INVITED SEMINAR

"RNA splicing of U12 introns is required for maize endosperm cell differentiation"

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10:00 - 11:00am Friday 7th March 2014

Room S11, Faculty of Agriculture
Hokkaido University, Sapporo Japan.

Abstract:

Splicing of pre-mRNA is critical to gene expression. Most plant genes contain introns, which need to be spliced from the pre-mRNA to code for proteins. A large fraction of plant genes are expressed with multiple, alternatively spliced, transcript variants that can post-transcriptionally regulate protein levels or protein function. The molecular mechanisms by which plant RNA splicing factors influence splice site selection and how alternative splicing influences plant phenotypes are largely unknown. We conducted screens for maize seed mutants influencing endosperm-embryo developmental interactions and identified the *rough endosperm3* (*rgh3*) locus. The *rgh3* mutant causes aberrant endosperm cell differentiation and prolongs a stem-cell like cell fate during seed development. The *rgh3* locus encodes an ortholog of the human ZRSR2 protein, which is a core RNA splicing factor. RNA-seq analysis of *rgh3* mutants found that *rgh3* specifically affects the splicing of genes containing U12 introns. U12 introns are removed by the minor spliceosome, represent <1% of maize introns, and are enriched for genes involved in cell cycle and growth.

Relevant Publications:

Fouquet *et al* (2011) Maize *rough endosperm3* encodes an RNA splicing factor required for endosperm cell differentiation and has a nonautonomous effect on embryo development. ***Plant Cell***, 23: 4280-4297.

Spielbauer *et al* (2013) Chloroplast-localized 6-phosphogluconate dehydrogenase is critical for maize endosperm starch accumulation. ***Journal of Experimental Botany***, 64: 2231-2242.

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