

Rice genetics: Dissecting complex rice traits

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Abstract

Mapping and identifying the genes responsible for the desirable attributes of local rice varieties will help to improve rice breeding

Original article citation

Huang, X. *et al.* [Genome-wide association studies of 14 agronomic traits in rice landraces](#). *Nature Genet.* **42**, 961–967(2010).

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Introduction



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By exploiting state-of-the-art DNA sequencing technology and sophisticated analytical methods, Bin Han at the Chinese Academy of Sciences in Shanghai and co-workers have mapped the genetic variation associated with important agronomic traits in rice¹.

The researchers sequenced the genomes of 517 local Chinese rice varieties (landraces) with one-fold coverage. They identified around 3.6 million single base-pair differences between these genomes and the previously published rice genome, which they used as a reference sequence. These genetic differences, known as single-nucleotide polymorphisms, are scattered throughout the rice genome, making them useful genetic markers.

They inferred missing genotypes from low-coverage sequencing with high confidence by applying a highly accurate computer algorithm to fill the gaps. The resulting dataset allowed them to genetically map multiple traits simultaneously.

Focusing on the *indica* (one of the two rice subspecies) landraces, they performed genome-wide association studies for 14 important agronomic traits related to plant architecture, grain yield, quality and colouration, or physiological features such as drought tolerance. They identified numerous chromosomal regions associated with these traits, including six regions close to genes known from previous studies.

The researchers are the first to have applied genome-wide association studies to dissect complex traits in a crop species. They believe that their study provides a fundamental resource for rice genetics research and crop improvement.

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Reference

1. Huang, X. *et al.* Genome-wide association studies of 14 agronomic traits in rice landraces. *Nature Genet.* **42**, 961–967(2010). | [Article](#)