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Rice genome revealed II: the *japonica* sequence

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Jean-Nicolas Volff

Abstract

Together with the draft sequence of the *indica* rice genome, the draft sequence of the *japonica* rice genome should advance understanding of this important crop plant

Significance and context

A team from the Swiss agricultural company Syngenta and the US biotechnology company Myriad Genetics has completed the draft sequence of the genome of *Oryza sativa* L. ssp. *japonica* Nipponbare, a rice cultivar very popular in Japan. The general background to the sequencing of the genome of rice (*Oryza sativa*) can be found in the Paper Report on the draft sequence of the *O. sativa* ssp. *indica* by a Chinese team (Yu *et al.*) that was published in the same issue of *Science* (see related report - [Genome Biology 3\(7\):reports0035](#)).

Key results

Using the whole-genome shotgun strategy, Goff *et al.* determined 390 million bases (Mb) of high-quality genomic sequence disrupted by about 42,000 gaps. The estimated number of genes was between 32,000 and 50,000. Goff *et al.* make a distinction between predicted genes (minimal length 300 bp) with high (34.3%), medium (27.0%) and low (38.7%) confidence scores on the basis of similarity to known genes, protein motifs and predicted genes from other species. As observed in *Arabidopsis thaliana*, numerous paralogous genes (duplicates) are present in the rice genome. About 22% of genes with high and medium confidence scores were present as duplicates on the same chromosome (local duplications). There is also evidence of larger chromosome/genome duplications having arisen after the separation of the *Arabidopsis* and rice lineages. Of *Arabidopsis* genes, 85% have at least one homolog in rice. Putative 'plant-specific' genes - that is, those present in both rice and *Arabidopsis* but apparently absent from the genomes of animals and microorganisms - were identified in *Arabidopsis* (8,000, or approximately 30% of predicted genes) and *O. sativa* ssp. *japonica* (13,000, approximately 20% of predicted genes with a minimal length of 300 bp). A substantial number of rice genes were not present in *Arabidopsis* or other organisms. The fact that most of these were classified as 'hypothetical' or 'unknown', or presented low confidence scores in rice, suggests that they may have been inaccurately predicted or may correspond to genes specific to particular plant lineages. Several classes of genes encoding families of proteins identified in other sequenced genomes (for example, nuclear steroid receptors, and the JAK and STAT

signaling molecules) were not found in either the rice or *Arabidopsis* genomes. This study confirmed that gene content and order are highly conserved between rice and other cereals, but that conservation is much more limited between rice and *Arabidopsis*.

Links

The research papers, news and commentaries about the sequencing of the rice genomes are available from [The rice genome](#) index page at the *Science* website. The draft *japonicarice* sequence reported by Goff *et al.* is available to academic researchers under certain conditions from the [Torrey Mesa Research Institute - the rice genome](#) page.

Reporter's comments

The restrictions over public access to Syngenta's data represent an unusual concession by the journal *Science*. As analysis of the two rice genomes proceeds, it will be interesting to see what differences there are between them.

Table of links

Science

Genome Biology **3**(7):reports0035

[The rice genome](#)

[Torrey Mesa Research Institute - the rice genome](#)

References

1. Goff SA, Ricke D, Lan TH, Presting G, Wang R, Dunn M, Glazebrook J, Sessions A, Oeller P, Varma H: A draft sequence of the rice genome (*Oryza sativa* L. ssp. *japonica*). *Science*. 2002, 296: 92-100. 0036-8075