



Editorial: Gene Flow Among Wild and Domesticated Plant Species in the Neotropical Region

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Keywords: primary gene pool, evolutionary changes, crop-wild-weed complex, hybridization, introgression

Editorial on the Research Topic

Gene Flow Among Wild and Domesticated Plant Species in the Neotropical Region

The importance of gene flow in plants has received oscillating recognition along the history of the Evolutionary Synthesis (Ellstrand, 2003), but lately the empirical literature has accumulated more powerful data-gathering methods and analytical tools (e.g., Birnbaum et al., 2003; van Heerwaarden et al., 2011; de Schawe et al., 2013; Félix et al., 2014; Guerra-García et al., 2017; Mardonovich et al., 2019). Besides its evolutionary role in natural ecosystems, gene flow and introgression are an important evolutionary factor in crop-wild-weed complexes, the crop's primary gene pool (Harlan and de Wet, 1971). Many crops coexist with their wild and weedy races (either escapes from the crops or wild-crop hybrids).

The requirements for crop-wild gene flow to occur are of five types (Bressan et al., 2020): (1) phylogenetic: at least one close wild relative must exist; (2) geographic: the wild and the crop species should be sympatric; (3) temporal: there should be flowering synchrony; (4) physiological/genetic: both the crop and the wild species must be sexual, fertile and compatible; (5) ecological: effective, if occasional, interspecific pollination should be spontaneous. Crop-to-wild gene transfer may flood the wild populations, even driving them to extinction, or making them weedy, while wild-to-crop gene transfer may also produce weeds or jeopardize the purity of a cultivar (Ellstrand and Rieseberg, 2016).

Together with West Central Asia, the Neotropics contains the highest number of native crops (Kloppenborg and Kleinman, 1987). Many of the thousands of crops domesticated in the Neotropics are considered neglected (Galluzzi and Noriega, 2014), which means they are understudied in relation to many scientific aspects, including crop-wild-weed gene flow. Even for the main crops, focus on this subject was intensified only with the growing concern about transgene contamination of wild populations from the 1990's on. We aim here at showing current investigations on crop-wild-weed gene flow in some of the main crops domesticated in the Neotropics.

Barroso et al. explore the gene flow between cotton, *Gossypium hirsutum*, and the wild *G. mustelinum*, having found the geographic and the genetic-physiological required conditions. Niche prediction allowed the authors to delimit their potential geographic distributions. Reasons for the local extinction of *G. mustelinum* are discussed, including removal of wild plants to avoid crop contamination. Regarding the second requirement, the advantage of same-species pollen usually hinders introgression.

The role of weedy cotton as a bridge between wild and domesticated cotton was the starting point for Alavez et al.'s investigation of *Gossypium hirsutum*'s primary gene pool dynamics in Mexico. Wild and domesticated cotton populations are frequently disjunct but the weedy populations,

OPEN ACCESS

Edited and reviewed by:

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Specialty section:

This article was submitted to
Evolutionary and Population Genetics,
a section of the journal
Frontiers in Ecology and Evolution

Received: 21 October 2021

Accepted: 28 October 2021

Published: 24 November 2021

Citation:

Oliveira GCX, Vieira ICG and
Tremblay RL (2021) Editorial: Gene
Flow Among Wild and Domesticated
Plant Species in the Neotropical
Region. *Front. Ecol. Evol.* 9:799071.
doi: 10.3389/fevo.2021.799071

which result from the hybridization between them, may intermediate gene flow. They used a niche prediction approach to map the potential distribution of weedy cotton and assess the transferability of genes from crop to wild cotton.

The evolutionary impact of gene flow on different pumpkin species was the objective of two papers. Martínez-González et al. studied the moderate to high levels of genetic diversity within and the low to moderate degrees of genetic differentiation among five infraspecific and infrasubspecific taxa of *Cucurbita pepo* from Mexico utilizing an extensive bioinformatics and population genetics toolbox to analyze SNP data. The authors propose that the reduced genetic differentiation may be caused by both historical and recent gene flow, in addition to incomplete lineage sorting and retention of ancestral alleles. Most of gene flow seems to occur from landraces to the other populations.

The independent domestication processes of the other two pumpkin species, *C. argyrosperma*, from Mexico, and *C. maxima*, from Argentina, were compared by Kates et al., who utilized 15,000 SNPs to assess the genetic diversity in landraces and improved cultivars and wild accessions of both primary gene pools. Wild-crop gene flow during and after domestication has shaped the primary gene pool of *C. maxima*, counterpoising the bottleneck caused by domestication and modern breeding. In sharp contrast, the bottleneck is evident in *C. argyrosperma*, whose cultivars show very little diversity in relation to the wild ancestor, suggesting wild-crop gene flow has been less critical in this species.

In an approach that combines ethnoscience and reproductive biology, Parra-Rondinel et al. documented the biocultural richness in potatoes (*Solanum tuberosum* and allies) found in the Peruvian Andes and the pollinators that visit the flowers of these varieties. The authors highlight the coexistence and consumption of many wild potatoes, landraces, and weedy derivations from non-collected tubers or recombinant seeds. All the conditions necessary for high levels of crop-wild-weed gene flow, leading to the great diversity in potatoes—sympatry, shared pollinators, flowering period overlap, sexual compatibility, and human-mediated transport of tubers among fields—were found.

Some of the main staple foods of Latin America, the five domesticated species of *Phaseolus* (the beans: *P. vulgaris*,

P. lunatus, *P. acutifolius*, *P. coccineus*, and *P. dumosus*), as well as the gene flow connections between them and their wild and weedy relatives, were the focus of Chacón-Sánchez et al.'s review. The authors centered their studies on aspects of the biological requisites for gene flow, especially pollination, male sterility, floral phenology and compatibility. The authors acknowledge the importance of gene flow for the wild populations' gains in adaptation and for the increase in diversity of the crops, with the ensuing expansion of their ecological and geographical range.

In an interesting contrast to the previous works, Ferrer et al. studied gene flow in arboreal species, exploring the effects that different reproductive systems and dispersal mechanisms may have on the maintenance of genetic diversity and on the differentiation between populations. The three species chosen are found in Yucatán and grow naturally in forests, being also planted by farmers in the agricultural matrix that interconnects the forests. The farm populations act as stepping-stones for two-way farm-forest gene flow, aided by the allogamy found in the species, which promote 100% crossing rates.

The papers in this Research Topic enrich our knowledge on crop-wild-weed gene flow of some of the most important crops domesticated in the Neotropic and we hope they inspire other groups to fill the huge scientific gap relative to the several hundreds of such species.

AUTHOR CONTRIBUTIONS

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

ACKNOWLEDGMENTS

We are grateful for the support of the entire Editorial board at Frontiers in Ecology and Evolution. We extend our special gratitude to Ewan Boden for his help all along the development of this Research Topic. Thanks also to the many peer reviewers whose work helped guarantee the quality of the texts presented in this collection.

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