

## ABSTRACT

### **Role of ALOG family genes in inflorescence patterning in Rice and Arabidopsis**

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Inflorescence architecture is a key agronomical trait that determines fruit and seed yield.

Understanding the genetic basis of inflorescence architecture will not only contribute to elucidate crop evolution/domestication mechanisms but also improve crop grain yield.

Flowering plants develop different type of inflorescences, such as racemes in Arabidopsis and panicles in Rice. The architecture is established during the early stages of reproductive development and it is determined by the activity of different meristem types and by the timing of transition between indeterminate meristems to determinate ones.

Inflorescence development is finely regulated by a genetic network that includes meristem identity genes and genes that regulate their expression; many genes are already known but others have to be unraveled to provide insight into how this process works and which are the molecular mechanisms behind it.

Transcriptomic analysis performed in rice and in Arabidopsis through laser microdissection technique in different meristematic tissues highlighted differentially expressed genes belonging to ALOG family.

The ALOG family genes encode nuclear proteins with unknown function and they seem to have a role in inflorescence patterning.

We focus on G1L1, G1L2 and G1L5, in rice and on LSH1, LSH3 and LSH4 in Arabidopsis. G1L5 is already known to be a major regulator of inflorescence architecture, whereas LSH3 and LSH4 seem to have a role in meristem maintenance and organogenesis.

RNAseq data were confirmed by in situ hybridization performed on meristematic tissues from both species.

We are also generating single and double/triple K.O mutants in different combinations by CRISPR/Cas9 genome editing technique to have a better understanding on their role in inflorescence patterning.

We show the data demonstrating a role of *GIL2* in inflorescence branching and spikelet numbers.