

## THE ALOG FAMILY MEMBERS OSG1L1 AND OSG1L2 REGULATE INFLORESCENCE BRANCHING IN RICE

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The ALOG family members *OsG1L1* and *OsG1L2* regulate inflorescence branching  
in rice

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Human population growth makes of primary importance to find new ways to improve agricultural crop production and meet the increasing food demand. In this context, inflorescence architecture is one of the key agronomical traits which determines grain yield; thus, it has been a major target for crop domestication and improvement.

In *Oryza sativa*, inflorescence architecture is established at early stages of reproductive development. During vegetative phase, the Shoot Apical Meristem (SAM) produces leaves. When a rice plant undergoes floral transition, the SAM differentiates into Inflorescence Meristem (IM), which in turn gives rise to Primary Branch Meristems (pBMs). The pBMs can produce Spikelet Meristems (SMs) or form a more complex architecture with Secondary Branches Meristems (sBMs), that will in turn produce SMs. When the SM differentiation occurs, the meristem loses its indeterminate state to become determinate, stopping all sorts of branching potential. This leads to the development of Floral Meristems (FM), that differentiate into floral organs.

The ALOG gene TAWAWA1 (TAW1) has been shown to be a regulator of meristem activity: it promotes IM activity and the suppression of the phase change to SM identity. Combining laser microdissection of rice inflorescence meristems with RNA-seq, we observed that other two members of the ALOG gene family, OsG1-like 1 (OsG1L1) and OsG1L2, present an expression profile similar to TAW1. Furthermore, the loss-of-function CRISPR mutants *osg1l1* and *osg1l2* present a phenotype similar to the *taw1* mutant, suggesting that these three genes may act in related pathways controlling inflorescence development.

A transcriptome analysis was performed on *osg1l2* mutant, suggesting the interaction of OsG1L2 with other genes known to control inflorescence architecture. The obtained dataset was also used to generate a gene regulatory network (GRN).

The analysis of the loss-of-function CRISPR mutant of the homeodomain-leucine zipper transcription factor gene OsH0X14 suggests that the proposed

GRN can be useful to identify players involved in inflorescence development in rice.