

## THE FLORIGEN-ACTIVATED GENE OSMAIL1 DETERMINES STIGMA NUMBER IN RICE FLORETS

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Rice (*Oryza sativa*) is a facultative short-day (SD) plant. Under a threshold of 13.5 hours of light per day, the plants flower. The flowering signal is perceived in the leaves, where a genetic cascade leads to the production of the florigenic proteins Hd3a and RFT1, that move to reach the shoot apical meristem (SAM) where they start the flowering process by activating floral identity genes such as *OsMADS14*, *OsMADS15*, *OsMADS18* and *PAP2*. The florigens are partially redundant, but where the differences in their upstream activation are known, little is known about the differences in their downstream functions. To address this gap, we generated transgenic lines selectively expressing either Hd3a or RFT1 upon spraying with dexamethasone (DEX). The transcriptomes of DEX-sprayed and mock-sprayed transgenic lines (DEX-Hd3a and DEX-RFT1) meristems were compared to find differentially expressed genes (DEGs), and the resulting data were crossed together with DEGs between SD-induced plants and long day (LD)-grown plants (which is a non-inductive condition). The intersection of these three datasets was composed of 16 DEGs, among which we found the aforementioned floral identity genes together with 10 uncharacterized genes, which became the focus of further studies.

Among them, an unannotated gene was found to be a orthologous of *A. thaliana* MAINTENANCE OF MERISTEM (MAIN), encoding for a plant mobile domain containing protein. Arabidopsis possess three other MAIN-like genes: *MAIL1*, *MAIL2*

and *MAIL3*. *MAIN* and *MAIL1* are involved in the maintenance of the meristem and the protection of the genome stability, acting by silencing potentially dangerous transposable elements. The rice gene was named *OsMAIL1* and its transcript was found in the ovary and the stigmas in microarray and RNA-seq data. CRISPR mutants were produced, and *osmail1* florets were found to have a defective ovary, which is smaller, and three stigmas instead of the regular two. RNA-seq on *osmail1* meristems sampled during the panicle development (dissected from plants exposed to 15SDs) has shown that genes involved in carpel morphogenesis and female reproductive organs development are downregulated in the mutants, after Gene Ontology was assessed. These data suggest a function that is not strictly related to flowering, but rather to a later stage of development that nonetheless is controlled by the photoperiod and the florigens.