

A DECADE OF INTROGRESSION: CROP ALLELES IN EXPERIMENTAL POPULATIONS OF WILD RADISH (*RAPHANUS RAPHANISTRUM*). Allison A. Snow<sup>1</sup>, Theresa M. Culley<sup>2</sup>, Lesley G. Campbell<sup>1</sup>, Norman C. Ellstrand<sup>3</sup>, Kristen L. Uthus<sup>1</sup>, and Subray Hegde<sup>3</sup>, Professor, Professor, Graduate Student, Professor, Research Associate, and Research Associate, <sup>1</sup>Ohio State University, Columbus, OH 43210; <sup>2</sup>University of Cincinnati, Cincinnati, OH 45221; <sup>3</sup>University of California at Riverside, Riverside, CA 92521.

Many cultivated species hybridize naturally with wild relatives, but little is known about the extent to which crop alleles can persist in wild populations, especially when F<sub>1</sub> hybrid progeny have reduced fitness. This process has important implications for understanding whether weedy populations can benefit from an influx of crop alleles, including fitness-enhancing transgenes. Wild radish (*Raphanus raphanistrum*) is a cosmopolitan, self-incompatible weed that is known to hybridize with cultivated radish (*R. sativus*) where these taxa co-occur.

We found that three crop-specific alleles persisted for at least a decade in crop-wild hybrid populations in Pellston, Michigan, USA. Four populations were established in 1996 using a 1:1 ratio of wild plants and F<sub>1</sub> crop-wild hybrids. The sites were tilled each spring, and flowers, pollen, and/or seeds were sampled each summer through 2005. Initially, F<sub>1</sub> hybrids had reduced fitness relative to wild genotypes, but the populations quickly regained wild-type fecundity by losing a reciprocal translocation and other deleterious crop genes. Initial frequencies of the three crop-specific alleles were 0.25 in each population. Recombination and natural selection allowed the populations to absorb the two crop-specific allozyme markers at relatively high frequencies in all populations. In the F<sub>8</sub> generation, for example, frequencies of crop-specific alleles averaged 0.26 for PGM and 0.14 for GPI. In contrast, frequencies of the crop-specific white petal allele (a dominant Mendelian trait) were only ~0.02-0.08 during the past five years.

Overall, frequencies of crop-specific alleles varied considerably among locations, years, and loci. This study provides a clear example of how easily certain crop alleles can become established in weed populations, while others remain rare or may even disappear.