

Digest: On the origin of a possible hybrid species

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Hybrid speciation—the origin of new species resulting from the hybridization of genetically divergent lineages—was once considered rare, but genomic data suggest that it may occur more often than once thought. In this study, Nogueras and Ortego found genomic evidence supporting the hybrid origin of a grasshopper that is able to exploit a broader range of host plants than either of its putative parents.

Our understanding of the role of hybridization in the evolutionary process has changed dramatically in recent years owing partly to wider access to genomic data and new methods for detecting signatures of admixture and introgression. For example, it is now widely accepted that hybridization can play a creative role in adaptation and speciation by bringing together novel combinations of alleles that arose in different populations (Marques et al. 2019). In extreme cases, this may lead to the formation of a new species that is ecologically distinct from its progenitors (Burke and Arnold 2001; Mallet 2007). However, compelling cases of hybrid speciation are still fairly rare.

In this study, Nogueras and Ortego (2022) find genomic evidence for the hybrid origin of a grasshopper from the genus *Chorthippus*. Their study focuses on eight taxa belonging to two named species—*Chorthippus saulcyi* and *Chorthippus binotatus*—that have allopatric or parapatric distributions in France, Spain, Portugal, and Morocco. These taxa have different host plant associations, with subspecies of *C. binotatus* feeding exclusively on scrub legumes and most subspecies of *C. saulcyi* feeding on gramineous herbs. The only exception is the subspecies *C. saulcyi algoaldensis*, which feeds on both scrub legumes and gramineous herbs. The question addressed by the authors was whether *C. s. algoaldensis*—and its dual feeding regime—may have originated through the hybridization of taxa that have narrower feeding preferences.

*This article corresponds to Nogueras, V., & Ortego, J. (2022). Genomic evidence of speciation by fusion in a recent radiation of grasshoppers. *Evolution*. <https://doi.org/10.1111/evo.14508>

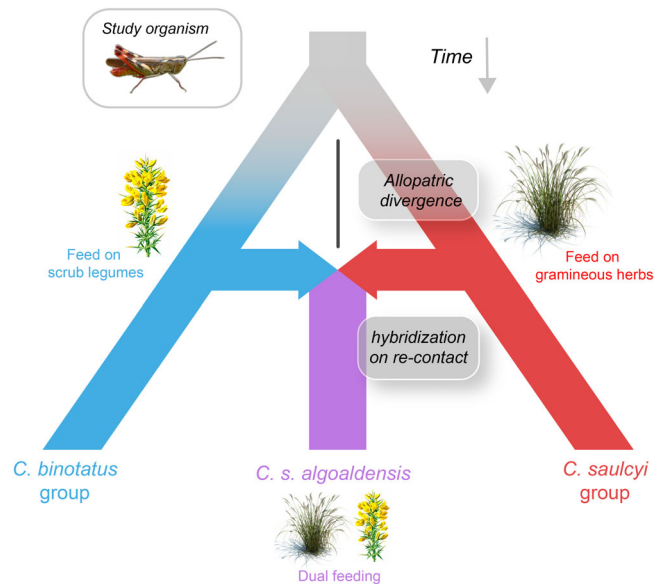


Figure 1. A graphical representation of the speciation history of *C. s. algoaldensis* inferred by the authors. Time runs down the page from a single common ancestor leading to the three contemporary groups. The initial divergence of the lineages leading to *C. binotatus* and *C. saulcyi* was facilitated by a period of geographic isolation (allopatry), which allowed feeding preferences to diverge. Upon secondary contact, hybridization led to the formation of a new lineage, ultimately giving rise to the dual-feeding *C. s. algoaldensis*.

To do this, the authors obtained double-digest RADseq data and morphological measurements from the eight subspecies and tested for signatures that are expected to arise following

hybridization. Although the patterns of morphological data could be adequately explained without invoking recent or past hybridization, the genomic data do suggest that admixture has played some role in the origin of *C. s. algoaldensis*. For example, an ABBA-BABA test revealed an excess of shared derived sites between *C. s. algoaldensis* and *C. binotatus*, which is consistent with past gene flow. The most compelling evidence comes from a demographic analysis, where several alternative three-population models of divergence were fit to the joint site-frequency spectrum. Of the models tested, those where *C. s. algoaldensis* arose from hybridization between the lineages leading to modern *C. saulcyi* and *C. binotatus* fit the data best (Fig. 1). Moreover, the inclusion of a period of isolation coinciding with the split in the common ancestor of *C. saulcyi* and *C. binotatus* improved the fit of the “speciation by fusion” model, suggesting that the hybridization event occurred upon secondary contact.

Although these results go a long way toward establishing the hybrid origin of *C. s. algoaldensis* and its dual-feeding regime, more evidence would certainly help strengthen that conclusion. For example, the RADseq method used by the authors covers just a tiny fraction of the massive *Chorthippus* genome (>10 Gbp). Whole genome-sequencing guided by a reference genome would help bolster signatures of hybridization and would also reveal how levels of *C. binotatus* and *C. saulcyi* ancestry vary across the *C. s. algoaldensis* genome. Feeding preference experiments using lab-reared hybrids (if possible) could help to determine if

the dual-feeding behavior of *C. s. algoaldensis* is a consequence of admixture between scrub legume and gramineous herb feeding lineages. More detailed quantitative data on the patterns of host plant use and availability may also help us understand if and why selection favored the dual-feeding behavior in *C. s. algoaldensis*.

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