

Hybridization provides climate resilience

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Hybrid populations have long been perceived as a threat to distinct lineages and undervalued from a conservation perspective. Now, research suggests that hybrid populations may harbour gene combinations that improve their ability to cope with changing climate conditions.

Climate change is altering the planet at an unprecedented rate, and organisms need every tool at their disposal in order to keep up. When faced with rising global temperatures, species may evade extinction by shifting their geographic ranges or relying on existing genetic variation to adapt to novel environmental conditions¹. One way in which beneficial gene combinations can quickly be introduced into vulnerable populations is through hybridization, or interbreeding between distinct lineages². Writing in *Nature Climate Change*, Brauer and colleagues³ demonstrate that hybridization between closely related species of rainbowfish spanning an elevational gradient in tropical Australia might make them better suited to adapt to shifts in climate.

Central to our understanding of how species may respond to climate change is the idea, originating in the early 1900s⁴, that organisms are associated with a specific ecological niche, or range of environmental conditions that enable survival and reproduction⁵. A species' ecological niche determines its distribution and abundance and can be quantified under current or ideal conditions to predict future species distributions under climate warming⁶. However, ecological niche models often treat organisms as static and uniform entities, overlooking the evolutionary processes that lead to heterogeneity in species' responses⁷. Recognizing that populations are locally adapted to specific environments, recent research has begun to integrate genomic data into these models to examine how responses to climate change may vary across a species' range^{8–10}. To achieve this, researchers first characterize the relationship between genetic variation involved in climate adaptation and current environmental conditions. Then, they apply this model to future climate projections to predict how much genomic composition must shift in order to keep pace with climate change (a metric referred to as genomic vulnerability)¹⁰.

While the incorporation of genomic data into assessments of climate vulnerability has greatly improved our ability to predict the fate of species, these models still ignore additional evolutionary forces, such as gene flow and hybridization, that can impact the distribution of adaptive genetic variation across space⁷. Brauer and colleagues explicitly address this gap in predictive models by investigating how natural hybridization influences vulnerability to climate change in five closely related rainbowfish species. Examining patterns of hybridization between *Melanotaenia splendida*, a widespread generalist species of rainbowfish, and four relatively restricted specialists (*Melanotaenia eachamensis*, *Melanotaenia utcheensis*,



Malanda rainbowfish and Tully rainbowfish), the authors detected 85 hybrids and 167 individuals of pure parental ancestry. They then determined what genomic variation was relevant for climate adaptation by examining genotype–environment associations with two climate variables. Using the relevant variation, they generated estimates of genomic vulnerability for both hybrid and pure parental populations. Populations of hybrid individuals possessed a greater number of beneficial climate-linked alleles and required a smaller shift in genomic composition to cope with changing climate conditions than pure populations of restricted specialists. Importantly, several adaptive genetic variants that they identified showed evidence of having been transferred from *M. splendida* to Malanda rainbowfish and *M. eachamensis* as a result of hybridization.

To further investigate the threat that climate change poses to the focal species of rainbowfish, the authors also quantified the environmental niche of the five species and constructed ecological niche models to track the presence of suitable habitat since the early Holocene and into the future. As expected, the niche analysis revealed that the generalist species, *M. splendida*, tolerates a much wider range of environmental conditions than the four specialist species. While habitat suitability has remained relatively stable for all five species over the past 10,000 years, a pattern that will continue for *M. splendida*, the restricted species are predicted to lose large portions of their current ranges under continued climate change.

Taken together, these findings suggest that hybridization, and the subsequent transfer of adaptive alleles from *M. splendida* to the restricted specialist species, may help mitigate the effect of climate change for threatened populations. While promising from a conservation standpoint, it is unclear to what extent these results can be generalized across other taxa. As the authors note, hybridization between these species of rainbowfish has likely occurred intermittently over an extended period of time. Interbreeding between more distantly related species abruptly brought into contact due to habitat loss and shifting geographic ranges may result in more negative outcomes.

Additionally, there are known limits to what we can infer from estimates of genomic vulnerability¹¹. For example, this approach assumes that the current relationship between environment and adaptive genomic variation holds beyond the present range of climate variables and can be extrapolated into the future. Furthermore, it is still uncertain exactly how the adaptive genomic variants used to estimate

vulnerability in this study are related to fitness in future climates. Additional experimental work aimed at testing the fitness of hybrid and parental populations under current and future climate conditions would provide further insight into the benefits of hybridization for climate adaptation in rainbowfish.

The conservation value of hybrid populations has long been controversial¹², as hybridization can lead to the extinction of rare plant and animal species¹³. Indeed, hybridization with introduced rainbow trout (*Oncorhynchus mykiss*) in North America has been implicated in the decline of native cutthroat trout (*Oncorhynchus clarkii*)¹⁴. However, for organisms faced with dwindling habitat and limited opportunities for dispersal, low levels of hybridization with closely related warm-adapted species may introduce the genetic variation necessary to remain in place and adapt to altered environmental conditions. The work of Brauer and colleagues highlights the importance of hybrid populations for conservation, revealing that, in some cases, they may hold the key to persistence under future climate change.

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Competing interests

The authors declare no competing interests.