Invited reply

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3. Phylogenetic position of Oryzias setnai

Second, we tested for the presence of LBA for O. setnai by estimating the phylogenetic position of this species after removing all outgroups, as proposed by [12]. We found that the position of O. setnai did not change (i.e. the branch leading to O. setnai split off from the internal branch that separates the latipes group from others; figure 2a), indicating that the effect of LBA, if any, is not substantial. It is also clear that fig. 1 in [1] did not successfully resolve deep divergences among families and orders within Atherinomorpha; for example, the flyingfish Cheilopogon pinnatibarbarus (Beloniformes) and the silverside Menidia menidia (Atheriniformes) were close to each other, implying that the finding of O. setnai nested among other adrianichthyids is unreliable.

We were aware that Parenti [13] estimated from morphological comparisons that O. setnai is sister to O. uawai, so we respectfully correct our assertion to ‘no molecular study has investigated its phylogenetic position’. We agree with [13] in terms of the view that O. setnai is a member of adrianichthyids, for which monophyly is supported by 17 synapomorphic characters, such as the lack of vomer and rostral cartilage. However, we disagree that O. setnai is phylogenetically located within other adrianichthyids [1,13], because it is highly autapomorphic. It is the only adrianichthyid species having internal fertilization, with male anterior anal-fin rays modified into an intromittent organ (figure 2b), and a bilaterally asymmetric female body [13].

Moreover, the number of abdominal and caudal vertebrae of O. setnai is disproportionately uncommon compared with other adrianichthyids (figure 2c). We also reported in [2] that mitochondrial genome gene order differs from that typical of vertebrates including other adrianichthyids (figure 2d; see also electronic supplementary material, figure S1 in [2]). These highly autapomorphic traits of O. setnai are consistent with our phylogenetic estimation that this species is sister to all other adrianichthyids.

4. Usage of †Lithopoecilus brouweri as fossil calibration

Third, we included †L. brouweri in our fossil calibration [2] because Parenti [13] had classified this species within Adrianichthyidae, but we realized that this classification was only tentative. We therefore re-estimated the divergence time of O. setnai, excluding †L. brouweri from the calibration. Excluding this fossil species did not greatly affect the divergence time estimation for O. setnai; it was estimated to have diverged about 71 million years ago (Mya) (electronic supplementary material, figure S1), whereas it was 74 Mya in [2]. This outcome indicates that although we still think that †L. brouweri is the common ancestor of O. sarasinorum and O. eversi (extant species endemic to Sulawesi [14]), the divergence time estimation for O. setnai is independent of its authenticity.
5. Conclusion

In summary, the points raised by Britz et al. [1] do not undermine our conclusions about the origin and evolutionary history of Adrianichthyidae (i.e. an eastward ‘out-of-India’ dispersal). We emphasize that ‘earth and life evolve together from something more ancestral’.

Data accessibility. Data available from the Dryad Digital Repository: https://doi.org/10.5061/dryad.nvx0k6dtx [15].

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