

Gene Flow dynamics between cultivated crops and wild plants - a review

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Abstract. Modern agriculture is related to genetically improved crops, but this progress faces a challenge: the gene flow. This phenomenon allows genes, like herbicide resistance, to transfer from GM crops to wild relatives via pollen or seeds. This review analyzes the impact of gene flow on biosafety in agriculture. The study used bibliographic research, analyzing scientific publications to understand the mechanisms and consequences of gene flow. Results show significant economic losses due to the emergence of resistant weeds, as it occurs with wild rice, a major weed in brazilian rice crops.. Gene flow has transferred herbicide resistance from the GM crop to the wild relative, creating a harder-to-control weed and reducing rice grain value. Similar cases involving corn, radish, sorghum, and cassava have also been documented. The study emphasizes the importance of studying gene flow patterns to minimize its negative effects. Potential strategies include physical barriers between crops and wild relatives, planting crops at different times to avoid pollen exchange, and utilizing diverse non-GM crop varieties to reduce selection pressure for resistance. Additionally, monitoring weed populations and employing integrated pest management are crucial for long-term sustainability. In conclusion, gene flow poses a significant threat to the effectiveness of GM crops and agricultural practices. Further research is needed to refine mitigation strategies and ensure the long-term viability of this technology in modern agriculture.

Keywords. Gene flow, weed, herbicide resistance.

1. Introduction

In modern and high-yield agriculture, the presence of improved crops in production fields is increasingly common, whether through genetic improvement via transgenics or hybridization, induced mutation, or genetic crossing. Examples of this are the "RR" or "RoundUpReady®" crops, which are indispensable in the current scenario of soybean production in Brazil, where no-tillage farming predominates, and in this case, the herbicide acts as the modern "plow" of the crop production. There are also other successful tools, such as the Clearfield® rice cultivation system, which exhibits tolerance to herbicides from the Imidazolinone chemical group through induced mutation, or hybrid maize cultivars with resistance to pests and insects, such as the BT the technology (with bacterium Bacillus thuringiensis).

However, it is known that the occurrence of loss of effectiveness of these improved crops has been increasing considerably, largely due to the development of resistance in target organisms. One of the ways this can occur in the field is through gene flow, which may happen due to selection pressure, causing wild plants to acquire resistance mechanisms or other characteristics of improved plants cultivated in the same area, potentially leading to significant economic losses.

Therefore, it is possible for wild plants to receive pollen from human-improved plants and acquire these characteristics, posing a major problem for farmers. An example of this is weeds acquiring herbicide resistance through this process.

1.1 Genetic Improvement of Plants in Modern Agriculture

Plant breeding constitutes a crucial tool for enhancing productivity, a primary objective of large-scale agriculture given the imminent population growth and the ever-increasing need for food production. Plant breeding can be conducted through various methods, including transgenics, where genes from other species with desired characteristics are inserted into the target plant. An example of this is the resistance to caterpillar attacks in hybrid maize. Currently, there are even modern gene editing techniques or genetic engineering methods such as CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)/CAS9, which have been studied with increasing frequency and intensity and have already shown significant results and enormous potential for utilization (XUAN LIU et al., 2017). With this technique, a wider range of possibilities is opened up for plant breeding.

It is also worth mentioning the technique of induced mutation, where genes are not inserted in the laboratory, and thus, the improvement process occurs through radiation bombardment such as gamma rays or chemically induced methods. Although these techniques require a certain degree of technology, research on them has been conducted at the Experimental Station of UFRGS since around the 1990s, aiming to demonstrate their importance for the genetic variability of crops (PANDINI et al., 1997). In this way, mutations that exhibit the desired characteristic in the crop are selected.

Another common technique, and one of the oldest in agriculture, is selective breeding, which has been practiced by early farmers since the beginning of agriculture as we know it today. Regarding genetic variability, induced mutation presents greater variability than artificial/induced crossing (COIMBRA et al., 2004). However, selective breeding remains in use to this day, and its variations can occur naturally in the field, such as gene flow.

1.2 Gene Flow

Gene flow, distinct from genetic drift, which can occur randomly, is a form of evolution in plant populations that can lead to phenotypic alterations. In gene flow, the tendency is for population homogenization (SOARES, 2009), thereby allowing resistance genes from improved/cultivated plants to "flow" into wild biotypes or species.

Gene flow can occur through pollen or seeds, with the latter being more significant in autogamous species (MARTINS, 1987). There are various methods and factors that researchers consider when quantifying or determining the rate or level of gene flow between populations, such as interactions among individuals, dispersion level, and reproductive success, with markers like microsatellites also being utilized (TCHAICKA, 2002).

Although it can affect large populations simultaneously, gene flow can still have its dispersal interrupted by barriers such as rivers or roads. While this wouldn't be a natural way to prevent it from occurring in cultivated plants in the field, it could be achieved through spacing between production areas or geographic discontinuity, avoiding dispersion, as the main determinant of the absence of gene flow is the distance between populations (TCHAICKA, 2002).

However, there is a tendency for plants to cross with the most distant plants possible, which increases the rate of gene flow within the population. This can be influenced by biotic and abiotic factors, causing seed and pollen dispersion to vary depending on wind and other environmental conditions. Wind, in particular, can play a fundamental role in population dispersion, potentially allowing for a larger area coverage in the production field. Additionally, the phenomenon of introgression may occur, which involves gene flow between different species, leading to population hybridization and even habitat alterations (MARTINS, 1987).

2. Methodology

This review was conducted through bibliographic research, utilizing online databases and repositories as sources, such as the freely accessible platform Google Scholar. Through these searches, information was compiled and specific points regarding the theme were analyzed, aiming to provide a scientific review of the topic.

3. Results and Discussions

Analyzing data regarding the occurrence of gene flow between improved plants and wild biotypes or non-genetically improved crops, it is known that when evolving towards cases of resistance, the scenario can result in significant losses and economic damages, reaching values of approximately R\$ 9 billion according to research by Agricultural Embrapa (Brazilian Research Corporation).

For instance, in cases where improved crops are cultivated close geographically to phylogenetically related species, gene flow between cultivated and wild plants can be a limiting factor for biosafety, causing significant disruptions to breeding programs, given the increased invasive behavior of wild populations (GOULART, 2011). Examples of this include cases of rice (Oryza sativa) crossbreeding with wild biotypes such as Wild Rice (Oryza sativa), a significant weed in rice production (MEROTTO et al., 2016), or hybridization with other species. Other extensively studied cases involve maize, radish, sorghum, and cassava, among others.

Even though species may exhibit a low gene flow rate, the large number of cultivated plants in the same area considerably increases this rate. In the specific case of rice, numerous reports and studies document wild cultivars acquiring herbicide resistance through gene flow from improved species, occurring not only between red rice and cultivated rice but also among cultivated rice and other species within the same genus (Oryza) (GOULART, 2011).

Such cases are typically quantified using markers, thereby confirming that the acquired resistance in wild plants originates from gene flow from cultivated plants. Furthermore, after acquiring resistance from cultivated rice plants, wild species or biotypes may not only perpetuate gene flow in the area but also be easily dispersed, primarily through seeds, leading to increasingly frequent resistance occurrences (GOULART et al., 2011).

A study conducted by Brunes et al. (2007) on gene flow between cultivated rice and red rice using microsatellite markers demonstrated that gene flow occurs within a distance of 10 meters between rice species. Additionally, individuals exhibiting commercial characteristics, such as plant and grain type, may possess red-colored grains, as genes from red rice can be transferred to cultivated rice. Consequently, it is possible for 75% of the progeny to be hybrid and acquire these characteristics.

Thus, the combination of dispersal distance and gene transfer capability aids in understanding the potential infestation of red rice plants in commercial cultivation areas, devaluing the worth of cultivated grains, increasing control costs, and reducing producer profits.

Moreover, understanding these gene flow events is crucial for maintaining the genetic diversity of non-GM plant varieties intact, allowing farmers to choose whether to produce conventional, genetically modified (GM), or organic crops (RIZWAN et al., 2019).

Gene flow, while an important evolutionary tool for plants, can be considered a significant problem when it comes to the biosafety of production systems, especially those involving intensive plant breeding. Given that it can occur among various species and in different ways, such as via pollen, greater importance and attention need to be given to this adaptive resource of cultivated and wild plant species.

In conclusion, gene flow remains a barrier to be explored in Brazilian agriculture, especially when considering the occurrence of important and equally concerning cases for food production, such as those involving red rice and cultivated rice, as well as others involving hybrid maize and native maize, cultivated sorghum, and Sorghum halepense, among others, where gene flow occurrences may complicate crop management methods, such as controlling resistant weeds.

4. Conclusions

In this scenario, studying the behavior of cultivated plants and wild plants, such as the occurrence and frequency of gene flow, is an important tool for achieving high productivity. Considering Brazil's status as one of the world's largest food producers, this tool holds immense importance for Brazilian fields. The horizon points towards the increasing need for further studies on these field occurrences.

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6. References

[1] Liu, X., Wu, S., Xu, J., & Sui, C. (2017). Application of CRISPR/Cas9 in plant biology. *Acta Pharmaceutica Sinica B*, 7(3), 292-302.

[2] Pandini, F., Carvalho, F. I. F., Neto, J. F. B., Mittelmann, A., & Amaral, A. L. (1997). Avaliação da variabilidade genética em triticale para ciclo e estatura de planta obtida a partir de mutações induzidas e cruzamentos artificiais. *Pesquisa Agropecuária Gaúcha*, 3(1), 55-61.

[3] Coimbra, J., Carvalho, F., Oliveira, A., & Guidolin, A. (2004). Criação de variabilidade genética no caráter estatura de planta em aveia: hibridação artificial x mutação induzida. *Revista Brasileira de Agrociência*, 10(3), 273-280.

[4] Soares, Thannya Nascimento. (2009). Estrutura genética populacional e fluxo gênico em Dipteryx alatavogel (Fabaceae) no Cerrado (*Doctoral dissertation*, Universidade Federal de Goiás, Goiânia, Brazil).

[5] Martins, Paulo Sodero. (1987). Estrutura Populacional, Fluxo Gênico e Conservação "in situ" (*Master's thesis*, IPEF).

[6] Tchaicka, Ligia. (2002). Análise de duas possíveis barreiras ao fluxo gênico entre populações de Ctenomysminutus (Rodentia-Ctenomyidae) da planície costeira do Sul do Brasil (*Master's thesis*, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil).

[7] Goulart, I.C.G.R., Kupas, V., Dias, L.P., Rosa, T.M., Borba, T.C.O., Menezes, V.G., & Merotto Jr., A. (2011). Análise da estrutura populacional e determinação do fluxo gênico entre populações de arroz vermelho. *Congresso brasileiro de arroz irrigado* 2011, anais, 1, 427-430. Balneário Camboriú.

[8] Goulart, Ives Clayton Gomes Dos Reis. (2011). Fluxo gênico e variação adaptativa de arroz vermelho (Oryza ativa l.) resistente aos herbicidas Imidazolinonas (*Master's thesis*, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil).

[9] Merotto, A., et al. (2016). Evolutionary and social consequences of introgression of nontransgenic herbicide resistance from rice to weedy rice in Brazil. Evolutionary Applications, v. 9, p. 837-846.

[10] Brunes, T. O., Rangel, P. H. N., Brondani, R. P., Neto, F. M., Neves, P. de C. F., & Brondani, C. (2007). Fluxo gênico entre arroz vermelho e arroz cultivado estimado por meio de marcadores microssatélites. *Pesquisa Agropecuária Tropical*, 37(2), 86-92.

[11] RIZWAN, M., et al. (2019). Gene flow from major genetically modified crops and strategies for containment and mitigation of transgene escape: a review. Applied Ecology and Environmental Research, v. 17, p. 11191-11208.