

# Comparative Genome-Wide Transcriptional Profiling of Rice Pollen and Sperm Cells(Frontiers in Rice Science -from Gene to Field-,The 100<sup>th</sup> Anniversary of Tohoku University, International Symposium)

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journal or publication title	Tohoku journal of agricultural research
volume	57
number	3/4
page range	18
year	2007-03
URL	<a href="http://hdl.handle.net/10097/40410">http://hdl.handle.net/10097/40410</a>

## **Comparative Genome-Wide Transcriptional Profiling of Rice Pollen and Sperm Cells**

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Transcriptional profiles of isolated sperm cells, pollen grains and seedlings of rice were analyzed using conventional amplification methods applied to the 51K GeneChip™ of Affymetrix Corporation (Santa Clara, US), which is a near genomic long (25-mer) oligonucleotide-based near genomic microarray which uses probeset technology to make presence/absence calls. As such, this represents the first near transcriptome level view of male gametophyte gene expression. Using the Affymetrix MAS5 algorithm, which incorporates single nucleotide polymorphism mismatches to discriminate sequence presence (matching 11 probe pairs for each probe set, using the PM-MM method), revealed 12,228 positive probe sets in pollen, 16,120 in sperm cells and 22,565 in seedlings. Contrasting detection methods based on other normalization models produced proportionally similar results, with exact numbers depending on stringency. The highest degree of probe overlap was found between sperm and seedling, followed by pollen and seedling, and lastly, sperm and pollen. There were 1027 positive probe sets in pollen, 2453 in sperm, 8395 in seedlings and 8334 in common. Pollen profiles reflect themes of upregulated expression in distinct pectinesterase inhibitor domain containing proteins, ubiquitin pathway products, pollen allergens, uniquely expressed unknown expressed proteins retaining probe similarity with related retroposon groupings, profilin A. Sperm upregulated or specific genes reflect a number of patterns, including routine cellular functions under unique control, relatively few sperm unique products (relative to other patterns), sperm adapted expression involving potential chromosome modeling, miRNA processing, cell cycle controls, and DNA repair.