The jury's in the details

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Abstract

Sánchez-Tójar et al. (2020, Ecol Lett) questioned 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 the misunderstanding of our peer-review process. General does not mean always; the jury of our study is in revealing when and where a transgenerational effect is beneficial, which enlightens future research.

Sánchez-Tójar et al. (2020) raised three main issues with our meta-analysis study (Yin et al. 2019): (1) the study did not fully account for non-independent, (2) it had limited coverage, and (3) it lacked transparency and the peer review process was ineffective. Here, I will focus this reply on these issues.

First, I appreciate Sánchez-Tójar et al. for their efforts in improving the data quality and reanalysing the data with models fully accounting for non-independence. However, I feel these efforts further demonstrate the robustness of our previous conclusions (Fig. 1). The re-analysis results show that all approaches generate similar estimates, and that the difference between "significant" and "non-significant" results only depends on different evolutionary assumptions rather than the data. As previously indicated in our paper, we did not account for phylogenetic non-independence because our data include many non-homologous traits that do not share a common ancestor. Furthermore, our data include both animals and plants, and in such a large phylogeny, the non-independence caused by sharing a common ancestor is probably very weak due to independent selection in different lineages (Fig. S1). The comment ignored the effect of selection by adopting the Brownian motion model (Felsenstein 1985), which overestimated the non-independence and substantially decreased the independent sample size and statistical power (Figs. S2 and S3). Although reducing the influence of phylogenetic non-independence or adopting different evolutionary models can generate significant results (Fig. 1), I do not consider these approaches necessary, as the critical assumption of sharing a common ancestor is still violated.

Second, I agree with Sánchez-Tójar et al. that our study has limited coverage. Such a limitation is more likely associated with restricting the subject areas (˜78% reduction in searching records) than with missing keywords (˜30% reduction). However, I disagree with the comment to focus the meta-analysis on F2 and F3 generations or to exclude the effects of parental condition transfer, as they will both greatly reduce the number of collected studies. One significant aspect of our study is the facilitation of acquiring comprehensive data by proposing a consensus conceptual framework of transgenerational effects (please see the discussion below). We, therefore, hope that our study and this reply can be an incentive as well as a reference for future more comprehensive meta-analysis in this field.

In particular, I disagree with the comment that our study lacks transparency or that the review is ineffective. Both the data and code were submitted in our first submission and completely open to the three reviewers, and their comments were critical but constructive (please refer to the 69-page reply letter in the supporting file). As a consequence, most issues raised by this comment, including those in the supplementary information,

have been identified and checked in the revision. More importantly, for controversial issues, e.g., expected fitness relationships (Supplementary Information 2.7 in Sánchez-Tójar et al. 2020), they even suggested using sensitivity analysis to evaluate the effect of our conductance. I emphasize that the decision of our manuscript is not established on the ignorance of these limitations, but the judgement by reviewers that the significance overwhelms the limitations and fits the criteria of Ecology Letters.

Finally, I feel that the comment underestimates the significance of our study. The real purpose of this meta-analysis is *NOT* to demonstrate a significantly positive overall effect. Such a positive effect has been anticipated by the previous meta-analysis, which revealed positive but non-significant estimates (Uller *et al.*2013; Radersma *et al.* 2018), possibly limited by the number of collected studies. One significant point of our study is that it raises a consensus conceptual framework to enable data collection from different environments, generations and types of designs, significantly improving the comprehensiveness of data. Furthermore, by analysing the heterogeneity underlining the comprehensive data, our study obtains the most detailed picture of transgenerational effects, which shows when and for which taxa such an effect is beneficial. The picture helps to weigh empirical evidence with theories and instructs future studies and is thus the real jury of our study. Intriguingly, our study also shows that transgenerational effects are found across the tree of life, a pattern consistent with previous studies (Salinas *et al.* 2013; Uller*et al.* 2013). This pattern suggests that these effects either have a deep evolutionary origin or have evolved repetitively.

To resolve the detailed scenarios that retain or drive the evolution of transgenerational effects, I fully agree with the comment that more comprehensive meta-analysis is necessary. Together, I hope that these discussions will promote open science practices, methodological development and the maturation of meta-analysis studies, which serve to bridge empirical evidence with theories and enlighten further research.

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REFERENCES

Blomberg, S.P., Garland, T. & Ives, A.R. (2003). Testing for phylogenetic signal in comparative data: Behavioral traits are more labile. *Evolution* , 57, 717-745.

Felsenstein, J. (1985). Phylogenies and the comparative method.*Am. Nat.* , 125, 1-15.

Pagel, M. (1997). Inferring evolutionary processes from phylogenies.*Zool. Scr.* , 26, 331-348.

Radersma, R., Hegg, A., Noble, D.W.A. & Uller, T. (2018). Timing of maternal exposure to toxic cyanobacteria and offspring fitness in*Daphnia magna* : Implications for the evolution of anticipatory maternal effects. *Ecol. Evol.* , 8, 12727-12736.

Salinas, S., Brown, S.C., Mangel, M. & Munch, S.B. (2013). Non-genetic inheritance and changing environments. *Non-Genetic Inheritance* , 1, 38–50.

Sánchez-Tójar, A., Lagisz, M., Moran N.P., Nakagawa, S., Noble, D.W.A & Reinhold, K. (2020). The jury is still out regarding the generality of adaptive "transgenerational" effects. *Ecol. Lett.*

Uller, T., Nakagawa, S. & English, S. (2013). Weak evidence for anticipatory parental effects in plants and animals. *J. Evol. Biol.* , 26, 2161-2170.

Yin, J., Zhou, M., Lin, Z., Li, Q.Q. & Zhang, Y.-Y. (2019). Transgenerational effects benefit offspring across diverse environments: a meta-analysis in plants and animals. *Ecol. Lett.* , 22, 1976-1986.

Figures Legends

Figure 1 Patterns analysed with different models. Model 1 uses the raw data uploaded by Yin et al. including 1170 effect sizes, and models 2-6 use the proofed data uploaded by Sánchez-Tójar et al. including 1059 effect sizes. Pagel's λ=0.5 halves the values of the variance-covariance matrix and thus relaxes the phylogenetic dependence (Pagel 1997). Blomberg's 0<g<1 assumes that the rates of evolution accelerate through time (Blomberg *et al.* 2003).