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# A TRANSCRIPTION FACTOR COORDINATING FLOWERING AND STEM ELONGATION IN O. SATIVA

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Rice is a facultative short day plant domesticated from its ancestor *O. rufipogon* in southeast Asia, a region characterized by tropical climate, where long day length coincides with rainy season. In order to avoid flowering during this unfavourable period, rice has developed a complex molecular network to synchronize flowering with short day length. When leaves are exposed to short days two florigen proteins are produced: Hd3a and RFT1. As they reach the shoot apical meristem (SAM) through the phloem the flowering transition begins: the SAM turns into an inflorescence meristem which will lead to the formation of the panicle. The panicle needs to be located at the top of the plant to allow heading and seeds dispersion. The elevated positioning of the panicle is ensured by the activity of the intercalary meristems, located between nodes and internodes. Therefore floral transition and stem elongation are two tightly linked phenomena, but the molecular link between the two remains still unclear.

During XX century Green Revolution rice yield has been substantially increased thanks to the introduction of defective alleles of *SEMI DWARF 1 (SD1)* gene, encoding for a GA20oxidase enzyme, responsible for the biosynthesis of active gibberellins. The cultivars developed during the Green Revolution required high nitrogen input in order to sustain a higher productivity. But the reduction in GA content provoked a decrease in cell wall lignin and culm diameter, thus not preventing the breaking of the stem by bending pressure and lodging. The identification of new genes involved in controlling plant height without an alteration in GA content may be

useful to reduce yield losses caused by lodging.

Through an RNA-seq experiment, we identified *PREMATURE INTERNODE ELONGATION 1 (PINE1)* as the master coordinator of flowering and stem elongation in rice. *pine1* knockout mutants show uncoupled stem elongation and flowering, presenting elongated internodes since seedling stage, while the overexpression of *PINE1* causes dwarfism. PINE1 is a growth repressor that, when expressed, maintains the stem unelongated. GAs are the principal plant hormones controlling cell division, stem elongation and growth. Since mutants do not present an increased GA content, PINE1 may be involved in GA signalling pathway, but how and when PINE1 is related to this pathway is still unknown. GA perception is mediated by the receptor GIBBERELLIN INSENSITIVE DWARF 1 (GID1) that binds GA, the growth repressor DELLA protein SLENDER1 (SLD1) that needs to be degraded, and the F-BOX protein GID2 that targets SLD1 to the proteasome when bound to the GID1-GA active complex. Creating double mutants of PINE1 and these genes will clarify which kind of relationship exists among them. In particular, we are generating CRISPR-Cas9 double mutants *pine1-sd1, pine1-sld1, pine1-gid1* and *pine1-gid2*. The comparison of double mutants phenotypes will help clarifying the relationship between these genes and PINE1.