Poster Communication Abstract – 1.32

CHARACTERISATION OF ALOG GENES CONTROLLING RICE INFLORESCENCE DEVELOPMENT&NBSP;FOR YIELD IMPROVEMENT

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rice, inflorescence architecture, functional genomics, grain yield

Plant inflorescence architecture is an important determinant of the reproductive success of a plant but also of agronomical interest, because it determines yield in many crops. Inflorescence development is a complex process and in the plant kingdom many variations in the developmental program have been observed.

In rice the inflorescence meristem, (rachis meristem) starts to develop primary branches. On these primary branches secondary branches are often formed which develop spikelet meristems that develop the florets and finally the grains. The result is a determinate inflorescence called panicle. The timing of spikelet meristem development determines the number of branches and grains that will develop. Our lab is interested in the molecular mechanisms that determine the identity of the different reproductive meristems since these stands at the base of the final architecture. Recently, we used laser micro-dissection for isolating the rice reproductive meristems and used this material for RNAseq analysis (Harrop et al., 2016). These experiments resulted in the identification of candidate genes involved in inflorescence development. We focused especially on the functional characterization of members of the ALOG gene family and the regulatory network in which they function. Approaches and recent results will be discussed.