

# **New methods to study 'genetic invasion' detect the escape of crop genomes into the wild**

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Agricultural fields create a patchwork landscape that increases the potential for domesticated crop DNA to flood wild plant gene pools. This allelic introgression can cause significant evolutionary change in wild plant populations, and jeopardize naturally occurring genetic material, which is needed for conservation and for future agricultural practices. The resulting changes in genetic diversity, which have been observed in common crop species like rice and cotton, reduce a population's ability to withstand sudden changes in the environment, such as climatic shifts, disease, and pest outbreaks.

Scientists have been tracking crop gene flow into the wild for years, but new research by Professor Lesley Campbell (Ryerson University) and colleagues found two major flaws in how crop gene escape is traditionally tracked, and inspired the formulation of a more sensitive method.

"The traditional scientific methods that measure allelic introgression are not sensitive enough to detect contamination in wild plants," notes Campbell. "Traditional methods are better at detecting decreases rather than increases in the genetic diversity, which could be more common, and detrimental, than previously thought."

As part of her research, Campbell pulled methods from a parallel field of study on global species invasions. The research team drew an analogy

between species that invade geographical landscapes and crop genes that invade "genetic landscapes." Campbell used indices that measure [species diversity](#) before and after invasions and applied them to measure genetic diversity before and after crop hybridization. The new approach is demonstrated in a recent issue of *Applications in Plant Sciences*.

"This is the first time anyone has used species diversity metrics to detect shifts in genetic diversity when there is hybridization and gene flow occurring," says Campbell.

Campbell and colleagues compared the traditional indices with the species diversity indices using European wild and domesticated beets. They found that traditional methods could not detect a loss of rare, potentially crucial, alleles in wild populations. The traditional indices were less sensitive to detecting hybridization, while the new approach was able to detect increased genetic diversity and increased genetic similarity of hybridizing populations to beet cultivars.

Campbell explains that an increase in wild plant genetic diversity can be detrimental if the quality of genetic material changes. A shift in the genetic composition of wild beet populations can lead to traits that negatively alter their evolutionary trajectory and eventually swamp out their original [genetic material](#). For example, hybrid beet populations only contained 25% of the rare alleles found in wild beet populations that had no crop gene contamination.

An inability to detect crop-wild hybridization prevents proper preservation of naturally occurring [genetic diversity](#) and material. Campbell affirms, "The new method is a more sensitive approach to use for risk assessment of the escape of crop transgenes prior to their release into the environment." The method should be used to test and re-test agricultural systems where there are baseline expectations about the wild plant genetic makeup that should be maintained.

**More information:** Lesley G. Campbell et al. An Ecological Approach to Measuring the Evolutionary Consequences of Gene Flow From Crops to Wild or Weedy Relatives, *Applications in Plant Sciences* (2016). [DOI: 10.3732/apps.1500114](https://doi.org/10.3732/apps.1500114)

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