

# Reply to Brush et al.: Wake-up call for crop conservation science

We strongly concur with Brush et al. (1) regarding the urgency for a new generation of studies (2), but reject claims that our findings are unsupported and our comparisons false, a misperception that could delay adequate academic and policy responses. First, spurious or not, it is not our interpretation that we put to the test but that of influential scholars who, notwithstanding studies' design and methodological differences, conclude that "there is increasing evidence that small-scale farmers throughout the world, and especially in areas of crop domestication and diversity, continue to maintain a diverse set of crop varieties" (3) and "after thirty years of crop collection and research ... the concept of genetic erosion remains more a presumption of what is likely to occur than a demonstrated fact" (4).

Our analysis supports the previous interpretation of trends in case-study data (figure 1A in ref. 5): it is significant that a single variable—time—explains 12% of variance (across studies and localities) for the highly multifactorial outcome of location-specific crop management (2), but analysis of Mexico National Household Survey's (ENHRUM) nationally representative, matched longitudinal data belies it (figure 1B in ref. 5). Brush et al. (1) provide no clear reason for suspecting errors to differ between survey rounds, the main pillar of their reasoning. So why should we suspect? Both rounds used the same instruments, farmer sample, and enumerator-training procedures. The diversity losses documented are large and statistically significant ( $P < 0.001$ ). The other pillar of Brush et al.'s (1) reasoning, the conjecture that ENHRUM data underestimate diversity,

is also unfounded. Our estimates are at least as high as Brush and coworkers for specific areas on similar or prior dates (table S1 in ref. 5). Significantly, even after declines, the estimates are noticeably higher for all southeast highlands than Brush and coworkers for highland Chiapas, where diversity is presumed highest in Mexico. However, the range of locality averages is wider for ENHRUM than for all previous studies combined. ENHRUM-based estimates of various other population parameters also are comparable to Brush and coworkers but of far greater scope (2).

Certainly, households could in principle regain discarded varieties via seed exchange, but this does not appear to be happening. In fact, reduced richness has been accompanied by farmers turning to alternative seed sources. Moreover, mathematical analysis of crop-metapopulation dynamics shows a complex relationship between seed exchange and genetic diversity that depends on a number of additional factors (6). The question no longer is whether genetic erosion remains a presumption but how to respond to it, particularly as the climate changes.

We concur with Brush et al. (1) in concluding that this question requires a new, inherently cross-disciplinary research agenda. Such an approach will need to: (i) map diversity measures using named varieties to measure genetic outcomes; (ii) monitor diversity using longitudinal, rather than cross-sectional, methods; (iii) account for markets and other determinants of on-farm diversity; (iv) model the linkages between incentives, agents' decisions, metapopulation dynamics, and diversity at various scales; and (v) predict the consequences of these interactions for

rural areas in the face of changing environments. The rapid loss of diversity documented in our study underlines the urgency of implementing this agenda.

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**1** Brush SB, et al. (2015) Assessing maize genetic erosion. *Proc Natl Acad Sci USA* 112:E1.

**2** Dyer GA, López-Feldman A (2013) Inexplicable or simply unexplained? The management of maize seed in Mexico. *PLoS ONE* 8(6):e68320.

**3** Bellon MR, Pham J-L, Jackson MT (1997) *Plant Genetic Conservation: The in Situ Approach*, eds Maxted N, Ford-Lloyd BF, Hawkes JG (Chapman and Hall, London).

**4** Brush SB (2004) *Farmers' Bounty: Locating Crop Diversity in the Contemporary World* (Yale Univ Press, New Haven, CT).

**5** Dyer GA, López-Feldman A, Yúnez-Naude A, Taylor JE (2014) Genetic erosion in maize's center of origin. *Proc Natl Acad Sci USA* 111(39):14094–14099.

**6** van Heerwaarden J, van Eeuwijk FA, Ross-Ibarra J (2010) Genetic diversity in a crop metapopulation. *Heredity (Edinb)* 104(1):28–39.

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The authors declare no conflict of interest.

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