Comparative population genomics of maize domestication and improvement.
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Early crossing studies between maize and teosinte led Nobel laureate George Beadle to assert that as few as 5 loci could be responsible for the dramatic morphological changes associated with maize domestication [1], a conclusion apparently supported by decades of subsequent genetic mapping [2]. Initial population genetic investigations of a limited number of loci, however, began to hint that other genes may have been targeted by selection [3, 4]. This paper reports the first whole-genome analysis of maize domestication, expanding signficantly on the results of earlier selection studies. We found evidence for hundreds of loci targeted by selection during domestication, and patterns of haplotype differentiation suggest the majority were subjected to stronger selection than the large-effect loci identified in previous mapping efforts. This result highlights the complexity of maize domestication, suggesting domestication has involved selection on a number of traits beyond the obvious morphological changes. The high resolution of our selection analysis enabled us to identify individual targets of selection, revealing that a substantial proportion were noncoding regions absent of genes. Our microarray evaluation of transcriptome-wide gene expression in both maize and its wild ancestor extended these results, finding that selection during domestication targeted cis-regulatory variation that changed expression patterns of selected loci.

Finally, this paper provided substantial evidence for the importance of diversity in crop wild relatives, documenting both the importance of standing genetic variation — as opposed to selection on new mutations — as well as the loss of functionally relevant diversity at genes linked to targets of selection.

The paper has been cited more than 180 times, and our population genetic approaches have since been broadly applied by other researchers to a number of other crops species [e.g. 5, 6, 7].

References

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