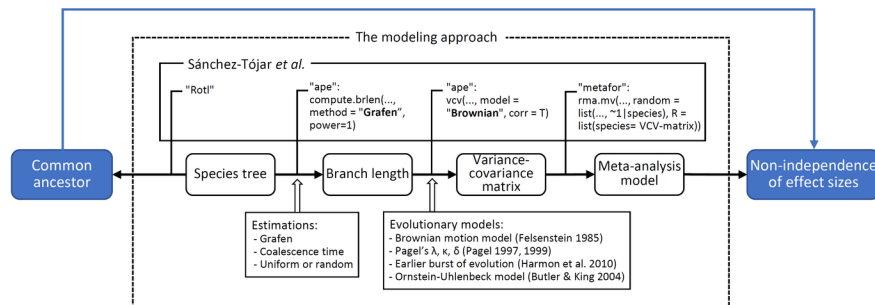

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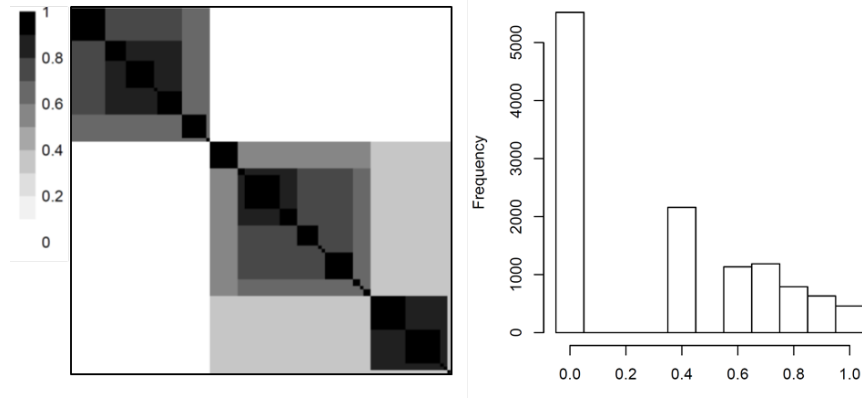
(b)

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