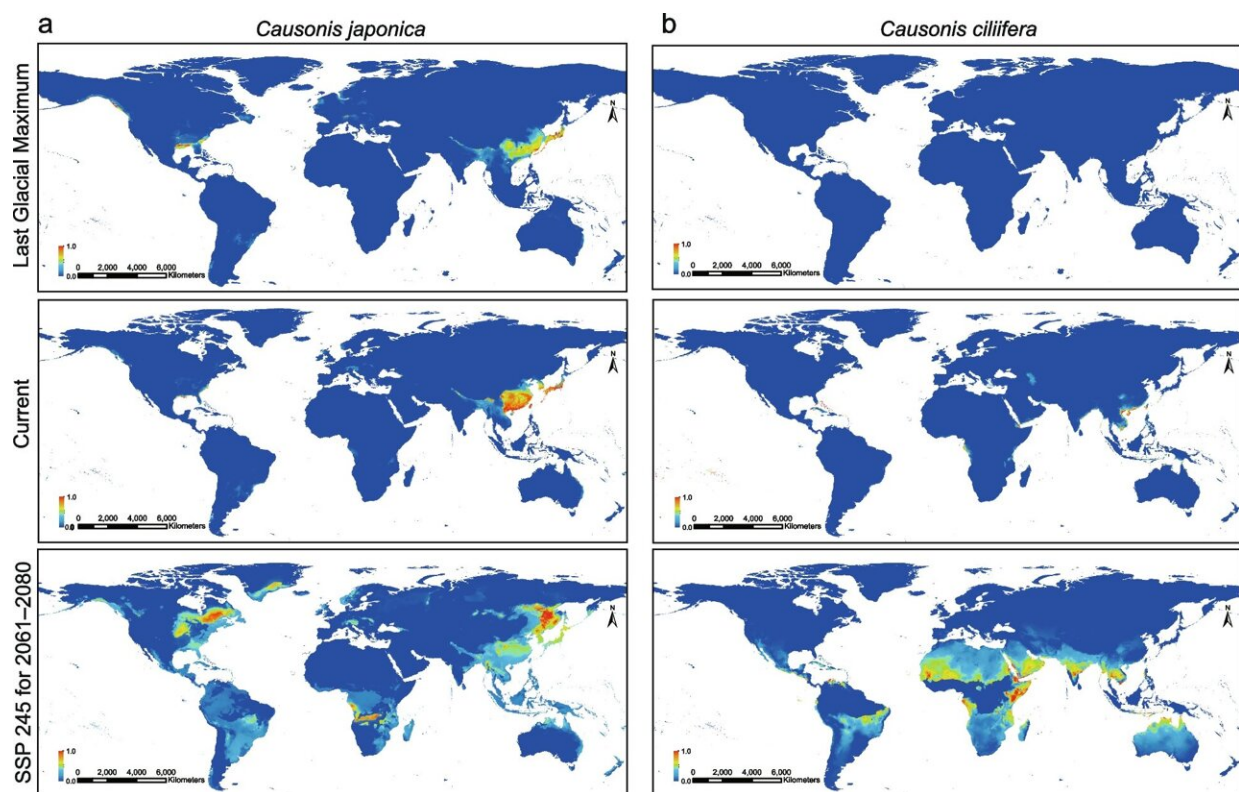


Study suggests potential role of hybridization and polyploidization in species range expansion

October 17 2023, by Zhang Nannan



The global potential distribution of a *Causonis japonica* and b *C. ciliifera* under the LGM (0.021 Ma), the current condition (1970–2000), and the future (2061–2080) on the shared socioeconomic pathway (SSP) 245 scenario, modeled using MaxEnt. The color panel in the bottom left refers to the level of climatic suitability, which increases with color from blue to red. Credit: *BMC Biology* (2023). DOI: 10.1186/s12915-023-01718-8

In a study published in [BMC Biology](#), Prof. Chen Zhiduan's team at the Institute of Botany of the Chinese Academy of Sciences (CAS), together with their international collaborators, used densely sampled nuclear and plastid data to reconstruct a reliable reticulate evolutionary history of *Causonis* in a robust biogeographic framework.

They detected nuclear gene tree conflicts throughout the [genus](#), especially in the core *Causonis* clade, which were identified as mainly caused by extensive hybridization events. Using comprehensive methods, they also revealed an allopolyploid origin of the widespread core *Causonis* clade, which may have promoted the accumulation of stress-related genes and thus facilitated the adaptation to changing environments.

Elucidating the mechanisms promoting [species](#) distribution range is crucial for understanding the dynamics of biodiversity under [climate change](#). Hybridization and polyploidization, two processes thought to accelerate the generation of adaptive innovations, have been proposed to play important roles in facilitating the expansion of species range distribution.

The genus *Causonis* of the grape family provides an opportunity to explore the mechanisms underlying the contrasting patterns of species distribution ranges. Species of *Causonis* show wide variation in distribution ranges, with most species in the "core clade" possessing much larger ranges than those in the early diverging lineages.

Previous studies have also suggested potential hybridization and polyploidization in *Causonis*, particularly in the core *Causonis* clade with more widespread species. Investigating the role of hybridization and polyploidization in species distributions requires strategies that bridge genomics and biogeography.

In this study, the researchers illustrated how [hybridization](#) and polyploidization may have contributed to the excessive disparity in species distribution ranges of *Causonis*. During the early Oligocene glaciation, most *Causonis* lineages underwent extensive extinction and distribution range contraction, while the core *Causonis* ancestor, equipped with duplicated genomes, may have survived the glaciation and flourished in continental Asia.

Using species distribution models, the researchers showed that the wide- and narrow-ranged species may have had different biogeographic pasts and may face different conservation challenges under future climate change. For example, the widespread species *C. japonica* tends to be more invasive in the future, while the narrow-ranged species *C. ciliifera* may be at risk of extinction due to the shrinking of adjacent suitable habitats.

This finding suggests the importance of considering the specific evolutionary history and genetic properties of the focal species when developing conservation strategies.

More information: Jinren Yu et al, Distinct hybridization modes in wide- and narrow-ranged lineages of *Causonis* (Vitaceae), *BMC Biology* (2023). [DOI: 10.1186/s12915-023-01718-8](https://doi.org/10.1186/s12915-023-01718-8)

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