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NEWS AND COMMENTARY

Polluting gene flow from crops
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Radishes gone wild

MA Chapman and JM Burke
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A recent study of wild and cultivated radishes in California provides some of the best evidence to date that natural hybridization is a legitimate conservation concern. Whereas plant and animal species typically harbor suites of traits that reduce or prevent genetic exchange with other species, these barriers are often imperfect and interspecific gene flow can be common. Theoretical studies have shown that such interspecific hybridization can lead to extinction of one or both hybridizing taxa via genetic assimilation (Wolf *et al.*, 2001), but data in support of this notion have been hard to come by. Perhaps the main reason for this is that extinction via hybridization is predicted to occur quickly, especially when reproductive barriers are weak. Researchers at the University of California at Riverside (UCR) have, however, recently documented the occurrence of this process in the flowering plant genus *Raphanus*.

The story begins well over 100 years ago, when two species of radish (*Raphanus raphanistrum* and the cultivated radish *R. sativus*) were introduced into California from Europe and became naturalized. By the early 20th century, a few apparent hybrids were observed in the wild, and by the 1960s some populations were completely composed of morphologically intermediate plants, which came to be known as 'wild radish' (Panetsos and Baker, 1967). Meanwhile, apparently pure populations of *R. raphanistrum* and *R. sativus* were maintained near the edges of the species' distribution in California. In a recent study published in the journal *Evolution*, however, Hegde *et al.* (2006) reported that in every population surveyed only hybrids were present, suggesting that wild populations of the parental species have been hybridized out of existence in California.

This investigation complements a number of studies on these radish species in California by UCR's Norman Ellstrand and colleagues. In recent years, these researchers have only been able to locate populations consisting of plants exhibiting an amalgam of the traits that distinguish *R. raphanistrum* and *R. sativus*. In their most recent paper, Hegde and Ellstrand, along with co-authors John Nason (Iowa State University) and Janet Clegg (UCR), collected seed from California wild radish populations as well as pure parental samples from elsewhere in the US and Denmark where hybridization is rare. When reared in a common greenhouse environment, the wild radishes maintained their distinctive morphology, indicating that their unique appearance is genetically conditioned. Because morphological measures can be unreliable indicators of hybridity (Rieseberg and Ellstrand, 1993), Hegde and colleagues complemented their greenhouse work with a molecular marker survey. As it turns out, the California wild radishes were genetically intermediate to their parents, and undoubtedly the product of hybridization between *R. raphanistrum* and *R. sativus*.

Looking more closely, the success of wild radish appears to result from a mosaic of parental-like, intermediate, and unique traits (Figure 1). Indeed, when compared to its parental species, wild radish exhibits a *raphanistrum*-like root (the root of *R. sativus* is susceptible to disease outside cultivation) and a *raphanistrum*-like flowering time (*R. sativus* has a longer time to flowering,

which allows for increased root growth for consumers). In contrast, although wild radish fruits have a diameter and shape similar to those of *R. sativus*, they have a spongy exterior unlike those found in either of its parents, and are also significantly heavier than those of both *R. raphanistrum* and *R. sativus*. Whereas Hegde *et al.* (2006) suggest that wild radish fruits are less susceptible to seed predation by birds, a better understanding of the significance of the unique fruit morphology in these plants will require formal investigation.

The overall absence of certain *sativus*-like (i.e., crop-like) traits in the hybrid wild radishes is interesting in another context, as well. More specifically, it has been suggested that the insertion of transgenes in close association with genes controlling crop-related traits might help to prevent transgene escape from crop plants into their wild relatives (Gressel, 1999; see also Chapman and Burke, 2006). The finding that wild radish tends toward its non-crop parent in a number of traits suggests that these traits are, in fact, negatively selected in the wild. Thus, genes underlying traits such as these might be candidates for use in future attempts at transgene mitigation.

Taken together, the findings of Hegde *et al.* (2006) have clear implications for the conservation of species. Although a handful of studies have used genetic markers to document instances in which two animal species are merging (e.g. Echelle and Connor, 1989; Taylor *et al.*, 2006), this study is the first to provide genetic evidence that two plant species can be simultaneously hybridized out of
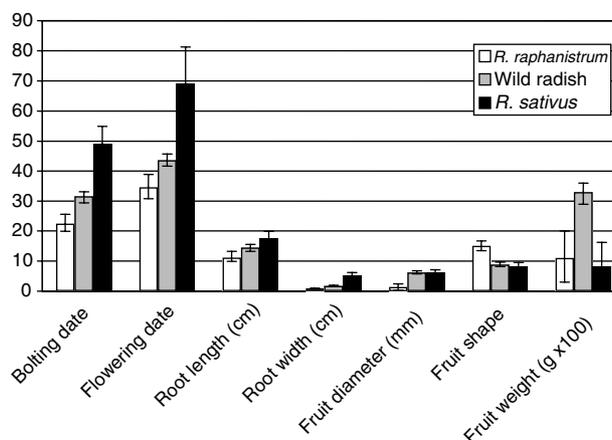

Figure 1 The success of hybrid wild radish may depend on a specific combination of parental-like, intermediate and unique characters. Values reported reflect the mean ± 95% confidence intervals for each taxon.

existence, at least locally. Given the rapidity with which extinction via hybridization can occur, it seems that genetic markers should now be brought to bear on other cases where, based on morphological grounds, persistent gene flow appears to be eroding species boundaries. In some cases, immediate action may be required to prevent a species' extinction (or two).

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