CellPress
Partner Journal

Uncover the mystery of pleiotropic effects of PROG1 during rice domestication

Rice is one of the earliest domesticated crops, and the plant and panicle architecture are critical domesticated traits that greatly affect yield (Xu and Sun, 2021). Previous studies revealed that PROSTRATE GROWTH 1 (PROG1) regulates tiller angle, tiller number, and panicle architecture during rice domestication (Jin et al., 2008; Tan et al., 2008). However, the detailed molecular mechanisms through which *PROG1* controls plant and panicle architecture have not yet been well documented. Recently, Wang et al. (2023) identified the direct downstream targets of PROG1 to illustrate the genetic basis of the pleiotropic effects of the gene *PROG1* in rice (Wang et al., 2023).

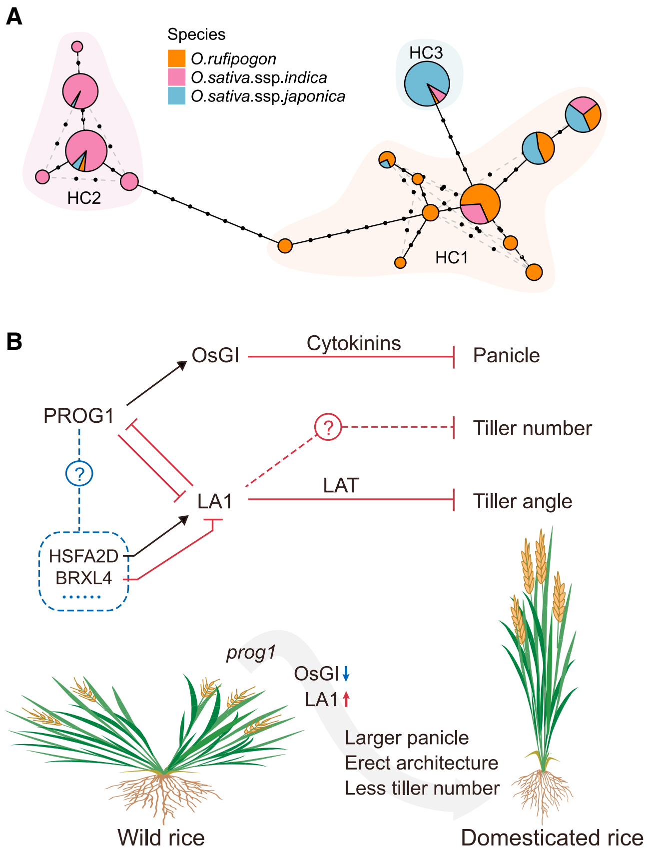

Figure 1. Molecular mechanism underlying plant and panicle architecture regulated by *PROSTRATE GROWTH 1* (*PROG1*)

(A) Haplotype network analysis of *LAZY1* (*LA1*) among the rice population. The pie plot of each node indicates the proportion of different species. Each edge represents the editing distances between two adjacent haplotypes.

(B) PROG1, HEAT STRESS TRANSCRIPTION FACTOR 2D (HSFA2D), and Brevis Radix Like 4 (OsBRXL4) act upstream of LA1 to regulate lateral auxin transport (LAT) and thus control tiller angle in rice. PROG1 can also regulate panicles by acting upstream of *OsGI* to affect the cytokinin levels. During the rice domestication process, the PROG1 inactivation led to an increase in *LA1*, resulting in the erect plant architecture and less tiller number. On the other hand, the reduction of *OsGI*, caused by the PROG1 change during rice domestication, results in panicle enlargement.

During the domestication of cultivated rice from wild rice, inactivation of PROG1 led to the transition from prostrate growth to erect growth, thereby facilitating the harvest (Jin et al., 2008; Tan et al., 2008). In rice, the *LAZY1* (*LA1*) gene regulates tiller angle by controlling lateral auxin transport (Li et al., 2007). Distinct from *PROG1*, haplotype network analysis showed that the haplotypes of *LA1* in *indica* were distinct from those in *japonica*, with various haplotypes in *Oryza rufipogon* as intermediates, indicating an *indica-japonica* divergence pattern of *LA1* (Figure 1A). Recent study revealed that *PROG1* acts upstream of *LA1* to regulate rice tiller angle by controlling the lateral auxin transport (Zhang et al., 2023). Consistently, Wang et al. (2023) verified that PROG1 and LA1 can directly bind to each other's promoter. Furthermore, Wang et al. (2023) also found PROG1 and LA1 can inhibit each other's expression to regulate rice tiller angle. Besides PROG1, HEAT STRESS TRANSCRIPTION FACTOR 2D (HSFA2D), and LA1-interacting protein named Brevis Radix Like 4 (OsBRXL4) also act upstream of LA1 to regulate the tiller angle in rice (Figure 1B). The gravistimulation-responsive *HSFA2D* acts upstream of *LA1* to positively regulate the expression of *LA1* (Zhang et al., 2018), and OsBRXL4 controls rice tiller angle by affecting nuclear localization of LA1 (Li et al., 2019). Although these factors all act upstream of *LA1*, their regulatory ways seem to be different, and their functional connection remains to be determined. These exciting discoveries provide fascinating new insights into the genetic regulatory network of tiller angle in rice.

Compared with wild rice, disruption of the PROG1 function also contributes greatly to a reduced number of unproductive tillers in the cultivated rice (Figure 1B). Surprisingly, Wang et al. (2023) found that *PROG1* and *LA1* may play antagonistic roles in regulating tiller number in addition to tiller angle. In fact, the tiller number phenotype regulated by *LA1* has not been reported in previous studies (Li et al., 2007, 2019; Yoshihara and Iino, 2007; Zhu et al., 2020; Zhang et al., 2023). Investigating whether PROG1-LA1 module is involved in the environmental plasticity regulation of rice tillering is fascinating.

Wang et al. (2023) also discovered that PROG1 controls panicle architecture by directly binding to the intragenic regulatory regions of *OsGIGANTEA* (*OsGI*) and subsequent activating its expression. A previous study found that *OsGI* negatively regulates panicle length and spikelet numbers (Itoh and Izawa,

Published by the Molecular Plant Shanghai Editorial Office in association with Cell Press, an imprint of Elsevier Inc., on behalf of CSPB and CEMPS, CAS.

2014). Wang et al. (2023) further showed that the OsGI acts downstream of PROG1 to regulate rice panicle architecture by affecting cytokinin levels. However, it is still unclear how *OsGI* regulates the levels of cytokinin in panicles.

The domestication of *PROG1* has effects on plant and panicle architecture, both of which ultimately contribute to rice grain yield. The driving forces underlying the domestication of complex agronomic traits have yet to be revealed. Efforts to investigate the potential post-domestication selected or co-domesticated patterns of *PROG1* downstream factors would shed light on the underlying mechanism of rice domestication and provide new information on precision breeding.

FUNDING

This work was supported by the grant from the National Key Research and Development Program of China (2022YFF1002903).

ACKNOWLEDGMENTS

No conflict of interest is declared.

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https://doi.org/10.1016/j.molp.2023.09.018

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