NEWS AND VIEWS

PERSPECTIVE

Unwanted Transgenes Re-Discovered in Oaxacan Maize

ALLISON SNOW

Department of Evolution, Ecology, and Organismal Biology, Ohio State University, Columbus, OH 43210

Received 7 November 2008; revision received 26 November 2008; accepted 27 November 2008

Transgenic [GM (genetically modified)] maize is shipped all over the world, and its ability to germinate, grow, and hybridize with local landraces of the crop has generated tremendous scientific, social, and political controversy. The great genetic diversity of farmer-produced landraces represents a vital resource for subsistence farmers, future crop breeding, and cultural heritage preservation. Although the Mexican government banned GM maize cultivation in 1998, vast quantities of living GM grain are imported from the USA and seeds can easily enter the country by other routes. In 2000, Quist & Chapela (2001) discovered transgenes in four ears of landrace maize and in seeds from a government-sponsored Distribution Centre in Oaxaca. Their controversial paper in *Nature* set off an explosion of publicity and speculation about how widely these novel genetic elements had proliferated, and what the consequences of ubiquitous gene flow might be. However, a more extensive survey of this region failed to detect transgenes in 2003 and 2004 (Ortiz-García et al. 2005a), suggesting that transgenic plants were rare or absent in the sampled fields. Here, Pineyro-Nelson et al. (2008) provide a valuable counterpoint to that survey, resolving apparent contradictions in the literature and raising the bar for subsequent studies of immigrating transgenes. They show that transgenes were present in Oaxaca in both 2001 and 2004. Their paper explains how sampling methods, statistical analyses, and problems with analytical techniques can lead to inconsistent estimates of transgene frequencies in maize populations. This is a must-read paper for those who follow genetically modified organisms (GMO) biosafety research.

Even with non-GM crops, researchers have worried about whether the diverse and locally adapted gene pools of landraces could be overwhelmed by abundant gene flow from modern cultivars. Indeed, another study in this issue of *Molecular Ecology* reports a significant amount of introgression from modern hybrid maize into ‘flint’ landraces that are preferred for making polenta in Italy (Bitocchi et al. 2008). Despite several decades of gene flow into Italian landraces, no evidence for genetic erosion has been found to date. A similar process could be taking place in Mexico, depending on the dynamics of gene flow via pollen and seeds, yet a more sensitive topic is the unintended spread of transgenes that are banned for cultivation. Several types of GM maize are grown in other countries, but the key role of landraces in Mexico, which is the centre of origin for this staple crop, has prompted caution for allowing GM varieties to be cultivated. Some environmental groups, in particular, view the spread of transgenes as genetic contamination, and many people are dismayed by the apparent futility of efforts to keep transgenes out of landrace gene pools.

Monitoring for the presence of transgenes in the Mexican countryside is a daunting task that requires teams of experts from several disciplines (e.g. Serratos-Hernández et al. 2007; Mercer & Wainwright 2008). Furthermore, the politically sensitive nature of this information has made it difficult for researchers to publish their findings. Here, Pineyro-Nelson et al. (2008) have carried out a masterful job of assembling a large data set that will help advance the scientific quality of future efforts to monitor the dispersal of GMOs in the environment. Nearly all GM maize varieties have the 35S promoter from the cauliflower mosaic virus, and most have a nopaline synthase (NOS) terminator from *Agrobacterium tumefaciens*. Thus, these elements are useful markers for other transgenes, and polymerase chain reaction (PCR)-based methods can be used to detect a single transgenic seed in a homogenized sample of several thousand seeds. However, the exquisite sensitivity of PCR amplification is both a benefit and a liability, as trace amounts of contamination can yield false-positives. Pineyro-Nelson et al. used duplicate or triplicate, blind-coded samples to address this problem, and positive PCR results from their 2001 samples were confirmed with Southern analyses and sequencing.

Pineyro-Nelson et al. (2008) found evidence for transgenes in three out of 20 different communities that were sampled in 2001 and/or 2002 (Table 1). When two of the three communities with positive results were sampled more intensively in 2004, transgenic plants were detected in 3 of 30 fields in Santiago Xiacui, and 8 of 30 fields in Santa Maria Jaltianguis. Based on interviews with farmers about seed exchange, the authors concluded that transgenes probably persisted in these communities after 2001, rather than having been re-introduced. They also present a simulation model showing that transgenes are likely to be highly aggregated geographically when pollen and seed mixing are limited, as appears to be the case in these communities. This finding challenges statistical methods for calculating the probability of detecting rare events based on assumptions of random or uniform geographical distributions (see Cleveland et al. 2005; Ortiz-García et al. 2005a). Indeed, the patchiness of transgenic plants could explain why none were detected by Ortiz-García et al. (2005a), even though they sampled several...
fields in Santiago Xiacui and Santa Maria Jaltianguis. If transgenic plants are aggregated within and among communities, future sampling efforts should include as many widely spaced fields and communities as possible (Pineyro-Nelson et al. 2008). Also, if aggregated distributions are common, estimates of the maximum frequencies at which undetected transgenic plants would be overlooked should be interpreted with strong caveats about the assumptions underlying these calculations.

Another important aspect of the study is the authors’ evaluation of various methods for reliably detecting transgenes within and among laboratories. A commercial seed-testing company reported negative results for the 35S promoter for three leaf samples that the authors confirmed as positive for 35S. Other findings from the company were supported by three leaf samples that the authors confirmed as positive for 35S. Other findings from the company were supported by three leaf samples that the authors confirmed as positive for 35S.

In summary, this study confirms what many people have long suspected—that transgenes have entered landrace maize populations in Oaxaca. Based on the scant published literature and the fact that Pineyro-Nelson et al. found some transgenic plants in three communities, we do not have enough information to estimate the frequencies of transgenic plants in this region or others, or to know whether introductions are still taking place. Mexican farmers are known to plant seeds of modern varieties of maize alongside their local landraces (Perales et al. 2003), thereby allowing genes from imported grain to introgress into landraces, perhaps irrevocably. Apparently, DICONSA no longer distributes GM maize, but Mexico still imports yellow GM maize from the USA for food and animal feed.

Looking towards the future, containment of commercial maize transgenes will be impossible and eradication from landraces will be difficult (CEC 2004), but preventative measures and confinement of introduced transgenes are viable goals (Bitocchi et al. 2008). Further surveys will be helpful for identifying centres of introduction and preserving essentially GM-free zones of maize landraces in Mexico. Meanwhile, the uneven acceptance of GM crops around the globe will continue to spawn disputes over the sovereignty of national gene pools.

### References


Allison Snow is a plant evolutionary ecologist. Her research focuses on (trans)gene flow and fitness consequences of hybridization in several crop-wild systems, including sunflower, radish, squash, rice, sorghum, and oilseed rape.

doi: 10.1111/j.1365-294X.2008.04063.x