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Transgene Flow into Native Seed and Ecosystems in Mexico

Ana Wegier

**National Institute for Research in Agriculture, Forests
and Livestock (INIFAP), Mexico**

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Introduction

To understand the context in which many of the centres of origin of important crops exist, we have to imagine how they emerged and the processes that have sustained them until today. Only by understanding their evolution we will know how to conserve them. Among the biological and cultural mega-diversity of Mesoamerica, one of the cradles of agriculture emerged. Mesoamerica is the centre of origin of about 150 crops like corn, beans, squash, chilli and several others that constitute the nutritional basis of the region. The environmental heterogeneity together with the diversity of customs and traditions maintain this centre of origin.

How can we identify areas that are centres of origin and diversity, to document and propose conservation strategies that include biosafety measures?

Nothing makes sense except in light of evolution. The conservation of genetic diversity is not a fad, since it represents the possibility of resisting new environmental scenarios. The higher the genetic diversity, the higher are the chances of surviving to new conditions by natural selection processes. In addition, *in situ* conservation is critical to the continuation of the process of domestication (another evolutionary process that is not static), because it offers not only the opportunity to make improvements with modern and traditional techniques, but the option to start the development again, in the event that something happens to all domesticated varieties (as has happened with the potato and banana), and as often as desired. However, if wild plants and traditional or native cultivars present transgenes, this possibility is ruled out, since these genes have been patented and nobody can make commercial use of the material while the protection period is effective.

Here we will discuss the case of cotton in Mexico from the beginning and then update the history of maize and its current consequences.

Cotton

At first, we investigated the actual and potential distribution of wild cotton populations, as well as the contribution of historical and recent gene flow in shaping cotton genetic diversity and structure. We evaluated historical gene flow using chloroplast microsatellites and recent gene flow through the assessment of transgene presence in wild cotton populations, exploiting the fact that genetically modified cotton has been planted in the North of Mexico since 1996. Assessment of geographic structure through Bayesian spatial analysis, BAPS and Genetic Algorithm for Rule-set Production (GARP), suggests that *G. hirsutum* seems to conform to a metapopulation scheme, with eight distinct metapopulations. Despite evidence for long-distance gene flow, genetic variation among the metapopulations of *G. hirsutum* is high ($H_e = 0.894 \pm 0.01$). We identified 46 different haplotypes, 78% of which are unique to a particular metapopulation, in contrast to a single haplotype detected in cotton cultivars. Recent gene flow was also detected ($m = 66/270 = 0.24$), with four out of eight metapopulations having transgenes. The percentage of positive individuals with “wild haplotypes” and the percentage of individuals with transgenes that are not commercially available, in combination or alone, show that evidently introgression has occurred and more research is needed (Wegier et al 2011 *Molecular Ecology* 20(19): 4182-94).

Many challenges arise from these findings: How can we know the impact of the insertion of a new gene in the ecosystem? How can we measure the environmental impact caused by GM in ecosystems?

Maize

Scientific papers documenting the presence of transgenes in Mexican native maize varieties: 1) In Sierra Juárez, state of Oaxaca in 2000: Quist and Chapela. (2001) *Nature*, 414, 541-543; 2) In the conservation area of the Federal District (Mexico City), in 2003: Serratos-Hernández et al. (2007) *Frontiers in Ecology and the Environment*, 5(5): 247–252; 3) In Sierra Juárez, state of Oaxaca in 2001 and 2004: Piñeyro-Nelson et al. (2009) *Molecular Ecology*, 18:50-761. ; 4) In localities of the states of Guanajuato, Veracruz, Oaxaca and Yucatán in 2002: Dyer, G. et al. (2009) *PlosOne*. Vol. 4(5): e5734 doi:10.1371/journal.pone.0005734; 5) Peer-reviewed papers addressing other transgene biomonitoring efforts made by governmental agencies and NGOs in Mexico: Mercer and Wainwright (2008) *Agriculture, Ecosystems and Environment*, 123, 109 – 115. To date, at least 12 papers can be found online on gene flow in Mexico. Recent projects, involving great sampling, have also found evidence of gene flow but indicate that they are still not ready for publication.

Since 2009, after demolishing several legal locks, the planting of GM corn in Mexico began. The Union of Scientists Committed to Society (UCCS, México) presented a document with a synthesis of the main issues that translate into important uncertainties and potential risks that have not been adequately addressed with scientific research:

1) There is still insufficient scientific evidence on the technological potential and risks of the present-day GM maize lines, and the ones being proposed for release are already obsolete. Alternative technologies should be explored before adopting this transgenic maize technology, which has been tailored for different environmental and socioeconomic conditions. Some examples that support this statement: Pests for which maize transgenic lines have been engineered are not important or present in Mexico. Local maize varieties are well adapted to resist important pests in each locality and the introduction of transgenic lines may also affect the ecological balance of different pests and create new pest problems for Mexican agriculture. The use of maize genetic variation combining bioinformatics, contemporary molecular biology approaches and the use of novel transgenic approaches that overcome some of the limitations and risks of the first generations of GMO is promising.

2) Uncertainties related to the interpretation of the law and its violation.

3) Recent scientific evidence has shown that transgenes have made their way into native maize varieties within several different agricultural zones in Mexico. This data suggest that coexistence of GM-maize lines with conventional maize varieties without gene flow is virtually impossible once the former are planted in the field.

4) Mexican Government agencies in charge of biosafety (Agriculture, Environment and Health, among others) have been unable to detect, investigate and prevent the introduction or impact of transgenes in Mexican native maize varieties.

5) Mexico comprises the centres of origin, domestication and diversification of maize and thus, harbours the majority of the genetic diversity of maize worldwide, while being home of all its known wild relatives. This genetic diversity is dynamically recreated in the fields of many small-scale farmers that produce maize for their subsistence, for local or regional markets. Farmers in the diverse agronomical systems present in different parts of Mexico, rely on saving seed from one agricultural season to the next as well as on frequent seed exchange among farmers within and outside of the communities. These activities are at the heart of the dynamic system that ensues the generation and maintenance of genetic diversity in maize. This system also implies that dispersal of GM maize and introgression of transgenes into native maize varieties cannot be avoided in Mexico if GM maize lines are planted in open fields.

6) Maize is a basic staple of the country, consumed daily with little processing and in large quantities, and thus possesses a critical agricultural, nutritional, economic and cultural significance for Mexican people. Furthermore, it's the third staple of the world, with increased consumption in countries within Africa and an important source of feed in many other nations. The health consequences of GMO consumption under these regimes have not been investigated thoroughly, but the few available appropriate experiments point to possible negative effects.

7) Multiple maize lines expressing pharmaceuticals and other industrial substances (so called pharma and industrial crops), should not be consumed by animals or humans. Companies have not been able to keep transgenic and non-transgenic lines segregated and several escapes from experimental plots of pharma-crops unauthorized for consumption have been reported. Therefore, even if such events could occur at very low probabilities and have limited impact on maize stocks in the USA, once in the Mexican territory, the frequency and dispersal of such sequences could be amplified. For that reason, the probabilities of occurrence of such escapes in Mexico should be estimated rigorously in order to establish efficient monitoring and biosecurity methods.

8) Once GM maize lines are released, transgenes will insert and accumulate in landraces and wild maize relative species (teosintes). It is well documented that the phenotypic effect of a transgene largely depends on the genome context and background where it is inserted.

9) There is ample evidence demonstrating that stable alternatives exist that meet and even exceed the needs which transgenic maize is purported to meet, without the risk its release involves.

In 2011, the global project about maize coordinated by CONABIO concluded. 235 researchers from 70 institutions participated (<http://www.biodiversidad.gob.mx/genes/proyectoMaices.html>). This effort culminated with a greater knowledge about the distribution of the native maize races of Mexico and the generation of multiple maps that are available at (<http://www.biodiversidad.gob.mx/usos/maices/razas2012.html>), however, the current initiative to determine the centre of origin and diversity of maize in Mexico, does not respect the results obtained in this project nor the rest of the scientific information generated on the subject.

Conclusions

The interplay of historical long distance gene flow and geographic barriers in Mexico has shaped the genetic structure of extant populations of *G. hirsutum*.

The hypothesis is rejected: geographic distance is not a measure that can prevent gene flow between cotton populations.

We need to incorporate ecological and evolutionary research to GMO risk assessments.

With this research, Mexico has demonstrated that it is not ready to release, monitor, or experiment with species of which it is the centre of origin or diversity, or that endanger human health or the ecosystems.

Literature

Wegier, A., Piñeyro-Nelson, A., Alarcón, J., Gálvez-Mariscal, A., Álvarez-Buylla, E. R. and Piñero, D. (2011). Recent long-distance transgene flow into wild populations conforms to historical patterns of gene flow in cotton (*Gossypium hirsutum*) at its center of origin. *Mol. Ecol.* 20 (19): 4182–4194.