

Genome-wide transcriptome analyses for intra/inter-species hybrids and cold stress responses at booting stage in rice

イネの穂ばらみ期における種内・種間雑種及び低温ストレスの網羅的なトランスクリプトーム解析

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1. Introduction

Microarray technology is a powerful tool for biological research, allowing the expression of many thousands of gene transcripts to be monitored simultaneously. By using 8x60k microarray slides designed mainly based on the genes and repeat sequences in the Nipponbare genome, we investigated transcriptome profiles in flag leaves and anthers of reciprocal hybrids for four cross combinations with different genetic distance. Also, we did transcriptome analyses for six cold-sensitive strains with diverse genetic background and different pollen sterility to study the complex molecular mechanism underlying cold tolerance.

2. Methods

To confirm the materials as F1 hybrids of different cross combinations, genotyping was done using their young leaves. Developing stage of microspore was checked by microscopic observation. Every microarray hybridization experiment was performed with flag leaves and anthers at the booting stage according to the manufacture's protocol. On the other hand, low-temperature treatment was applied for six cold-sensitive strains. Anther samples were taken for microscopic observation of anther morphologies, and pollen fertility was investigated by staining with I₂-KI.

3. Results

Comparing the expression profiles in F1 plants, three elements showed that their expressions in the leaves of all six hybrids were higher than those of their parents. The number of differentially expressed elements after cold stress in leaves tended to be greater than in anthers. The up- and down-regulated gene expression patterns appeared in microarray profiles allowed us to characterize gene ontologies involved in several functions. The microarray profiles also predicted candidate genes for seven hybrid sterility loci between *Oryza sativa* and *O. glaberrima*. We found two types of genome-wide expression patterns in the cold-sensitive strains after a cold treatment: four strains displaying abnormal anther morphologies tended up-regulated expression, while the other two cold-sensitive strains left unchanged anther morphology showed a down-regulated expression.

4. Conclusion

Our discovery of three genes showed common higher expression in rice F1 hybrids may be contributed to particular role in heterosis. Besides, the finding of two types of cold-sensitive rice strains may help to elucidate the complex molecular mechanism underlying cold tolerance.