Abstract

ISSN 1178-9905 (print edition)

ZOOSYMPOSIA

ISSN 1178-9913 (online edition)

https://doi.org/10.11646/zoosymposia.22.1.63 http://zoobank.org/urn:lsid:zoobank.org:pub:4850B3EF-1681-4D92-AD71-8C4A82313A21

Host plants contribute to the global pattern and diversification of herbivorous eriophyoid mites*

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*In: Zhang, Z.-Q., Fan, Q.-H., Heath, A.C.G. & Minor, M.A. (Eds) (2022) Acarological Frontiers: Proceedings of the XVI International Congress of Acarology (1–5 Dec. 2022, Auckland, New Zealand). Magnolia Press, Auckland, 328 pp.

Eriophyoid mites (Acari: Eriophyoidea) comprise approximately 5000 named species, leading to the most speciesrich superfamily in the Acari. They are strictly herbivorous with a high level of host specificity, reflecting 89% of these mites attack only one or two congeneric host species (Yin *et al.*, 2022). However, their global patterns of species diversity and factors contributing to the diversification remain poorly known. We adopted multiple approaches to determine the extent of potential factors affecting their diversification, including contemporary climate, Quaternary climate change, habitat heterogeneity, and host plants. Our results show the center of eriophyoid species diversity in the temperate region, which is opposite to the patterns in center of diversity for plants and some other organisms (Li *et al.*, 2022). Environmental factors (abiotic factors) can indirectly influence the species richness of eriophyoid mites by affecting the host plants (biotic factors) (Li *et al.*, 2022). Multiple host shifts as well as speciation constrained by hosts were probably the main drivers behind eriophyoid mite diversification (Xue *et al.*, 2022). Our study provides new evidence regarding the global pattern of herbivorous mite diversity and highlights the evolutionary trajectory of eriophyoid mites.

References

- Yin, Y., Yao, L.-F., Hu, Y., Shao, Z.-K., Hong, X.-Y., Hebert, P.D.N. & Xue, X.-F. (2022) DNA barcoding uncovers cryptic diversity in minute herbivorous mites (Acari, Eriophyoidea). *Molecular Ecology Resources*, 22, 1986–1998. https://doi.org/10.1111/1755-0998.13599
- Xue, X.-F., Yao, L.-F., Yin, Y., Liu, Q., Li, N., Hoffmann, A.A., Sun, J.-T. & Hong, X.-Y. (2022). Macroevolutionary analyses point to a key role of hosts in diversification of the highly speciose eriophyoid mite superfamily. *Molecular Phylogenetics* and Evolution. Major revision.
- Li, N., Sun, J.-T., Yin, Y., Hong, X.-Y. & Xue, X.-F. (2022) Global patterns and drivers of herbivorous eriophyoid mite species diversity. *Journal of Biogeography*. Accepted.