Transgenic Maize in Mexico

In a recent article in *BioScience,* Soleri and colleagues (2006) cite our research and challenge our conclusions concerning the presence of transgenic maize in Oaxaca, Mexico (Ortiz-García et al. 2005a). As Soleri and colleagues stated, we concluded that the frequency of transgenic seeds was near zero, or extremely rare, and there was no current evidence for transgene introgression into maize landraces in the studied region of Sierra de Juárez, Oaxaca. However, Soleri and colleagues have misinterpreted or misunderstood many of our results, and we would like to clarify some points.

Citing their own work as evidence (Cleveland et al. 2005), Soleri and colleagues argue that our conclusions are "not scientifically justified." However, they fail to note that (a) their paper was part of an editor-reviewed roundtable discussion and not a peer-reviewed scientific analysis, and that (b) their criticisms were appropriately answered in a reply published together with their discussion paper (Ortiz-García et al. 2005b). Soleri and colleagues reiterate arguments that have already been addressed in our published reply, which was omitted from the citations in their *BioScience* article. In order not to wade again through a prolonged technical discussion, we would like to refer readers to their original paper and to our detailed rebuttal.

Despite Soleri and colleagues' conclusions, the results of our study are quite clear-cut: In 2000, Quist and Chapela (2001, 2002) sampled six maize ears in some plots near Ixtlán de Juárez in Oaxaca and found transgenic constructs in four of them. Then, when we sampled the same area in 2003 and 2004, we did not find a single transgenic construct among 153,746 seeds from more than 870 plants growing in 125 fields (Ortiz-García et al. 2005a). This, of course, is not proof that transgenes were completely absent from the area (as we clearly mention in our paper), but our results certainly imply that if transgenes were present in these plots, they persisted at frequencies that were, in all likelihood, far lower than they were in 2000. This absence of detectable transgenes is consistent with recent reports cited on the ETC Group Web page (*www.etcgroup.org/documents/ETCMaizeNRfinal.pdf*), and no peer-reviewed papers have appeared to either confirm or refute our findings.

To reiterate, at the scale and the resolution at which we did our analysis, transgenes that seemed to be common in traditional maize varieties in the year 2000 can no longer be regarded as common, and earlier assumptions that they had introgressed widely (e.g., Quist and Chapela 2001) have not been confirmed. We are now refining our sampling procedures for this region to gain even greater precision in our detection capacity by sampling fewer seeds from a larger number of maternal plants. However, this effort does not invalidate the results we have published so far. We hope that other research groups will publish related studies promptly to provide a better understanding of the generality of our findings from the Sierra de Juárez of Oaxaca.

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Response from Soleri and colleagues

Ortiz-García and colleagues (2005a) agreed with us that variance effective population size ($N_{e(v)}$), not census population size (n), should be used to estimate transgene frequency (Vencovsky and Crossa 1999), and reanalyzed their data using $N_{e(v)}$ with two additional statistical tests. The first was based on the assumption that sampled maize populations had no significant structure, which is not valid (Cleveland et al. 2005). The second, Fisher's combined probability test, gave a minimum detection level for seeds in 2004 of approximately 1% (0.00775, $P < 0.05$) (Ortiz-García et al. 2005b), close to our estimate of approximately 1%–4% (0.00961–0.03586, $P < 0.05$) across individual locations, accounting for popula-

tion structure (Cleveland et al. 2005), and contrasted with their original estimate of 0.01%, P = 0.00003 (Ortiz-García et al. 2005a). Therefore, there is no evidence to refute our conclusion that "we still do not have any data to support the proposition that transgenes are not present at other localities, or at frequencies below 1–4% in the localities in the Ortiz-García et al. study" (Cleveland et al. 2005, p. 205).

Although Ortiz-García and colleagues assume that Quist and Chapela's study showed transgenes "common in traditional maize varieties," that study was based on a very small, nonrandom sample; the study showed only transgene presence and thus cannot be used to estimate changes in transgene frequency (Cleveland et al. 2005).

It is important to see the debate about transgene presence from unintended gene flow in a wider policy context: Commercialization of transgenic varieties, especially in centers of origin, may have difficult-to-predict effects—many irreversible—on landrace diversity and farmer well-being. Therefore, wide scientific discussion of research methodologies and results is critical.

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The Value of Barcoding

Kirk Fitzhugh (2006a, 2006b) has recently offered a novel critique of DNA barcoding based on his own carefully considered interpretation of species as "explanatory hypotheses." Though he is not alone in questioning a method that claims to identify species based on a single genetic locus (Lipscomb et al. 2003, Mallet and Willmott 2003, Wheeler 2005), I fear that Dr. Fitzhugh's particular philosophical interpretation of the problem may prove more than he intends.

According to that interpretation, since species as explanatory hypotheses are the products of abductive reasoning, they cannot be identified on the basis of DNA data alone without running afoul of Rudolf Carnap's requirement of total evidence, which holds that "for one to rationally believe a conclusion on the basis of some set of evidence, then all available relevant evidence must be taken into consideration" (Fitzhugh 2006a). But DNA barcoding is hardly unique in failing to meet this requirement. If barcoders cannot rationally defend species identifications based solely on DNA sequence because this ignores "other relevant properties in need of explanation" (presumably morphological, biochemical, behavioral, or other non-DNA properties), then surely morphological taxonomists are also irrational if their identifications fail to consider DNA sequences, which are similarly properties in need of explanation.

Dr. Fitzhugh is thus unfair to level his criticism specifically at DNA barcoding, as it should be aimed instead at any nonintegrative taxonomic method. More to the point, there has never been—nor will there ever be—a taxonomic hypothesis that did not exclude some available relevant evidence. Since any practicable taxonomic approach will inevitably fail the strict requirement laid out in Dr. Fitzhugh's critique, and as the scientific community is unlikely to classify all taxonomy as irrational, I submit instead that Carnap's principle is perhaps not the most satisfying way to assess the rationality of scientific thought.

In addition, I think it important to note that the validity of DNA barcoding does not rest entirely (and perhaps not even primarily) on its success in species identification. Many proposed applications of this technology focus instead on the identification of individuals to the species level. In these applications the identification of species is done quite independently, typically by traditional and integrative taxonomic methods; in fact, most applied barcoding assumes the validity of species identifications made by such methods. Such applications of DNA barcoding could prove enormously useful in a variety of contexts, despite the tendency of some to consider them scientifically uninteresting (e.g., Wheeler 2005, Will et al. 2005). Technically, as individuals are neither hypotheses nor explanatory constructs, Dr. Fitzhugh's philosophical objections do not apply to the adoption of barcoding as a means to identify them. Even if successful, then, his critique is not a wholesale indictment of DNA barcoding, and should not on its own forestall the pursuit of that technology.

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