

RICE SEPALLATA GENES OSMADS5 AND OSMADS34 COOPERATE TO LIMIT INFLORESCENCE BRANCHING BY REPRESSING THE TERMINAL FLOWER1-LIKE GENE RCN4.

ZHU W.*, YANG L.*, WU D.*, MENG Q.*, DENG X.*, HUANG G.*, CHEN X.*,
FERRA'NDIZ C.***, LIANG W.*, DRENI L.***, ZHANG D.*

*) School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, 200240, China.

**) Instituto de Biología Molecular y Celular de Plantas, CSIC-UPV Valencia 46022, Spain.

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The spatiotemporal control of meristem identity is critical for determining inflorescence architecture, and thus yield, of cereal plants. However, the precise mechanisms underlying inflorescence and spikelet meristem determinacy in cereals are still largely unclear. The rice (*Oryza sativa* L.) inflorescence is a raceme with two orders of branching, built by the sequential activity of the indeterminate inflorescence meristem (IM), determinate primary branch meristems (PBMs) and determinate secondary branch meristems (SBMs). *SEPALLATA* MADS-box genes are well known for their conserved role in conferring floral organ identity but, among them, the rice *OsMADS34* (also known as *PAP2*, *PANICLE PHYTOMER2*) seems to have evolved new functions in inflorescence development (1, 2). Recently, we described in detail the role of *OsMADS34* in controlling different aspects of inflorescence architecture: *OsMADS34* acts as a repressor of both primary branching and secondary branching (3, 4), while promoting branch elongation (4). We also reveal that its paralog *OsMADS5* contributes partially redundant to the process (4).

To do so, we have generated loss-of-function and overexpression mutants of the paralogous *OsMADS5* and *OsMADS34* genes in rice, and analysed their phenotypes. Using chromatin immunoprecipitation, electrophoretic mobility-shift and dual-luciferase assays, we have also identified *RICE CENTRORADIALIS 4*

(*RCN4*), a *TFL1* (*TERMINAL FLOWER1*) -like gene, as a direct downstream target of both *OsMADS* proteins, and have analysed *rcn4* mutants.

The *osmads5 osmads34* mutant inflorescences had significantly enhanced branching with increased secondary, and even tertiary and quaternary, branches, compared to wild-type (WT) and *osmads34* plants. The *osmads34* mutant phenotype could largely be rescued by also knocking out *RCN4*. Moreover, transgenic lines overexpressing *RCN4* had significantly increased branching, and initiated development of c. 7× more spikelets than WT.

Furthermore, we have isolated new co-factors interacting with *OsMADS5* and *OsMADS34* proteins.

Our results reveal that *OsMADS5* and *OsMADS34* play similar functions in limiting branching and promoting the transition to spikelet meristem identity, in part by repressing *RCN4* expression (4). These findings provide new insights to better understand the molecular regulation of rice inflorescence architecture.

REFS. (@, corresponding authors)

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