第101回　システム自然科学研究科セミナー

Regulators of Reproductive Development in Rice

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　　From a microarray-based expression analysis of more than 30 rice transcriptomes, corresponding to both vegetative and reproductive developmental stages/tissue types, we have shortlisted a number of genes on the basis of their tissue-specific expression, or prior knowledge of their involvement in reproductive development, to serve as nucleation points for delineation of the underlying regulatory networks. In my presentation, I would primarily focus on (a) transition of somatic cells into germline tissue that leads to male gametophyte development and (b) functional delineation of embryo and endosperm development nucleating on a seed-specific MADS box transcription factor, OsMADS29, that has been implicated in the regulation of embryo development and grain filling by affecting hormone homeostasis during seed development in rice. The analysis of anther transcriptomes has indicated that specific components of the 26S ubiquitin proteasome complex could play role in the sporophytic to gametophytic phase transition. As for seed development, MADS29 seems to play central role by modulating auxin and cytokinin ratios. Suppression of MADS29 expression by RNAi severely affects seed set. The surviving seeds are smaller in size, with developmental abnormalities in the embryo and reduced size of the endosperm cells. The packaging of starch in the endosperm is also not as compact as in the wild type. Microarray analysis of the overexpression and knockdown lines indicated differential expression of genes involved in plastid biogenesis, starch biosynthesis, cytokinin signaling and biosynthesis pathways. Rice MADS29 has also been found to interact with several seed-expressed transcription factors and its capability to localize in the nucleus is affected by these interactions. Taken together, these data suggest that high throughput transcriptomics data can serve as a good source for mining novel regulatory mechanisms that modulate plant growth and development.