S4-03

The genome sequences of *indica* and *japonica* rice

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We have produced sequences for the genomes of *indica* and *japonica* rice, using a whole-genome shotgun (WGS) method. Tested against a non-redundant set of 19,079 full-length cDNAs, 98.1% of the genes are found in one or the other genome, without fragmentation and anchored to the existing maps. We introduce a gene identification procedure for plant genomes that does not rely on similarity to known genes to remove erroneous predictions. Estimated gene counts range from 49,088 (*indica*) to 45,824 (*japonica*). Only a percent or so of either gene set is unique to one subspecies. Although there is little variation in gene content, there is massive variation in intergenic regions, to such an extent that at least one third of the two genomes cannot be aligned.

S4-04

Prospects and Direction of Brassica Genome Sequencing

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The complete genome sequence of an organism provides unlimited information in the sequenced organism as well as the related taxa. Multinational Brassica Genome Project (MBGP) are aiming to sequence complete genome of Brassica rapa using variety Chiifu (http://www.brassica.info). Korea Brassica Genome Project (KBGP) is aiming to complete sequencing the chromosome 1. we have developed a comparative genetic map between Arabidopsis and B. rapa using EST markers. The comparative map reveals the collinear chromosomal regions between two species. The sequenced BAC clones on chromosome 1 that are identified by genetic markers and confirmed by BAC-FISH technique, are placed on the collinear chromosomal regions of Arabidopsis and finally provide starting point for selection of seed BAC clones extending to flanking sides with minimum overlap. We have developed an advance method for complete sequencing using comparative physical map on Arabidopsis, a model plamt genome. This strategy was applied successfully for in silico chromosome walking and for clone validation on chromosome 1 using bacterial artificial chromosome (BAC) end sequences.