IN BRIEF

Flowering time and photoperiod sensitivity in rice: Key players and their interactions identified

Kutubuddin A. Molla

1 Assistant Features Editor, The Plant Cell, American Society of Plant Biologists, USA.
2 ICAR-National Rice Research Institute, Cuttack, India

Rice is one of the most important cereal crops and has wide adaptability in diverse climatic regions ranging from 44°N to 35°S and 6 ft below to 2700 ft above sea level (Pathak et al., 2021). Which traits and mechanisms confer this adaptability is a major question in rice biology. Heading date (or flowering time) is a crucial trait for the regional and seasonal adaptation of rice and influences grain yield. Rice is a facultative short-day plant; short-day (SD) conditions promote, and long-day (LD) conditions inhibit flowering. On receiving day-length signals, leaf cells produce a mobile flowering activator, florigen, that is transported to the shoot apex to initiate the flowering transition. In rice, Hd3a and RFT1 are the two proposed florigens, which function under SD and LD conditions, respectively (Zhou et al., 2021). Transport of Hd3a from leaves to the shoot apex is essential for flowering under SD conditions. However, how this transport occurs and what factors facilitate the movement of Hd3a are unknown. In this issue, Liang Zhang and colleagues (Zhang et al., 2022) identified proteins responsible for florigen trafficking through the phloem from the leaves, where it is synthesized, to the shoot apex, where flower development occurs.

To decipher the mechanism of Hd3a movement, the authors first identified and isolated proteins that directly interact with Hd3a. Employing a series of molecular biology techniques, they confirmed that OsFTIP9 (FT-INTERACTING PROTEIN 9) physically interacts with Hd3a. An earlier study showed that FTIPs play an important role in protein trafficking (Liu et al., 2019). Zhang et al. (2022) generated CRISPR-mutants for Osftip9 and observed that these mutants display late-flowering compared to wild-type plants under SDs. This phenotype was rescued when the Osftip9 mutant was transformed with a genomic construct (gOsFTIP9) harboring the upstream and coding sequence of OsFTIP9. This result demonstrates that the late-flowering phenotype of the mutant under SDs is due to the loss of function of OsFTIP9.

Hd3a mRNA accumulation was not affected in the Osftip9 mutant, suggesting that OsFTIP9 may modulate Hd3a function at the post-transcriptional level. Immunoelectron microscopy of an Osftip9 mutant overexpressing HA-tagged FTIP9 (Osftip9 4HA-gOsFTIP9) revealed that FTIP9 is located in phloem companion cells but not in sieve elements. The authors then generated gHd3a-3FLAG expressing lines in both hd3a and hd3a Osftip9 backgrounds and used immunoelectron microscopy to check if OsFTIP9 facilitates Hd3a export from companion cells to sieve elements. With anti-FLAG antibodies, the Hd3a-3FLAG signal was detected in both companion cells and sieve elements. Interestingly, the signals in sieve elements were greatly reduced in the hd3a Osftip9 background compared to hd3a, whereas the signals in companion cells were more intense in the hd3a Osftip9 background than in hd3a. In addition, Hd3a-3FLAG accumulation was reduced in shoot apices, but not in leaves, in the hd3a Osftip9 background compared to hd3a. When a functional copy of OsFTIP9 was introduced into the hd3a Osftip9 background, the accumulation of Hd3a-3FLAG was restored in shoot apices. These results suggest that OsFTIP9 mediates Hd3a transport from phloem companion cells to sieve elements and impacts Hd3a accumulation in the shoot apices.

Further investigation identified a hitherto unknown tetra-tricopeptide repeat (TPR) protein, OsTPR075, as an interacting partner of OsFTIP9. The Ospr075 mutants displayed late-flowering under both SDs and LDs. Retransformation with a functional copy of OsTPR075 rescued the late-flowering phenotype in both SDs and LDs. Interestingly, the OsTPR075 overexpressing line exhibited early-flowering under both SDs and LDs.

Collectively, these results suggest that OsTPR075 promotes flowering in rice. A number of independent investigations revealed that OsTPR075 physically interacts with both OsFTIP1 and OsFTIP9 in vitro as well as in vivo. The authors’ earlier study showed that
OsFTIP1 binds another florigen RFT1 and facilitates RFT1 export under LDs (Song et al., 2017). Co-immunoprecipitation assay with epitope-tagged lines showed that OsTPR075 is essential for the Hd3a-OsFTIP9 interaction and enhances the RFT1-OsFTIP1 interaction. In the absence of a functional OsTPR075, the abundance of florigen, Hd3a, and RFT1 was significantly lower in shoot apices but not in leaves. These results indicate that OsTPR075 strengthens physical interactions between FTIPs and florigen, and positively affects the abundance of florigen in the shoot apex. Comparing the flowering times of various single, double, and triple mutants under SD and LD conditions led the authors to conclude that OsTPR075, OsFTIP9, and Hd3a act in the same pathway under SDs, while OsTPR075, OsFTIP2, and RFT1 function in a common pathway under LDs.

In summary, the authors demonstrated that OsFTIP9 interacts with florigen Hd3a and enables its transport from companion cells to sieve elements and ultimately to shoot apices, where the florigen activates genes related to floral meristem initiation and development. Hence, the study by Zhang et al. (2022) filled a vital gap in understanding the regulation of florigen transport and flowering time under SDs in rice and identified a common factor, TPR075, that increases florigen transport efficiencies under both SDs and LDs (Figure). This work will inspire investigation of a similar module in other crop plants and facilitate breeding efforts to increase the adaptability of rice under diverse agroclimatic regions by controlling flowering time in response to day length.

REFERENCES


