




Maize looks set to amaze



A genome sequence for maize has long been expected to provide valuable information for both breeding strategies and basic research. Now, publication of the sequence of the B73 inbred maize line, a maize haplotype map and a collection of related papers have demonstrated the breadth of novel insights that can be obtained from this resource.

The Maize Genome Sequencing Consortium (Schnable *et al.* and the authors of the *PLoS Genetics* 2009 Maize Genome Collection) assembled the 2.3 Gb genome by shotgun sequencing of bacterial artificial chromosome (BAC) clones, followed by further sequencing to improve coverage of unique regions. They used evidence-based and *ab initio* approaches to identify 32,450 protein-coding and 150 microRNA genes — this increases the number of microRNA genes by ~50%. A striking ~85% of the genome consists of transposable elements, the influence of which is highlighted in companion papers that discuss centromeric structure and patterns of recombination. These elements will need to be considered in future studies of genome evolution and dynamics.

The maize haplotype map is a complementary research tool that has been generated by Gore *et al.*

The authors identified and genotyped several million sequence polymorphisms in 27 diverse inbred lines and generated SNP data sets that can be used for genome-wide association (GWA) studies and for characterizing genome-wide variation patterns.

The authors found evidence that hundreds of genomic regions are likely to contribute to geographic diversity in maize phenotypes, and it is hoped that future GWA studies will identify the genetic basis of complex traits that are relevant to breeding programmes.

From an agricultural perspective, an important but poorly understood aspect of maize biology is heterosis — the enhanced vigour of a hybrid relative to its inbred parents. Using their newly generated map of variation, Gore *et al.* found that recombination rates vary considerably across the maize genome and that a low recombination rate is the major factor that contributes to the retention of residual heterozygosity in the pericentromeric regions. This finding might help to explain heterosis, as insufficient recombination would prevent the creation of the most vigorous allelic combinations, so vigour is achieved by outcrossing. Swanson-Wagner and colleagues explored heterosis in

hybrids of the inbred lines B73 and Mo17. They identified loci at which expression differs quantitatively between the parental lines and found that, in most cases, transcriptional control seems to be mediated by the paternally transmitted allele. The authors suggest that imprinted small RNAs might contribute to these effects, opening up new avenues for research into the molecular basis of heterosis.

These are just a few examples of the already impressive body of knowledge that the genome sequence has contributed to. Many other topics — including domestication, copy-number variation and transposition dynamics — are being investigated, and maize research looks set to flourish.

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ORIGINAL RESEARCH PAPERS

Schnable, P.S. *et al.* The B73 maize genome: complexity, diversity, and dynamics. *Science* **326**, 1112–1115 (2009) | Gore, M. A. *et al.* A first-generation haplotype map of maize. *Science* **326**, 1115–1117 (2009) | Swanson-Wagner, R. A. *et al.* Paternal dominance of trans-eQTL influences gene expression patterns in maize hybrids. *Science* **326**, 1118–1120 (2009)

FURTHER READING *PLoS Genetics* 2009 Maize Genome Collection: <http://collections.plos.org/plosgenetics/maize.php> | Vielle-Catada, J.-P. *et al.* The Palomero genome suggests metal effects on domestication. *Science* **326**, 1078 (2009) | Yang, L. & Bennetzen, J. L. Distribution, diversity, evolution, and survival of *Helitrons* in the maize genome. *Proc. Natl Acad. Sci. USA* **106**, 19922–19927 (2009) | Du, C., Fefelova, N., Caronna, J., He, L. & Dooner, H. K. The polychromatic *Helitron* landscape of the maize genome. *Proc. Natl Acad. Sci. USA* **106**, 19916–19920 (2009)