

Category	: 8th Rice Genetics Symposium
Select Theme	: Genetics of Yield: Grain quality and quantity
Endorsement email	:
Genetics of Yield Grain quality and quantity Keyword 1	: Grain weight and size
Genetics of Yield Grain quality and quantity Keyword 2	: Starch
Genetics of Yield Grain quality and quantity Keyword 3	: Grain yield
Title of Entry	: Insights into the Function and Regulation of OsMADS29, a Major Regulator of Seed Development in Rice
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: By using high-throughput microarray-based transcriptomic analyses, our group has identified a novel MADS-box transcription factor, OsMADS29, that plays multiple regulatory roles during embryo development and grain filling by affecting hormone homeostasis during seed development in rice. In situ immunolocalization experiments revealed that OsMADS29 protein accumulates mainly in the embryo and aleurone and sub-aleurone layers of the endosperm. Suppression of OsMADS29 expression by RNAi severely affects seed set. The surviving seeds are smaller in size, with developmental abnormalities in the embryo and reduced size of endosperm cells. The packaging of starch in the endosperm is also not as compact as in the wild type. The most intriguing insight into its function was observed when OsMADS29 was ectopically expressed in rice transgenics under the control of maize ubiquitin promoter. The resultant plants were severely stunted; however, their innate developmental program was not compromised. We discovered that these plants accumulated very high levels of cytokinin along with 2-3-fold reduction in the levels of auxin. These data suggested that OsMADS29, when expressed outside its natural domain of action, is able to regulate cytokinin biosynthesis pathway to achieve higher cytokinin levels in the target cells. Transcriptome analysis of overexpression and knockdown lines have indicated genes involved

in plastid biogenesis, starch biosynthesis, cytokinin signaling and biosynthesis pathways as probable targets of OsMADS29. The OsMADS29 expresses specifically in seeds and its mRNA starts to accumulate few hours after pollination and within a day increases by several hundred folds. Our data has further revealed that even though OsMADS29 is a transcription factor, that would require to move into the nucleus to regulate its downstream targets, its monomers are incapable of localizing in the nucleus. However, when a OsMADS29 monomer interacts with another monomer of OsMADS29 or with any of the 11 other seed expressing MADS-box proteins, the resultant dimers localize very specifically in the nucleus. This indicates that there could lie another level of control at the post-translational level that might influence OsMADS29's activity. Role of MADS29 in developing endosperm into a sink tissue will be discussed.

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