

 CROP GENETICS

# Resequencing sows the seeds

Next-generation sequencing is rapidly expanding our knowledge of genetic variation in crop plants. Recent resequencing studies in rice and maize illustrate the promise of this new phase of crop genomics to further our understanding of the genetic basis of agronomically important traits.

Rice landraces are inbred lines that show variation in traits that are relevant to their specific environments. Genome-wide association (GWA) studies are a potentially powerful tool for uncovering the genetic variation that underlies these phenotypic differences, but these studies require a much more detailed picture of genetic variation than has been available until now for rice. To address this situation, Huang and colleagues resequenced 517 diverse rice landraces, each to ~onefold coverage. They identified approximately 3.6 million SNPs, which they estimate represent ~80% of the worldwide genetic diversity. To compensate for the low sequence coverage — which

led to a substantial number of missing genotypes — the authors used imputation to fill in the gaps and construct a detailed haplotype map.

Using this map, Huang and colleagues carried out GWA studies for 14 agronomically relevant traits. Altogether, 80 robust association signals were identified; for six of the traits, signals were located at or close to genes that were previously identified as affecting the trait. On average, for each trait the association signals explain ~36% of the phenotypic variance, a much higher figure than the equivalent for human GWA studies.

In a second study, resequencing in maize has revealed potentially informative genetic differences between commercially important lines. Lai and colleagues sequenced six elite maize inbred lines to an average of 5.4-fold coverage and identified more than 1.2 million SNPs and over 30,000 indels. Sequence comparisons between lines also uncovered hundreds of presence/absence variations (PAVs) of intact expressed genes — in

which an entire gene is present in some lines but missing in others. The authors speculate that the effects of these PAV genes, along with SNPs that have potentially large effects on protein function, might be important contributors to heterosis in maize — that is, crosses between lines that differ in these variants may lead to masking of their detrimental effects in hybrids (see also ‘Further reading’).

Both studies provide results that can be immediately followed up to gain new biological insights. They also highlight the use of resequencing in providing tools for future crop GWA studies.

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**ORIGINAL RESEARCH PAPERS** Huang, X. *et al.* Genome-wide association studies of 14 agronomic traits in rice landraces. *Nature Genet.* **42**, 961–967 (2010) | Lai, J. *et al.* Genome-wide patterns of genetic variation among elite maize inbred lines. *Nature Genet.* **42**, 1027–1030 (2010)  
**FURTHER READING** Swanson-Wagner, R. A. *et al.* Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. *Genome Res.* 29 Oct 2010 (doi:10.1101/gr.109165.110)

