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EDITED AND REVIEWED BY
Maria Ina Arnone,
Stazione Zoologica Anton Dohrn, Italy

*CORRESPONDENCE

Thiago André
✉ thiago.andre@unb.br

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Editorial: The future of the homology concept under novel evolutionary paradigms

Thaís Elias Almeida¹, Thiago André^{2*} and Roxana Yockteng³

¹Departamento de Botânica, Universidade Federal de Pernambuco, Recife, Brazil, ²Departamento de Botânica, Universidade de Brasília, Brasília, Brazil, ³Corporación Colombiana de Investigación Agropecuaria, Centro De Investigación Tibaitata, Mosquera, Cundinamarca, Colombia

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Editorial on the Research Topic

[The future of the homology concept under novel evolutionary paradigms](#)

Homology, the sameness or similarity of traits found in different organisms that are inherited by continuous descents from a common ancestor where the trait was present or originated (DiFrisco, 2021), has been a central concept in evolutionary biology for many decades (reviewed by Bellego-Campos et al., 2023). Nevertheless, contemporary findings in evolutionary developmental biology (Brakefield, 2006; Müller, 2007; Svensson, 2018) and the mounting evidence of hybridization across the history of life (Mallet et al., 2016) challenge traditional knowledge on trait evolution, in particular, the concept of homology. Phylogenetic networks (Huson and Bryant, 2006) extend phylogenetic trees to allow for reticulate evolutionary processes such as hybridization and horizontal gene transfers, which can also produce original traits. Recent years have also seen the rise of creative molecular, genomic, and developmental approaches that enabled integrated exploration of the mechanisms by which apparent similarity arises throughout life. Transgenerational epigenetic inheritance, physiological inheritance, ecological inheritance, behavioral transmission, and cultural inheritance can play significant evolutionary roles by biasing phenotypic variants subject to selection (Laland et al., 2013, Laland et al., 2014, Laland et al., 2015).

Conceptual frameworks advance in response to new data, theories, and methodologies. The Research Topic *The future of the homology concept under novel evolutionary paradigms* presents fresh perspectives from diverse organisms, leveraging modern theory and technologies in comparative biology.

The author Göpel, with the hypothesis and theory article titled “*Synthesizing foundations in evolutionary morphology and a plea for conceptual explicitness regarding homology concepts*” focuses on the scientific discipline of morphology, which is concerned with describing and comparing organismal form. It highlights morphology’s historical and contemporary significance within biological sciences, emphasizing its revival through advancements in imaging techniques and the rise of phenomics. The author discusses the scientific discipline of evolutionary morphology, emphasizing its importance in understanding organismal form and its evolutionary implications. Göpel argues that morphology has historically been undervalued as merely descriptive. Traditionally linked with the concept of homology, morphology has evolved from being perceived merely as an auxiliary discipline to being recognized as an explanatory science capable

of providing insights into the evolutionary processes. The paper argues against reducing morphology to descriptive, non-explanatory endeavors, illustrating its role in understanding biological diversity through evolutionary perspectives. It highlights the challenges faced in defining and using the concept of homology—essential for understanding biological similarities and differences—due to its diverse interpretations across different studies. The manuscript further explores the integration of modern technological approaches such as 3D digital data and computational methods like ontologies. These cutting-edge tools have not only expanded the scope and accuracy of morphological studies but also opened up new avenues for research. Using ontologies—structured knowledge bases that define terms and their relationships—holds immense potential to enhance conceptual clarity and foster better communication within the scientific community. This approach is seen as a promising solution to the challenge of diverse interpretations associated with critical morphological concepts, especially homology. The manuscript underscores the thrill of these advancements and the importance of maintaining conceptual clarity, especially in the use of terms like ‘homology,’ which have varied interpretations across different studies. It advocates for conceptual explicitness to facilitate clearer communication and understanding within the scientific community.

In the opinion article “*Homologous vs. homocratic neurons: revisiting complex evolutionary trajectories*”, [Moroz and Romanova](#) provide a brief historical overview of the homology concept and discusses its applications to diverse nervous systems of invertebrates targeting the level of individual functionally characterized neurons. They make an argument against a single origin of neurons, which they claim is not supported by existing data. These authors then bring two cases: First, [Romanova and Moroz](#) discuss the “*Parallel evolution of gravity sensing*”. In this article, they highlight the evolution of gravity sensing and the comparative biology of gravity reception, by tracing the parallel evolution of gravity sensing. Early diverging metazoans evolved alternative solutions toward spatial orientation. Gravitational sensitivity and locomotory integrative systems studies should target the understanding of convergent evolution at all levels of biological organization. Secondly, in the opinion article on “*Syncytial nets and chemical signaling: emerging properties of alternative integrative systems*”, [Moroz](#) presents the Ctenophora chemical language for intercellular communications as a unique and mostly unknown subset of signal molecules for neural

architecture. The molecular deciphering of neural toolkits in ctenophores includes a reduced representation of canonical bilaterian neurogenic and synaptic gene complement, with an apparent lack of classical low molecular weight transmitters ([Moroz et al., 2014](#); [Moroz et al., 2020](#)). Moroz introduces these comb jellies with unique neural organizations of enigmatic origins; and lacking recognized homologies to any other animal phylum.

Overall, the papers presented in this Research Topic make strong cases for the renewed recognition of morphology as a vital scientific discipline that contributes significantly to our understanding of biological forms and their functional, developmental, and evolutionary contexts. Definitions of homologous features should extend beyond similarity in appearance and shared position to encompass shared genetic arrangements, integrating developmental approaches alongside phylogenetic methods. Therefore, we advocate for the advance of a dynamic conceptual framework of homology will certainly revitalize morphology as a discipline and its role in explaining evolutionary processes at the same level as molecular biology.

Author contributions

TEA: Conceptualization, Writing – original draft, Writing – review & editing. TA: Conceptualization, Writing – original draft, Writing – review & editing. RY: Writing – original draft, Writing – review & editing.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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References

- Ballego-Campos, I., Bonifácio, S. K. V., and Assis, L.C.S.. (2023). A unified view of homology? *Cladistics* 39, 398–417. doi: 10.1111/cla.12541
- Brakefield, P. (2006). Evo-devo and constraints on selection. *Trends Ecol. Evol.* 21, 362–368. doi: 10.1016/j.tree.2006.05.001
- DiFrisco, J. (2021). “Developmental homology,” in *Evolutionary developmental biology*. Eds. L. Nuño de la Rosa and G. B. Müller (Springer Nature, Switzerland), 85–97. doi: 10.1007/978-3-319-32979-6_74
- Huson, D. H., and Bryant, D. (2006). Application of phylogenetic networks in evolutionary studies. *Mol. Biol. Evol.* 23, 254–267. doi: 10.1093/molbev/msj030
- Laland, K., Odling-Smee, J., Hoppitt, W., and Uller, T. (2013). More on how and why: cause and effect in biology revisited. *Biol. Philos.* 28, 719–745. doi: 10.1007/s10539-012-9335-1
- Laland, K., Uller, T., Feldman, M., Sterelny, K., Müller, G., Moczek, A., et al. (2014). Does evolutionary theory need a rethink? *Nature* 514, 161–164. doi: 10.1038/514161a
- Laland, K., Uller, T., Feldman, M., Sterelny, K., Müller, G., Moczek, A., et al. (2015). The extended evolutionary synthesis: its structure, assumptions and predictions. *Proc. R. Soc. B Biol. Sci.* 282, 1–14. doi: 10.1098/rspb.2015.1019
- Mallet, J., Besansky, N., and Hahn, M. W. (2016). How reticulated are species? *Bioessays* 38, 140–149. doi: 10.1002/bies.201500149
- Moroz, L. L., Sohn, D., Romanova, D. Y., and Kohn, A. B.. (2020). Microchemical identification of enantiomers in early-branching animals: Lineage-specific diversification in the usage of D-glutamate and D-aspartate. *Biochemical and Biophysical Research Communications* 527(4), 947–952. doi: 10.1016/j.bbrc.2020.04.135
- Moroz, L., Kocot, K., Citarella, M., Dosung, S., Norekian, T. P., Povolotskaya, I. S., et al. (2014). The ctenophore genome and the evolutionary origins of neural systems. *Nature* 510, 109–114. doi: 10.1038/nature13400

Müller, G. B. (2007). Evo-devo: extending the evolutionary synthesis. *Nat. Rev. Genet.* 8, 943–949. doi: 10.1038/nrg2219

Svensson, E. I. (2018). On reciprocal causation in the evolutionary process. *Evol. Biol.* 45, 1–14. doi: 10.1007/s11692-017-9431-x