

# Plant Physiology



## Molecular cloning and functional analysis of a novel rice gene, OsZmGL1, involved in drought tolerance

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Research Article

### Abstract

Drought has become one of the most severe abiotic stresses experienced in agricultural production across the world. Plant response to water deficit is a complex process involving multiple mechanisms in the leaves, which are mainly regulated by transcription factors (TFs). Previous studies from Arabidopsis have shown that ZmGL1 is a novel TF gene involved in drought tolerance. In this study, we identified a novel rice gene, OsZmGL1, which encodes a protein with a high degree of similarity to ZmGL1. We found that OsZmGL1 is highly expressed in rice leaves under drought stress. We further found that OsZmGL1 overexpression in rice significantly improved drought tolerance. To investigate the function of OsZmGL1, we performed RNA-seq analysis of rice leaves under drought stress. The results showed that OsZmGL1 overexpression significantly up-regulated the expression of genes involved in drought tolerance, including those related to hormone signaling, cell wall synthesis, and osmolyte synthesis. These results demonstrate that OsZmGL1 is a novel TF gene involved in drought tolerance in rice. This study provides a new candidate gene for drought tolerance breeding in rice.

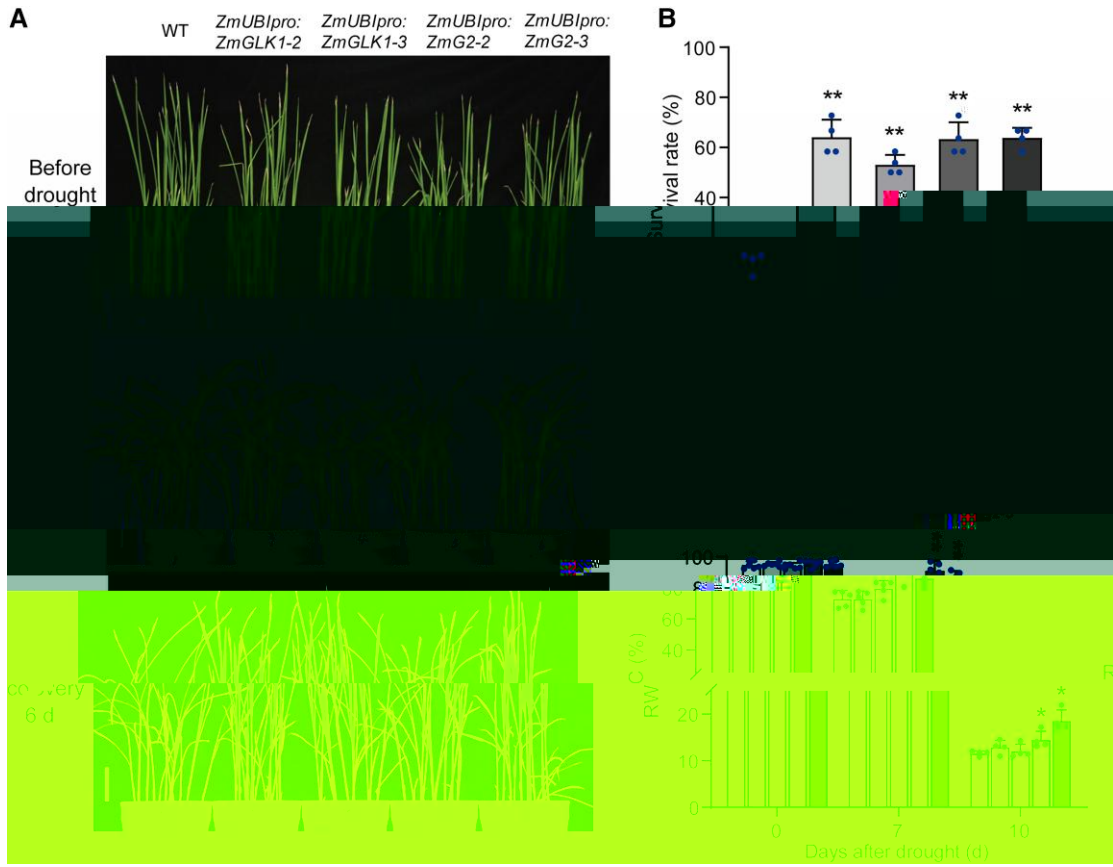
### Introduction

Global crop production must be approximately doubled by 2050 to meet the demand for the increasing human population (FAO 2009; Timlin et al. 2011). However, yield improvement is hindered by the expected climate change, including drought stress (Rötter et al. 2013). Yield stress is a major constraint to crop production (Edmeades et al. 2009). Drought is one of the most severe abiotic stresses in agriculture; it has been extensively studied in rice (Li et al. 2019).

Water deficit is a major abiotic stress in rice (Li et al. 2019). Rice (Oryza sativa) is a major staple food for nearly half of the world's population, but it is highly susceptible to drought stress (Over 50% of the world's rice production is estimated to be affected by drought stress (Mba et al. 2011). Development of drought-tolerant rice varieties is urgently needed to meet the demand for rice under changing climate conditions (Tang et al. 2019).  
Stomatal regulation is a key mechanism for water exchange between plants and the atmosphere. When plants suffer from water

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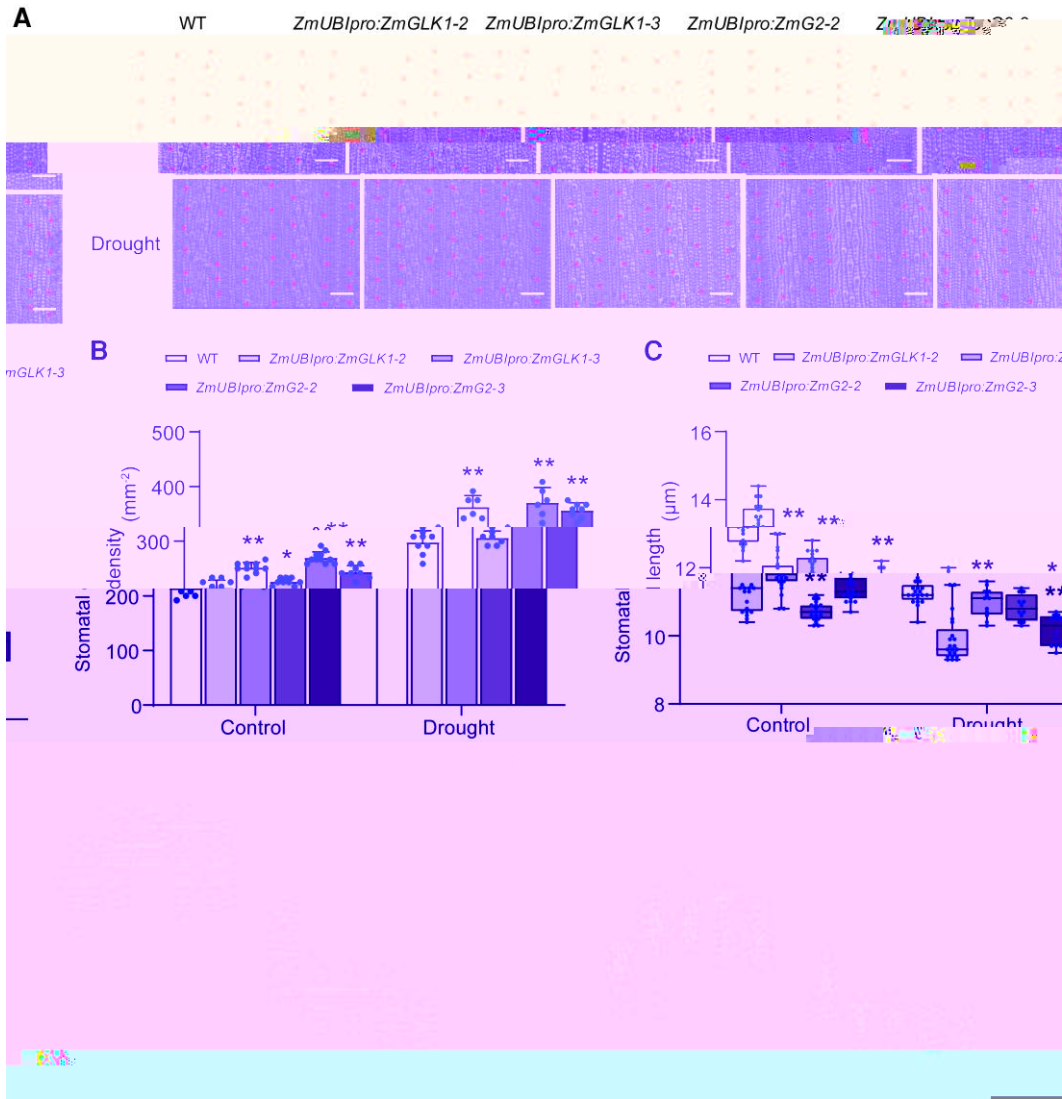


**Figure 1.** Overexpression of ZmUBIpro lines increases drought tolerance. **A)** Phenotypes of WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants during drought and recovery. Three weeks later, WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice seedlings were grown in pots and subjected to waterlogging for 10 d, then watered for 6 d to recover. The upper, middle, and lower panels show representative photos before drought, after 10 d of drought, and after the 6 d recovery, respectively. Scale bar = 2 cm. **B)** Survival rates of WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants after 10 d of drought. All were by 6 d of recovery. Data are presented as the mean  $\pm$  SD for three biological replicates. **C)** The RWC of WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice leaves after 0, 7, and 10 d of drought. Data are presented as the mean  $\pm$  SD.

10 d of PEG treatment. Supplement 1 F1. S1B. We found that the RWC of rice seedlings during PEG treatment. The results show that the drought-tolerant plants recover more quickly than the WT. Specifically, RWC values were 11.0%  $\pm$  0.1% and 9.5%  $\pm$  0.7% higher than WT, respectively, compared with the WT. Supplement 1 F1. S1C. These results further indicate that overexpression of ZmUBIpro lines increases drought tolerance.

ZmGLK1 and ZmGLK2 are known to regulate stomatal opening and closing. To further investigate the physiological mechanism underlying the elevated drought tolerance conferred by ZmGLK1 and ZmGLK2, we evaluated the effects of drought on stomatal conductance ( $g_s$ ) and transpiration rate ( $T_r$ ) in the pots in which the plants were respired in pots, serving as the control. In addition, photosynthesis under drought. We therefore measured

stomatal conductance and photosynthesis-related parameters under control conditions using LICOR 6400XT portable photosynthesis system. The results revealed that the stomatal conductance in ZmUBIpro:ZmGLK1-2 and ZmUBIpro:ZmGLK1-3 rice seedlings (0.118–0.130 and 0.126–0.131, respectively) compared with the WT (0.083) under control conditions; while the drought-tolerant plants performed better photosynthesis rates, net cell CO<sub>2</sub> concentration (C<sub>i</sub>) and transpiration rates (Supplement 1 F1. S2), in the plants grown in the pots (L1 and L2) (0). In contrast, after 7 d of drought treatment, ZmUBIpro:ZmGLK1-2 and ZmUBIpro:ZmGLK1-3 rice plants displayed a significantly decrease in stomatal conductance (0.06–0.073 and 0.05–0.050, respectively), where the WT remained relatively stable under drought conditions (0.087; Supplement 1 F1. S2B). The photosynthesis rates, C<sub>i</sub>, and transpiration rates showed corresponding declines in ZmUBIpro:ZmGLK1-2 and ZmUBIpro:ZmGLK1-3 rice plants during water deprivation (Supplement 1 F1. S2, C, and D). We next compared the stomatal conductance between WT and ZmUBIpro:ZmGLK1-2 and ZmUBIpro:ZmGLK1-3 rice plants under

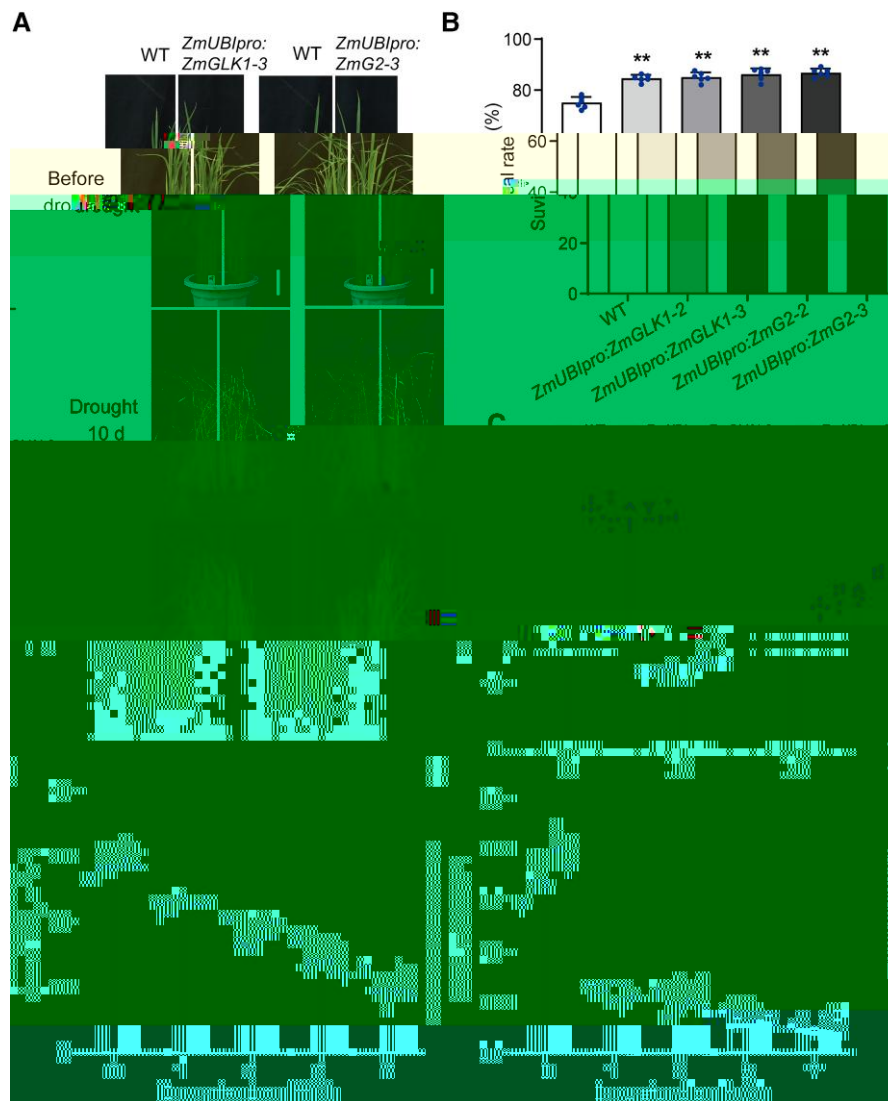


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both control and drought conditions. Transgenic plants presented higher stomatal densities in the leaves but significantly higher stomatal conductance of the WT regardless of conditions (Fig. 2, B & C). Interestingly, the stomata were prominently wider in WT under control conditions (Fig. 2D), where, under air humidity stress, the stomatal widths were significantly decreased in transgenic plants. Lower level of WT, consistent with the stomatal pore size of the Fig. 2E.

Considering the relative width increases in the chamber conductance of the stomatal pore, we further conducted an experiment in which we used a humidifier to exclude the influence of air humidity. As expected, the results

showed consistency with the chamber experiments (Fig. 1). All plants were severely impacted due to the partial loss of water during the 10-day air humidity treatment (Supplemental Fig. S3; Fig. 3). After rewatering for 7 d, we observed the higher survival rate in WT (Fig. 3A) and transgenic plants (Fig. 3B), as well as the significantly higher RWC of the leaves of the WT after during the air humidity stress (Fig. 3C). Moreover, we measured the dynamics of photosynthesis rate of the stomatal conductance during the air humidity treatment (Fig. 3D). Transgenic plants performed higher photosynthesis rate of the stomatal conductance under surface water conditions. Nevertheless, the photosynthesis rate of the stomatal conductance of all plants were equally declined during the

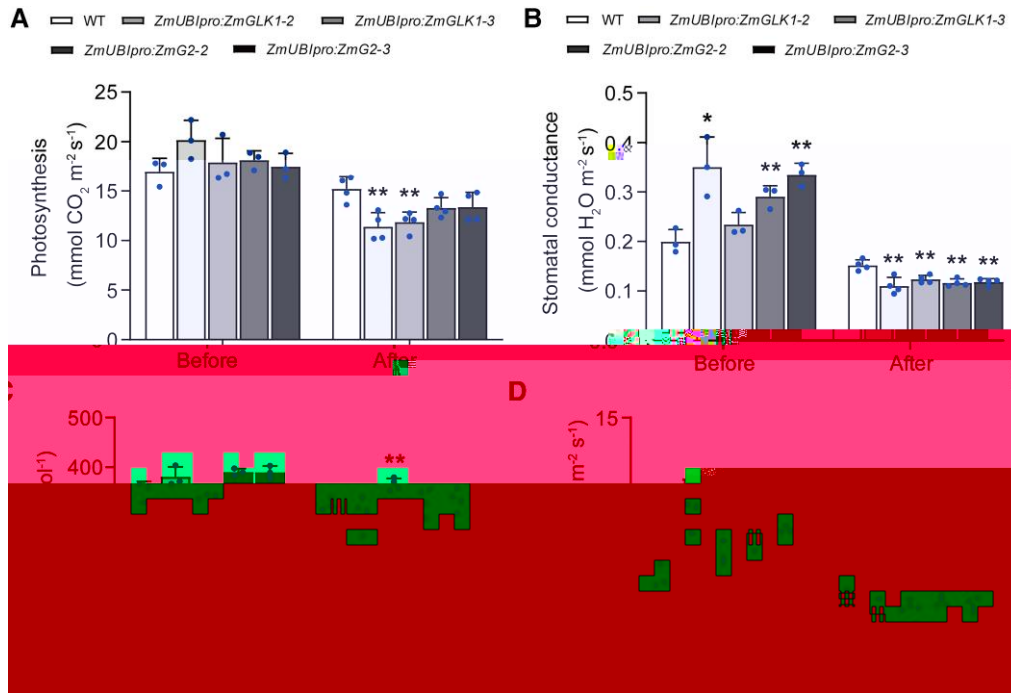


**Figure 3.** ZmGLK1-3 and ZmGLK2-3 overexpression in rice prevents water loss and increases survival during drought. **A)** Phenotypes of WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants during drought. Sixty-day-old WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants were grown in the greenhouse under well-watered conditions. Sixty-day-old rice plants were transferred to pots containing 10 cm of water for 10 days before drought. After 10 days of drought, the rice plants were transferred to pots containing 7 cm of water, respectively. Scale bar: 10 cm. **B)** Survival rates of WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants after 10 days of drought. All were by 7 days of recovery. **C)** The RWC of WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants after 0 and 7 days of drought and 7 days of recovery. **D, E)** Dynamic changes of photosynthesis rate. **D)** Photosynthetic rate. **E)** WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants during drought. Data are presented as the mean  $\pm$  SD for 3 to 6 biological replicates. \* < 0.05, \*\* < 0.01 Student's t-test.

drought deeper, which indicates that ZmUBIpro:ZmGLK1-2 and ZmUBIpro:ZmG2-2 rice plants present a lower photosynthesis rate after 2.5 h of drought. These results further clearly indicate that ZmGLK1-3 and ZmGLK2-3 overexpression was effectively induced by water deficiency in WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants, further confirming the elevated drought tolerance.

**Regulation of photosynthesis and ABA-mediated gene expression in ZmUBIpro:ZmGLK1 and ZmUBIpro:ZmG2-2 rice plants**  
 During drought, both the photosynthesis rate and the regulation of stomatal movement respond to drought

Chen et al. (2020). To further dissect the underlying mechanism of stomatal closure and photosynthesis reduction by ZmGLK1-3 and ZmGLK2-3 overexpression, we first determined whether the photosynthesis and stomatal closure were induced by BABA. After 2.5 h of applying 100  $\mu$ M BABA, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants showed significantly decreased photosynthesis rates, compared with the reduced stomatal conductance (Fig. 3, D and B). Accordingly, the chlorophyll fluorescence were significantly lower in ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants compared with the WT after BABA application (Fig. 3, C and D). The effects of exogenous BABA application on photosynthesis and stomatal conductance in



**Figure 4.** Exogenous B application reduced the photosynthesis rate and stomatal conductance in rice plants overexpressing ZmGLK1 and ZmG2 compared with the WT. **A)** Photosynthesis rates, **B)** stomatal conductance, **C)** and **D)** chlorophyll content (SPAD) of 3-week-old WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants before and after 3 h B treatment. Error bars represent standard deviation. \*  $p < 0.05$ , \*\*  $p < 0.01$  Student's *t*-test.

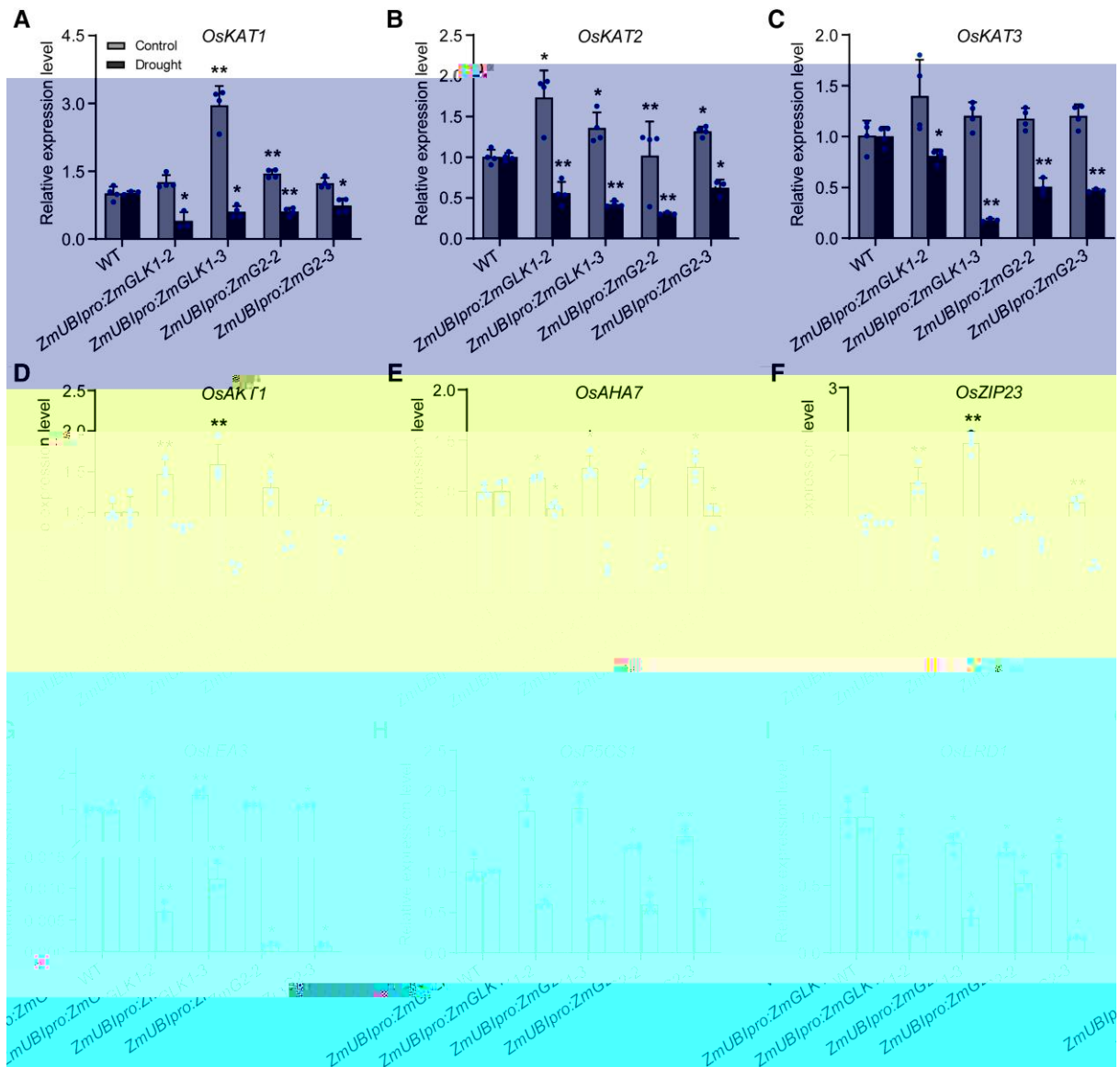
The WT rice plants under B treatment showed a significant decrease in photosynthesis rate and stomatal conductance compared with the WT. In contrast, the ZmGLK1 and ZmG2 overexpressing rice plants showed a significant increase in photosynthesis rate and stomatal conductance after B treatment.

### ZmL1 and ZmG2 overexpression reduces stomatal conductance

To further understand the mechanism of stomatal closure induced by ZmGLK1 and ZmG2 under B stress, we next compared the expression levels of several key genes associated with stomatal movement in WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, and ZmUBIpro:ZmG2-3 rice plants under control and B stress conditions. Under control conditions, several key genes were highly expressed in the rice plants compared with the WT but primarily in response to B stress. These common genes include *PC*, *OST1*, *SLAC1*, *OST2*, *OST3*, *OST4*, *OST5*, *OST6*, *OST7*, *OST8*, *OST9*, *OST10*, *OST11*, *OST12*, *OST13*, *OST14*, *OST15*, *OST16*, *OST17*, *OST18*, *OST19*, *OST20*, *OST21*, *OST22*, *OST23*, *OST24*, *OST25*, *OST26*, *OST27*, *OST28*, *OST29*, *OST30*, *OST31*, *OST32*, *OST33*, *OST34*, *OST35*, *OST36*, *OST37*, *OST38*, *OST39*, *OST40*, *OST41*, *OST42*, *OST43*, *OST44*, *OST45*, *OST46*, *OST47*, *OST48*, *OST49*, *OST50*, *OST51*, *OST52*, *OST53*, *OST54*, *OST55*, *OST56*, *OST57*, *OST58*, *OST59*, *OST60*, *OST61*, *OST62*, *OST63*, *OST64*, *OST65*, *OST66*, *OST67*, *OST68*, *OST69*, *OST70*, *OST71*, *OST72*, *OST73*, *OST74*, *OST75*, *OST76*, *OST77*, *OST78*, *OST79*, *OST80*, *OST81*, *OST82*, *OST83*, *OST84*, *OST85*, *OST86*, *OST87*, *OST88*, *OST89*, *OST90*, *OST91*, *OST92*, *OST93*, *OST94*, *OST95*, *OST96*, *OST97*, *OST98*, *OST99*, and *OST100*. These results demonstrate that ZmGLK1 and ZmG2 overexpression primarily affects the expression levels of stomatal movement genes when subjected to B stress.

Gene ontology (GO) analysis was conducted to identify the biological processes enriched in the ZmGLK1 and ZmG2 overexpressing rice plants. The results showed that the most enriched GO terms were related to stomatal movement, including stomatal closure, stomatal opening, and stomatal conductance. These results are consistent with the observed increase in stomatal conductance in the ZmGLK1 and ZmG2 overexpressing rice plants under B stress.

In addition, we performed a transcriptome analysis of the ZmGLK1 and ZmG2 overexpressing rice plants under B stress. The results showed that the ZmGLK1 and ZmG2 overexpressing rice plants had a significantly higher number of differentially expressed genes (DEGs) compared with the WT. The DEGs were primarily enriched in biological processes related to stomatal movement, including stomatal closure, stomatal opening, and stomatal conductance. These results are consistent with the observed increase in stomatal conductance in the ZmGLK1 and ZmG2 overexpressing rice plants under B stress.



**Figure 5.** Relative expression levels of genes in rice under drought stress in WT, ZmUBIpro:ZmGLK1-2, ZmUBIpro:ZmGLK1-3, ZmUBIpro:ZmG2-2, ZmUBIpro:ZmG2-3 rice under normal conditions and after 7 d of drought stress. Expression levels of (A) *OsKAT1*, (B) *OsKAT2*, (C) *OsKAT3*, (D) *OsAKT1*, (E) *OsAHA7*, (F) *OsZIP23*, (G) *OsFA3*, (H) *OsPDS1*, and (I) *OsLAD1*. Gene expression levels were measured with RT-qPCR in the leaves of 3-week-old rice plants grown in soil under normal conditions or drought stress for 7 d. Drought stress was induced by withholding water for 7 d. Data are presented as the mean  $\pm$  SD from 3 biological replicates. \* < 0.05, \*\* < 0.01 Student's *t*-test.

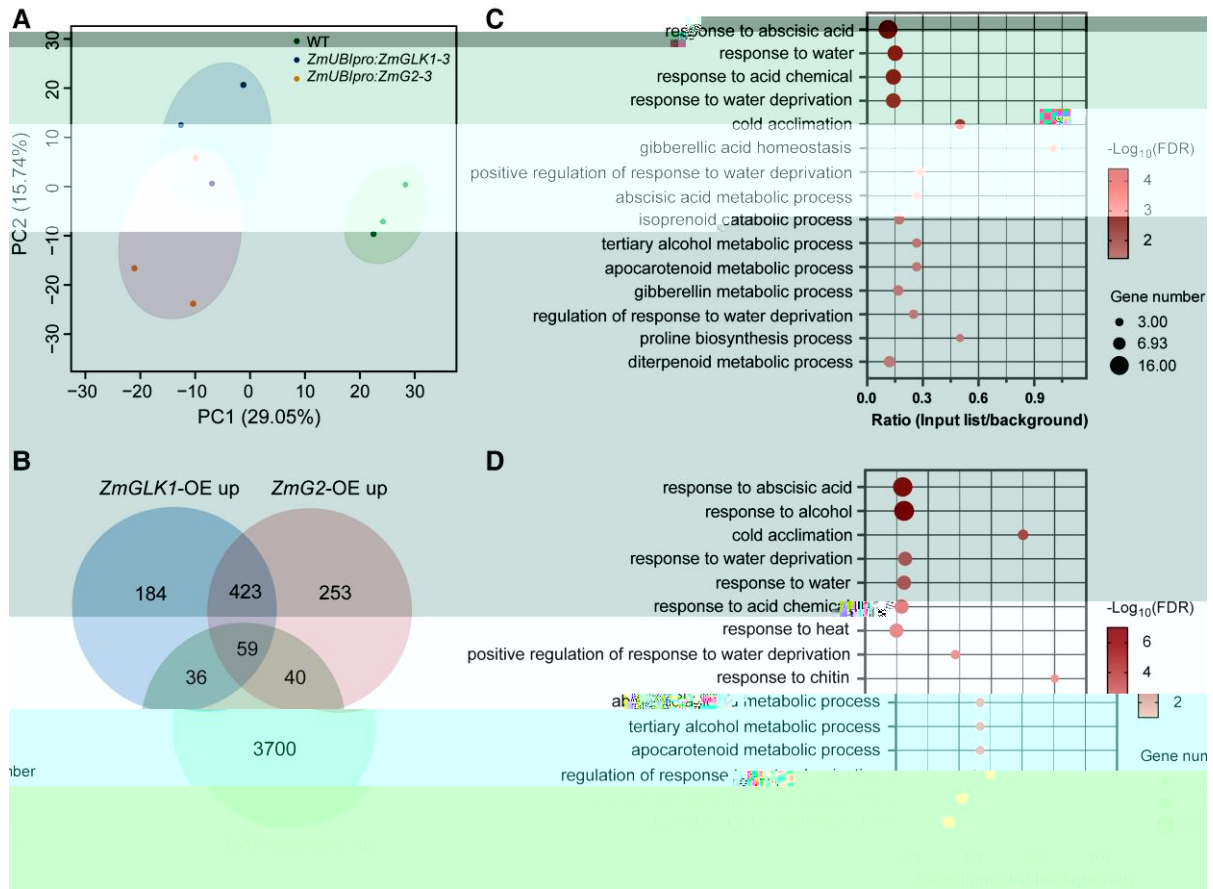
in plants overexpressing *ZmGLK1* or *ZmG2-3* (Fig. 6B; Supplemental Table S1). We then identified upregulated DEGs were significantly downregulated in rice under drought stress by using bioinformatics analysis. Therefore, these genes were identified as potential drought stress-related genes in rice, including rice genes

*OsKAT1*, *OsKAT2*, *OsKAT3*, *OsAKT1*, *OsAHA7*, *OsZIP23*, *OsFA3*, *OsPDS1*, and *OsLAD1*. The gene expression from RNA-seq of these genes was primarily higher in rice under drought stress (Fig. 7, E & F). Further reverse transcription

quantitative PCR (RT-qPCR) analysis verified that these genes were highly induced in rice under drought stress conditions (Fig. 7, I & L). These putative drought stress-related genes may contribute to enhance drought tolerance by enhancing protein synthesis when suffering from water deficit.

### Discussion

GL TFs have long been recognized as the most important regulatory factors for plant growth and photosynthesis. In this study, we have identified a number of novel genes in rice that are highly induced in rice under drought stress. These genes may contribute to enhance drought tolerance by enhancing protein synthesis when suffering from water deficit.



**Figure 6.** Transcriptomic analysis of WT, ZmGLK1-OE, and ZmG2-OE plants. **A** PCA plot of gene expression in WT, ZmGLK1-OE, and ZmG2-OE plants. **B** Venn diagram showing unique and shared DEGs upregulated in ZmGLK1-OE and ZmG2-OE plants. **C** and **D** GO functional enrichment analysis of upregulated DEGs in ZmGLK1-OE and ZmG2-OE plants, respectively. Bubble size indicates the number of DEGs in the category; bubble color indicates the  $-\log_{10}$  FDR value; and the  $x$ -axis indicates the  $-\log_{10}$  FDR value.

Ross et al. 2001; Wells et al. 2009; Powell et al. 2008. In rice, ectopic expression of *OsDRE1* genes in Arabidopsis promotes expression of stress-responsive genes in the leaf and root, and increases chlorophyll and carotenoid levels in rice vascular sheath cells (Wang et al. 2017). Previously, we have shown that overexpression of *ZmGLK1* and *ZmGLK2* genes in rice increases biomass yield and results in improved photosynthetic capacity and reduced photo-inhibition under high light fluctuation conditions (Liu et al. 2020).

In the present study, we investigated the overexpression of *ZmGLK1* and *ZmGLK2* genes in rice and their effect on rice yield and stress tolerance. Specifically, when plants were grown under stress conditions, we observed similar stress tolerance in rice plants overexpressing *ZmGLK1* or *ZmGLK2* compared with WT plants (Fig. 2, B and E). These results were consistent with the previous studies showing that overexpression of *ZmGLK1* and *ZmGLK2* genes in rice increases biomass yield and results in improved photosynthetic capacity and reduced photo-inhibition under high light fluctuation conditions (Liu et al. 2020).

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### Spontaneous emergence of WT sc in cocultures

Red lentils were dissected from control and treated cultures. For plating, 100 mg of milled lentils (3 x 3 mm pieces, excluding the veins) were placed in a 250 ml flask containing 100 ml of 0.1 M phosphate buffered pH 7.0. The lentils were washed with 1% sodium hypochlorite. After washing, the lentils were placed in 0.1 M phosphate buffered, samples were collected for 15 min, 30 min, 1 h, 2 h, 4 h, 6 h, 8 h, 10 h, and 100% for 15 min. Then, samples were collected using a centrifuge, pelleted, and stored in the sample storage buffer. The samples were observed under phase contrast microscope using a SU 8010 scanning electron microscope. The size, number, and pressure of the samples were calculated using ImageJ software.

### Time course of exogenous ABA response

The uppermost explants were cultured in control and treated conditions. Grunt samples (100 mg) were extracted with 10 ml of 100% methanol. Samples were centrifuged and the resulting supernatant was evaporated. The combined extracts were purified on a C18 silica column and dried in a rotary evaporator. The residue was dissolved in 100 µl of 50% acetonitrile. The samples were analyzed using a reversed-phase HPLC-MS/MS system as described by Liu et al. (2018).

### Exogenous ABA response

Fifty red lentil seeds were surface-sterilized with 100 mg of 100% methanol and 0.5% [v/v] Tween 20 surfactant. The lentils were washed. The volume of 100% methanol applied was consistent between seeds. After 2.5 h, the explants were exchanged in 100 µl of water and were evaluated as described above.

### RNA extraction and RT-qPCR

The uppermost fully explanted lentils were harvested from 3-week-old red lentil seeds in control and treated conditions. Samples were flash-frozen in liquid nitrogen and stored at -80°C. Total RNA was extracted with TRIzol reagent. RNA purities were evaluated using a Nanodrop 2000 spectrophotometer. Thermofisher Scientific, USA. Total RNA was reverse transcribed from 1 µg of total RNA per sample using the RevertAid First-Strand cDNA Synthesis kit (ThermoFisher Scientific, USA). RT-qPCR was performed using OD SYBR Green mix with the ROX TOYOBO in the ABI QuantStudio 6 Flex instrument. Relative gene expression levels were calculated using the  $2^{-\Delta\Delta CT}$  method of Livak and Schmittgen (2001) with 3 biological replicates. The lentils were grown using the same protocol. Primers are listed in Supplemental Table S1.

### RNA sequencing

Three fully explanted lentils were harvested from 3-week-old red lentil seeds in control and treated conditions. Total RNA was extracted with TRIzol reagent. RNA purities were assessed with the NanoDrop 2100. The libraries were prepared using the TruSeq Library Prep v2 kit (Illumina, USA) with 3 biological replicates per line. The resulting libraries were sequenced on the Illumina HiSeq X Ten sequencing platform. After removing the adapter sequences and low quality reads, clean reads were mapped to the Arabidopsis thaliana cv. Nipponbare reference genome using the HISAT2 (Mao et al. 2015) and Bowtie2 (Langmead et al. 2009). Gene expression levels were calculated in reads per kilobase transcript per million mapped reads (RPKM) using cuffdiff. DEGs were identified with the "DESeq" R package. The thresholds for classification of a DEG in the transcript lines compared to the WT were  $p < 0.05$  and  $|\log_2(\text{fold change})| > 1$ .

### DAP sequencing analysis

The full length cDNA sequences of the genes were amplified from cDNA of the mature seeds in B73. Each sequence was recombined into the pX-HLO vector using LR Cloning II In vitro. The pX-HLO ZmGL1 and pX-HLO ZmG2 primers were generated using 500 ng of each of the pX-HLO ZmGL1 and pX-HLO ZmG2 plasmids. ScnVOE



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