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A TRIPLE FLORIGEN SYSTEM IS ESSENTIAL FOR FLOWERING AND PANICLE ARCHITECTURE IN RICE

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To allow rice (Oryza sativa) to shift from vegetative to reproductive phase, a physiological event called floral induction is required. When two essential genes, HEADING DATE 3a and RICE FLOWERING LOCUS T1, encoding the florigens and belonging to the phosphatidyl ethanolamine binding protein (PEBP) family, are expressed, can this event take place. Hd3a and RFT1 are transcribed and translated in the leaf before moving to the shoot apical meristem (SAM) through the phloem. After reaching the shoot apical meristem they form an heterohexameric complex named Florigen Activation Complex (FAC), binding to two 14-3-3 proteins and to two bZIP transcription factors. Conversion of the shoot apex into a panicle is induced by this complex by promoting expression of panicle-identity genes. Along with these two florigens, both well-known and well-characterized, there is a third PEBP gene, identified thanks to a transcriptional screen at the rice SAM, FLOWERING LOCUS T-LIKE 1 (FT-L1). FTL1 expression during floral commitment is strongly induced at the SAM. Following a phase of isolation and thorough analysis of different EMS mutant alleles, I could conclude that FT-L1 shows floral promoting activity under different day-length conditions, but some of the common characteristics of a typical florigen are not shown, as FT-L1 holds a few distinctive traits. Expression data both from qRT-PCR and in situ hybridization studies indicated that its mRNA is mainly expressed in the SAM rather than in the leaves during all developmental stages; and secondly, its mutants, phenotypically analyzed with the P-TRAP software, show panicles with a higher number of secondary and tertiary branches. Throughout my research I'm defining FT-L1 function and its position in the flowering pathway and I'm discovering how it regulates panicle architecture by analysing its regulators.