Regulation of primary metabolism in response to low oxygen availability as revealed by carbon and nitrogen isotope redistribution

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Résumé en anglais
Intersubspecific (indica×japonica) autotetraploid Oryza sativa (rice) hybrids have greater biological and yield potentials than do diploid rice. However, the low fertility of intersubspecific autotetraploid hybrids, which is largely due to high pollen abortion rates, limits their commercial utility. To decipher the cytological and molecular mechanisms underlying allelic interactions in autotetraploid rice, we developed an autotetraploid rice hybrid that was heterozygous (SiSj) at F1 pollen sterility loci (Sa, Sb, and Sc), using near iso-genic lines. Cytological studies showed that the autotetraploid had a higher percentage (>30%) of abnormal chromosome behavior and aberrant meiocytes (>50%) during meiosis than did the diploid rice hybrid control. Analysis of gene expression profiles revealed 1888 genes that were differentially expressed between the autotetraploid and diploid hybrid lines at the meiotic stage, among which 889 and 999 were up- and down-regulated, respectively. Of the 999 down-regulated genes, 940 were associated with the combined effect of polyploidy and pollen sterility loci interactions (IPE). Gene Ontology enrichment analysis identified a prominent functional gene class consisting of seven genes related to photosystem I (GO: 0009522). Moreover, 55 meiosis-related or meiosis-stage-specific genes were associated with IPE in autotetraploid rice, including Os02g0497500, which encodes a DNA repair-recombination protein, and Os02g0490000, which encodes a component of the ubiquitin-proteasome pathway. These results suggest that polyploidy enhances epistatic interactions between alleles of pollen sterility loci, thereby altering the expression profiles of important meiosis-related or meiosis-stage-specific genes, and resulting in high pollen sterility.

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