

# What can plants reveal about gene flow? That it's an important evolutionary force

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This is the May issue cover of the *American Journal of Botany*. Credit: Hazel Wetzstein.

A plant breeder discovers his experimental crops have been "contaminated" with genes from a neighboring field. New nasty weeds sometimes evolve directly from natural crosses between domesticated

species and their wild relatives. A rare plant is threatened due to its small population size and restricted range. What do all these situations have in common? They illustrate the important role of gene flow among populations and its potential consequences. Although gene flow was recognized by a few scientists as a significant evolutionary force as early as the 1940s, its relative role in maintaining a species' genetic integrity and/or its diversity has been debated over the decades, vacillating from trivial to critical.

So how much gene flow is there between [plant populations](#)? How important is gene flow for maintaining a species' identity and diversity, and what are the implications of these processes for evolution, conservation of endangered species, invasiveness, or unintentional gene flow from domesticated crops to wild relatives?

Norman Ellstrand, a plant geneticist at the University of California, Riverside, is interested in many aspects regarding gene flow, especially in applied plant biology, and has spent more than 25 years considering the possibility and potential impacts of unintended gene flow from genetically engineered crops. As part of the *American Journal of Botany's* Centennial Review series, Ellstrand reviews the history of gene flow, focusing on plants, and provides evidence for its importance as an evolutionary force.

Selection, mutation, gene flow, and genetic drift, are the four mechanisms that lead to biological evolution, or a change in allele frequencies in a population over time. Just how important are each of these forces relative to each other?

Interestingly, Ellstrand points out that evolutionary biologists' view on the importance of gene flow has waxed and waned over the last century. Although it was first seen in the 1940s to be the evolutionary glue that held species together, and thus a significant evolutionary force, a few

decades later when quantitative data on gene flow in plant populations began being collected, this view changed as evidence seemed to indicate that gene flow was not all that significant.

Not only was intra-specific gene flow among populations seen to be minimal at that time, but, somewhat incongruously, inter-specific hybridization, or the movement of genes among species, was seen to be a much larger force in evolution than intra-specific allele movement. At the time the main concern for plant breeders was pollen movement between different strains of crops—if a variety of sweet corn was contaminated by pollen from a popcorn variety, then the resulting hybrid offspring would produce seeds that were unusable for market purposes or for selecting new varieties. Increasing the distance between plots of different varieties was seen to be the best solution to this problem.

However, beginning in the 1980s the tide turned again due to mounting evidence from new approaches: parentage and spatial population genetic structure studies.

"When I first started doing plant paternity studies in the 1980s," Ellstrand comments, "our lab assumed that gene flow was limited. But we kept identifying 'impossible fathers' that could not be assigned to our study population. Surely, these couldn't be fathers from outside of our wild radish populations—hundreds of meters away? But after excluding all other possibilities, the improbable turned out to be the answer. And the paradigm of limited gene flow in plants began to crumble."

Indeed, one of the amazing things that parentage studies revealed is just how far genes could flow—from hundreds to thousands of meters in some cases. In one extraordinary case, a study found that the nearest possible paternal sire of an individual fig tree was 85 km away!

With the advent of more and more sophisticated ways to measure

genetic variation and relatedness using molecular markers, such as allozyme polymorphisms and DNA-based markers, not only can individuals be tracked as to their parentage, but changes in allele patterns over time and thus the effects of evolution on populations can be "seen" in the genetic information.

As it turns out, despite the initial skepticism about the importance of gene flow, modern empirical and theoretical research using up-to-date molecular and DNA techniques have shown us not only how surprisingly far the flow of genes between distant plant populations can be, but also that the flow of alleles among populations is just as important, if not more so in some cases, as natural selection. Indeed, even just a low level of gene flow between populations can counter opposing forces of mutation, genetic drift, and selection.

"Just like selection, gene flow is one of the evolutionary forces—and a potentially important one," notes Ellstrand. And plants are very well suited for studies on gene flow because individuals are stationary yet pollen and seeds are mobile.

However, an important caveat that Ellstrand reports in his review is that the relative importance of gene flow can vary tremendously among species and among populations, and can be as low as no gene flow at all to very high rates of gene flow.

"This review paper tells the story of [gene flow](#)'s rise to respect among plant evolutionary biologists," he concludes, "a fact that hasn't yet penetrated biology in general that is still mired in selection/adaptation-only thinking."

**More information:** Norman C. Ellstrand. 2014. Is gene flow the most important evolutionary force in plants? *American Journal of Botany* 101:737-753. [DOI: 10.3732/ajb.1400024](https://doi.org/10.3732/ajb.1400024)

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