LONG-TERM FIELD STUDIES OF THE EVOLUTION OF CROP-WEED HYBRIDS IN RADISH: IMPLICATIONS FOR INVASIVENESS. Allison A. Snow, Lesley G. Campbell, Theresa M. Culley, and Caroline E. Ridley, Professor, Department of Evolution, Ecology, and Organismal Biology, Ohio State University, Columbus, OH 43210, Postdoctoral Associate, Departments of Plant Science, Landscape Architecture, and Entomology, University of Maryland, College Park, MD 20742, Assistant Professor, Department of Biological Sciences, University of Cincinnati, Cincinnati, OH 45221, and Graduate Student, Department of Botany and Plant Sciences, University of California, Riverside, CA 92521.

Many cultivated plants hybridize naturally with wild and weedy relatives, but little is known about the evolutionary effects of this process on recipient populations. To examine the dynamics of introgression in a natural setting, we monitored crop-specific genetic markers in replicated field populations of weedy Raphanus raphanistrum in Michigan, USA, for ten years. Four isolated hybrid populations were established in 1996 using a 1:1 ratio of *R*. raphanistrum and F_1 crop-wild hybrids (*R*. raphanistrum x R. sativus). The sites were tilled and fertilized annually to mimic agricultural fields, and plants were exposed to local biotic and abiotic selective pressures. Initially, F₁ hybrids had reduced fitness relative to wild genotypes, but the populations quickly regained wild-type pollen fertility, presumably by losing a crop-specific reciprocal translocation. Recombination and natural selection allowed the populations to absorb two crop-specific allozyme markers at relatively high frequencies in all populations, even exceeding their initial frequency of 0.25 in a few cases. Frequencies of a crop-specific white petal color allele were much lower, but this allele also persisted in all populations. Overall, frequencies of the three crop-specific alleles varied considerably among locations, years, and loci. In the tenth year, plants from each hybrid population were grown in a common garden experiment along with wild genotypes. The lifetime fecundity of these advancedgeneration hybrids was similar to that of the wild genotypes. This long-term study provides a unique example of how easily certain crop alleles can become established in weed populations while others remain rare or disappear.

In a second study, we tested the hypothesis that crop-wild hybridization can allow weeds to be more successful. A third study was carried out simultaneously to determine whether cultivated radish could generate feral populations. We established replicated populations of wild, hybrid, and "volunteer" cultivated radishes in Michigan and let them evolve for three growing seasons, starting in 2002. Three of the five volunteer populations died out. The two remaining populations became contaminated with wild genes and evolved traits that were similar to crop-wild hybrids (Campbell and Snow, in prep.). Although we did not find evidence for ferality in the absence of hybridization with R. raphanistrum, further studies involving more populations and locations might detect ferality. Results from the wild and hybrid populations were reported in Campbell et al. (2006) and are summarized briefly here. The initial frequency of crop alleles in these hybrid populations was 0.50 (twice the level in our introgression study above) because all plants were F₁ hybrids. Frequencies of white-flowered plants declined slightly, unlike our previous study, and then remained relatively constant. We suspect that the sharp drop in white-flowered plants in our earlier study was due to the fact that many hybrid plants flowered very late or not at all, and the white petal allele is linked to delayed reproduction [Campbell, 2007]. In 2005, advanced-generation hybrid and wild seedlings were grown in common garden experiments in Michigan and California. Hybrid-derived plants had slightly lower fecundity than wild plants in Michigan, but exhibited ~270% greater lifetime fecundity and ~22% greater survival than wild plants in California. These results support that hypothesis that crop-wild hybridization may create genotypes with the potential to displace parental taxa in new environments, which is consistent with other studies of hybrid-derived wild radish populations in California (C. E. Ridley et al., in prep.). In summary, our combined field studies of evolving crop-wild hybrids show that conventional crop

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alleles can persist in wild populations and may increase the fitness of wild relatives in some cases. Further research is needed to confirm the common assumption that enhanced fitness results in more abundant weed populations.

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