



Balancing high grain yield and early maturity: The *OsFTL1* allele *TGW1a*^{JZ}_{FA}

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Global food demand is projected to increase by 30%–50% by 2050, posing a major challenge to agronomic systems with limited arable cropland (FAO, 2018). Enhancing cropping intensity (also known as annual crop harvests per unit area of arable land) is one effective way to improve production in multiple cropping systems (FAO, 2018). However, high yield usually relies on prolonged growth periods, which largely affects timely rotation for subsequent seasonal crops and compromises cropping intensity. Thus, breeding high-yield crops with short growth duration is a vital goal for improving annual yield in sequential cropping systems.

In rice breeding, high yield and early maturity are inherently antagonistic since shortened vegetative growth periods usually result in a yield penalty, making it difficult to achieve both breeding objectives simultaneously. A core part of reconciling this contradiction is early flowering accompanied by rapid nutrient accumulation during the limited growth periods, especially carbon and nitrogen, two of the most essential macronutrients for plant growth and development. This is tightly correlated with key physiological processes, including high photosynthesis rate and nitrogen use efficiency (NUE) during the entire growth stage (Li et al., 2025). Correspondingly, several crucial flowering regulators were reported to participate in these two processes. For instance, the long noncoding RNA *Ef-cd* shortens maturity duration without yield penalty by enhancing nitrogen utilization and improving photosynthesis rate (Fang et al., 2019). The key transcriptional regulator OsDREB1C facilitates photosynthetic carbon assimilation and NUE, thus contributing to early flowering with high yield (Wei et al., 2022). These studies have demonstrated the theoretical feasibility of breeding high-yield and early-maturity rice varieties.

A recent study from Jian Zhang's group has identified a flowering locus T-like encoding gene *TGW1a* (*thousand-grain-weight 1a*), the elite allele of which could simultaneously increase NUE, grain weight, and promote flowering time, contributing to high yield and early maturity in rice. More excitingly, favorable allelic combination of *TGW1a* and its tightly linked locus *Gn1a* (responsible for grain number) in different modern cultivars led to superior yield performance, suggesting its great promise for practical application in agriculture (Figure 1).

To dissect the genetic basis of flowering and grain yield, the authors performed fine mapping using BC₃F₄ population derived from Jizi1560 (JZ, donor) and recurrent parent Huanghuazhan (HHZ, receptor) (Li et al., 2026), and identified *TGW1a*, also known as *OsFTL1* (LOC_Os01g11940), which encodes a flowering locus T-like, phosphatidylethanolamine-binding protein (Giaume et al., 2023; Wei et al., 2025). Introducing *TGW1a* from JZ (*TGW1a*^{JZ}) into HHZ led to approximately 6 d earlier heading, a 5.3%–7.5% increase in thousand-grain weight (TGW), and an ~11% increase in grain yield per plant relative to the control. These results demonstrate that *TGW1a*^{JZ} can simultaneously shorten growth duration and boost grain yield, thus holding considerable breeding potential. Notably, previous studies reported that simple overexpression of *OsFTL1* caused extremely early flowering time but suffering a substantial yield penalty (Giaume et al., 2023; Wei et al., 2025; Liu et al., 2026). Here, *TGW1a*^{JZ}—the elite allele of *OsFTL1* with optimal expression level—effectively uncouples the trade-off between growth duration and yield, underscoring the importance of identifying suitable alleles for translational breeding applications.

In addition to the short growth duration, the authors also found that NUE was improved in NIL-*TGW1a*^{JZ} compared to NIL-*TGW1a*^{HHZ}. To further investigate the physiological and molecular basis of *TGW1a*^{JZ}-conferred higher NUE, the authors performed RNA sequencing and found that *TGW1a* promoted the expression of plenty of nitrogen utilization genes, such as *OsAMT1.2*, *OsNRT1.1B*, and *OsNADH-GOGAT*, resulting in higher nitrogen absorption and assimilation capacity. Moreover, *TGW1a* interacted with *Ghd7* and *Hd1*, two crucial flowering regulators determining heading and grain yield in rice, and enhanced their protein stability (Xue et al., 2008). Interestingly, *Ghd7* and *Hd1*, as transcription factors, were both found to target plenty of NUE genes, which include the eight genes that *TGW1a* regulated. Therefore, the *TGW1a*–*Ghd7*/*Hd1* module confers high NUE by positively affecting nitrogen utilization. Collectively, *TGW1a*^{JZ} is involved in the crosstalk between flowering and nitrogen use, optimizing both to balance early flowering and high yield.

Notably, the authors found that *TGW1a* is closely linked to *Gn1a*, a locus responsible for grain number (Ashikari et al., 2005). Although *TGW1a*^{JZ} confers high yield and early

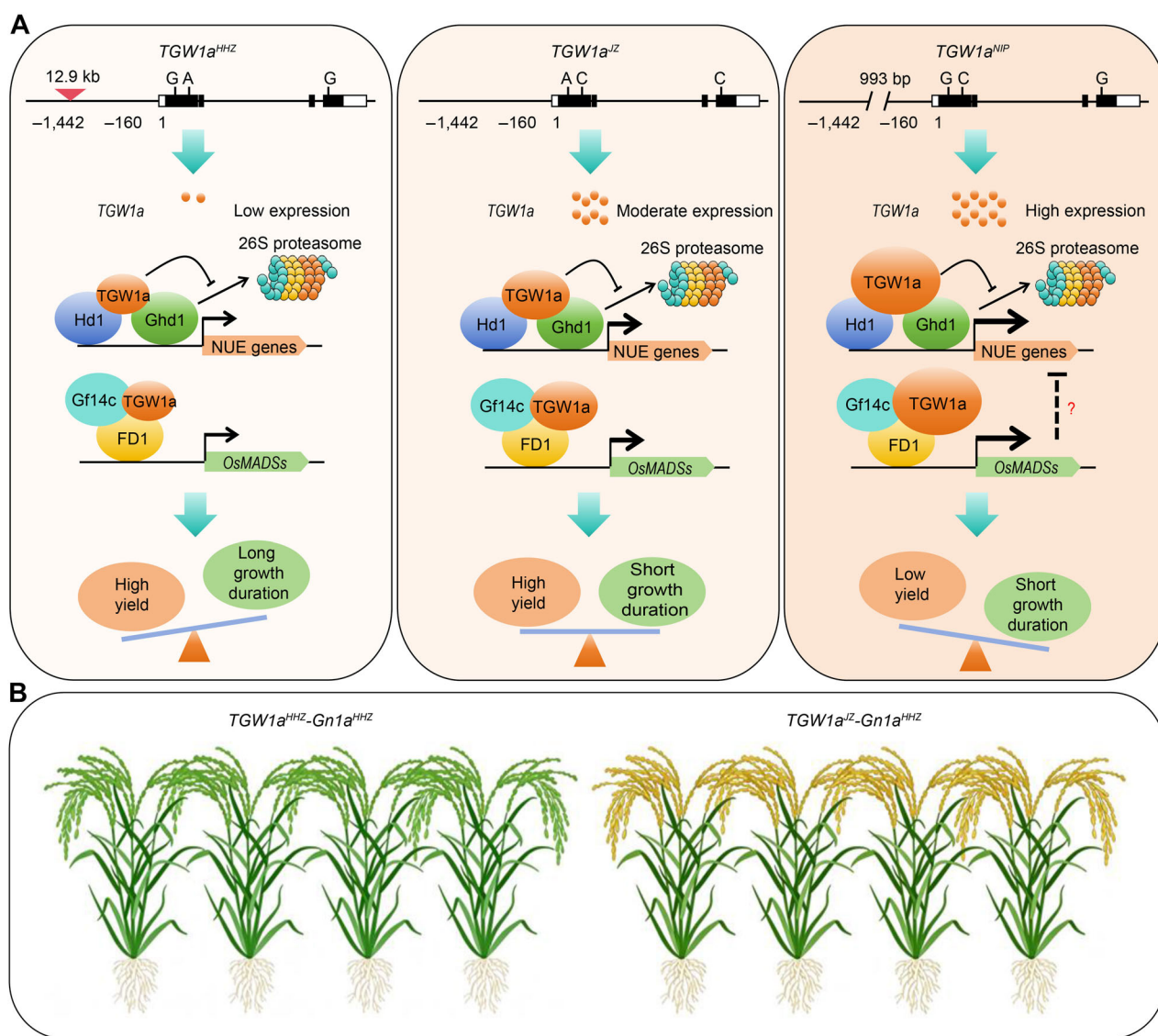


Figure 1. A schematic model depicts the critical functions of *TGW1a^{JZ}* in shortening growth duration and increasing grain yield

(A) The optimal allele *TGW1a^{JZ}*, with a moderate expression level encoding a flowering locus T-like protein, can interact with and stabilize Ghd7 and Hd1 to activate the NUE genes (*OsNRT1.1B*, *OsAMT1.2*, *OsNADH-GOGAT*, etc.) to increase nitrogen utilization. Simultaneously, *TGW1a^{JZ}* can form a FAC (Florigen Activation Complex) with Gf14c and OsFD1 to activate the expression of *OsMADS14/15* to accelerate the flowering time. Hence, it can be inferred that *TGW1a^{JZ}* is involved in regulating NUE and flowering time, and could optimize both to shorten growth duration and enhance grain yield. In contrast, low or high expression of *TGW1a* is unable to balance flowering time and NUE, leading to high yield with a long growth duration or extremely low yield caused by very early flowering time. **(B)** The application of elite alleles *TGW1a^{JZ}* and *Gn1a^{HHZ}* in four cultivars demonstrated their huge breeding potential. The figure was created partly using BioRender (<https://biorender.com>).

maturity, its linkage to the inferior allele *Gn1a^{JZ}* with limited grain numbers hindered further yield improvement. Therefore, the allelic combination of *TGW1a^{JZ}* with the elite allele *Gn1a^{HHZ}* is expected to generate a synergistic effect. To this end, *TGW1a^{JZ}* was introduced into four cultivars, including Zhongjiazao17, Zhongzao39, Huazhan, and R173 (all *TGW1a^{HHZ}-Gn1a^{HHZ}* background) to construct NILs-*TGW1a^{JZ}-Gn1a^{HHZ}* (Ashikari et al., 2005). Compared to controls, NILs-*TGW1a^{JZ}-Gn1a^{HHZ}* shortened the flowering time from 3.08 to 7.83 d and growth duration ranging from 3.67 to 8.67 d, increased thousand grain weight by at least 3.81%, and increased yield per plot ranging from

4.22% to 11.00%. Moreover, they crossed Huazhan-*TGW1a^{HHZ}-Gn1a^{HHZ}* and Huazhan-*TGW1a^{JZ}-Gn1a^{HHZ}* with an elite male-sterile line QiA and found that F₁ lines (Huazhan-*TGW1a^{JZ}-Gn1a^{HHZ}* × QiA) flowered and harvested earlier about 4 d; there was an increase in grain weight (4.38%) and grain yield (5%). These discoveries strongly suggest that *TGW1a^{JZ}-Gn1a^{HHZ}* shows promising potential in high-yield and early-maturity rice breeding, especially the principal role of *TGW1a^{JZ}*.

In summary, the work by Li et al., (2026) represents a major breakthrough in breeding for high-yield and early-maturity rice, as it identifies a specific allele that simultaneously enhances

grain yield and shortens the growth duration via improving NUE. Despite previous work confined to mechanistic characterization (Giaume et al., 2023; Wei et al., 2025; Liu et al., 2026), the present work, for the first time, translates this knowledge into practical breeding applications. More importantly, the authors offer critical insights into precision breeding: Optimal expression of a given gene in specific tissues at specific developmental stages is essential for fine-tuning a target trait without compromising others, thus allowing balanced improvement across multiple traits. Furthermore, this study underscores the value of specialized genetic resources and germplasm, which harbor unique alleles with untapped breeding potential. Systematic discovery, functional understanding, and utilization of such alleles will greatly accelerate translational breeding efforts. Collectively, this work provides a feasible theoretical framework and valuable genetic resource for future breeding of high-yield and early-maturity rice varieties, marking a significant milestone in the field.

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CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS

W.Z. conceived and revised the manuscript. S.W. and Y.L. drafted the manuscript. All authors have read and approved the contents of this paper.

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