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Transgenes in Mexican maize

To the editor:

Genetic flow between transgenic and native maize has apparently occurred in Mexico[1], resulting in wild strains containing one or more transgenic sequences (most likely encoding *Bt* toxin). These "transgenic" native maizes not only have every single trait that has been selected and preserved for thousands of years (making them perfectly adapted to specific geographic regions), but now also possess an additional and desirable characteristic—insect resistance, a trait likely to be consciously preferred by Mexican peasant farmers. Diversity will not be affected. On the contrary, we can predict that this useful transgene will be found in increasing numbers and types of native maizes.

We believe it is important to stress this is not genetic contamination! Contamination means unexpected, undesirable, and uncontrollable spread; that is not happening. The spread will be induced because of the advantage of having a native corn with resistance to insects.

Maize is so dependent on human intervention that it cannot survive in the wild. Maize seeds are attached to a cob and cannot free themselves: it absolutely requires human intervention. As maize was first domesticated more than 6,000 years ago, only genes and alleles that are important for humans have been selected and preserved.

Still, if someone wants to remove the transgene from these plants, the procedure would be simple: select and multiply those susceptible maizes and do not harvest and multiply the insect-resistant ones. That is something no Mexican farmer will do.

Teosintes, ancestors and close relatives of corn, do not seem to be affected by genetic flow from (any) maize. Teosintes growing naturally in cornfields yield a very poor hybrid progeny. They do not release their seeds, and therefore the probability is very low for natural genetic introgression (incorporation of a gene or allele in a population) into teosintes. We also have found that teosintes are highly susceptible to insects and pathogens when growing under more intensive experimental field conditions, but they appear to be resistant to them when growing naturally in the wild.

Thus we conclude that even if the *Bt* transgene could be introgressed into teosintes, it will provide no biological advantage and thus would be lost by natural evolution. To reiterate[2], there is no need for concern.

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Errors in genomics and proteomics

To the editor:

Large-scale studies of gene expression on the RNA, protein, and/or metabolite level should greatly help to understand complex biological processes. However, it now becomes apparent that the correlation between mRNA and protein levels is remarkably and unexpectedly low; for example, the moderate correlation between levels of transcript and protein in yeast[1] has confirmed an earlier study using serial analysis of gene expression (SAGE)[2].

This low correlation is generally hypothesized to result from post-translational modifications, which therefore seem more frequent than previously assumed. It would also imply that RNA studies are less predictive, notably for complex traits, than protein studies are. But should we discount RNA expression profiling and favor proteomics? We think it is too early to conclude and believe that different distributions of experimental noise can contribute to the lack of correlation between RNA and protein data.

In large populations of transformed tobacco plants carrying the β-glucuronidase (GUS) and the luciferase (LUC) reporter genes, enzyme activities correlate poorly with the respective mRNA levels ($R = 0.46$–0.67). In contrast, GUS enzyme activities correlate well with LUC activities ($R = 0.80$), and GUS mRNA levels correlate well with LUC mRNA levels ($R = 0.94$). As neither of the proteins undergoes any post-translational modification, the counterintuitive result of the poor RNA/protein correlation cannot be due to changes at this level.

In this case, we postulate the existence of "error pipelines" that mask a biologically relevant correlation. Assays of mRNA, by whatever method, involve experimental steps in common for each mRNA. Each step will have its own errors associated with it. Some of these errors will be systematic in nature and point in the same direction. The crux is that in correlation analysis, such errors will cancel out, resulting in better correlations. The same holds for protein assays. However, when mRNA assays are correlated with protein assays, different methods of analysis are combined and the errors do not cancel out. This way, relevant correlations can become blurred by what is essentially experimental noise and not necessarily post-translational modification(s).

Our concept of error pipelines predicts that similarly low correlations will be found between genomics or proteomics and future metabolomics data (as in ref. 3). Preventing a blur due to error pipelines requires the careful assessment of the hierarchy in, and quality of, data sets. Reducing experimental noise by further technical improvements and/or increased replication, for example, with the use of segregating populations[4], will prove important for any associative study of different data types in genomics to become meaningful. Many more mRNA assays may correlate much more nicely with their corresponding protein assays, and the still easier/cheaper large-scale RNA analyses can remain the method of choice.

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