

Mae OLDEN-LIE loses its seedling tolerance by homozygosity

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Abstract

Drought has become one of the most severe abiotic stresses experienced by agricultural production across the world. Plants respond to water deficit via stomatal movements in the leaves, which are mainly regulated by abscisic acid (ABA). In a previous study from our lab, we showed that constitutive expression of maize *ZmOLDEN-LIE* (*ZmOL*) transcription factors in rice (*Oryza sativa*) can improve stomatal conductance and plant photosynthetic capacity under field conditions. In the present study, we uncovered a function of *ZmOL* regulation of stomatal movement in rice during drought stress. We found that elevated drought tolerance in rice plants overexpressing *ZmOL* or *ZmOL2* is conferred by rapid ABA-mediated stomatal closure. Comparative analysis of RNA-sequencing (RNA-seq) data from the rice leaves and DNase-seq analysis of DNase-seq results obtained *in vitro* revealed that *ZmOL* played roles in regulating ABA-related stress responsive pathways. Four upregulated genes closely related to abiotic stress tolerance in strongly drought peaks in the DNase-seq data were identified as putative targets of *ZmOL1* and *ZmOL2* in rice. These results demonstrated that maize *OL* plays an important role in regulating stomatal movements to coordinate photosynthesis and stress tolerance. This trait is a valuable target for breeding drought-tolerant crop plants without compromising photosynthetic capacity.

deficit or are exposed to other environmental stimuli, including high temperature, low relative humidity, high CO₂ levels, and pathogens, stomata are rapidly closed, especially in guard cells (Sera et al. 2018). This dynamic movement is driven by turgor pressure changes in the guard cells, as a result of the activation of anion channels and the inhibition of anion efflux channels, which are coded by

genes (Miyamoto et al. 2010). The efflux of anions and small metabolites, including Cl⁻, NO₃⁻, and malate, causes membrane depolarization to activate the outwardly rectifying K⁺ channel and Cl⁻ channels. K⁺ efflux, further reducing turgor pressure in the guard cells and leading to the stomatal closure (Pardey et al. 2007). Under water deficit conditions, the phytohormone abscisic acid (ABA) plays as the primary regulator of stomatal movement to prevent water loss, which elevates ABA levels are controlled by a precise balance between biosynthesis and catabolism, which is also influenced by transport and catabolic processes (Ushiro et al. 2007; Hsu et al. 2011). Biosynthesis starts from C₆ carotenoids to form xanthophylls (e.g., violaxanthin and zeaxanthin); a C₁₅ terpenoid, xanthoxin, is formed in the plastids via oxidative cleavage catalyzed by zeaxanthin epoxidase (ZEP). NCED1 in the cytosol is the exported to the cytosol and converted to ABA through a 2-step reaction via xanthoxin dehydrogenase/reductase 1 (SDR1/BDT) and ribulose biphosphate dehydrogenase 3 (RBDH3) (Seo and Yoshida 2000; Ory and Zhou 2003).

Transcription factors (TFs) are crucial regulators of many biological processes, including responses to environmental signals and hormone regulation. These regulatory functions are accomplished through binding to specific DNA elements in the promoter regions of target genes (Todorova et al. 2017). Numerous abiotic stress responsive TFs have been identified in plants; for instance, WRKY, MYB, and DREB/CBF TFs have all been reported as key regulators of plant stress responses (Miyamoto et al. 2011). OLDEN-LIKE 1 (OLEN1) TFs are directly acting transcriptional activators of chloroplast development and biogenesis (Ross et al. 2001; Wang et al. 2013) and play important roles in regulating nuclear photosynthesis related genes (Chen et al. 2016). In maize (Z. m.), ZmOLEN1 genes

have shown differential expression patterns between mesophyll cells and the bundle sheath (Huang et al. 2008; Chang et al. 2017). Ectopic overexpression of maize ZmOLEN1 gene reduces chloroplast development in bundle sheath cells and activates intracellular plasmodesmal connections, considering the key step in forming the tripartite protoperchloroplast anatomy, the transition from C₃ to C₄ photosynthesis (Wang et al. 2017). Our previous study from our lab showed that constitutive ZmOLEN1 expression in rice leads to increased xanthophyll content and further mitigates the photo-inhibition under high light conditions, resulting in enhanced photosynthetic capacity with higher stomatal conductance and improved biomass and grain yield in the field (Liu et al. 2020). Moreover, ZmOLEN1 also functions in abiotic stress responses (Huang et al. 2019) and pathogen resistance

(Murmu et al. 2017); for example, ZmOLEN1 affects stomatal movement in rice (Liu et al. 2020). In this study, we uncovered the dual function of maize ZmOLEN1 and the ectopic overexpression of ZmOLEN1 in rice conferred improved drought tolerance by promoting stomatal closure response to water deficit while maintaining high stomatal conductance to obtain efficient photosynthesis in the sufficient water available. We further showed that rapid stomatal movement is mediated by B-kinase involved pathway under drought conditions. These results suggest that ZmOLEN1 may be promising candidate for breeding rice varieties with high stomatal flexibility and sustainable yield, which could strongly improve agricultural production and increase food security in the context of climate change.

Results

Zm L 1 and ZmOLEN1 confer improved drought tolerance in rice

In our previous study, ZmOLEN1 transgenic rice lines constitutively expressing ZmOLEN1 were driven by the maize promoter performed improved photosynthesis rates and higher stomatal conductance (Liu et al. 2020). We further explored the stomatal responses of transgenic rice plants to water deficit in pot experiments in the growth chamber. Surprisingly, transgenic rice plants exhibited stronger drought tolerance than wild-type (WT) plants after recovery from a 10 d drought treatment (Fig. 1). Specifically, the survival rates of WT, transgenic, and control plants were 53.0% to 67.0% after the 6 d recovery period, which were significantly higher than the WT (47.3%; Fig. 1B). Moreover, the relative water content (RWC) of the leaves of WT and transgenic plants ranged from 87.7% to 95.3% before drought but decreased to 73.1% in the WT after water withheld for 7 d. In comparison, transgenic plants maintained relatively high RWC, especially after 10 d drought, ranging from 86.1% to 90.9%. After 10 d of drought stress, the RWC values of WT and control plants decreased to 11.6% to 17.9%, which were significantly lower than those of transgenic plants (47.5% to 18.6%; Fig. 1C). These results indicated Zm L 1 and ZmOLEN1 both conferred higher capacities for water conservation and thus drought tolerance.

We next tested the growth performance of WT, transgenic, and control rice plants to PE-induced osmotic stress as a drought simulation. After growth in 20% PE (6000 for 10 d), transgenic plants showed less leaf and chlorosis compared to the WT (Supplemental Fig. S1). The maximum quantum efficiency of photosystem II (PSII) (F_v/F_m) as measured as an important indicator of plant physiological state under stress conditions, and the

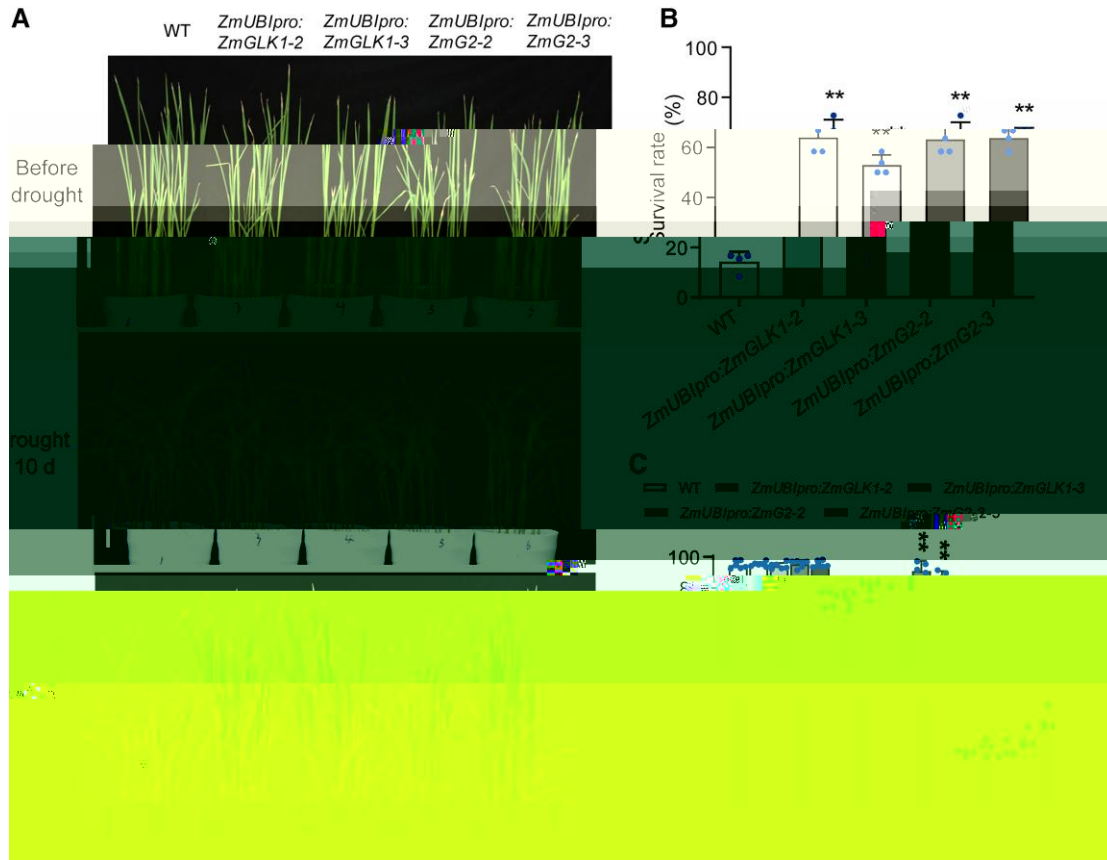


Figure 1. Overexpression of *ZmUBIpro* and rice genes increased drought tolerance. **A)** Phenotypes of WT, *ZmUBIpro:ZmGLK1-2*, *ZmUBIpro:ZmGLK1-3*, and *ZmUBIpro:ZmG2-2* rice plants during drought stress. Three-week-old WT, *ZmUBIpro:ZmGLK1-2*, *ZmUBIpro:ZmGLK1-3*, and *ZmUBIpro:ZmG2-2* rice seedlings were soil-drought stressed by withholding water for 10 d and then transferred for a 6 d recovery period. The upper, middle, and lower panels show representative plants before drought stress, after 10 d of drought stress, and after the 6 d recovery, respectively. Scale bar = 1 cm. **B)** Survival rates of WT, *ZmUBIpro:ZmGLK1-2*, *ZmUBIpro:ZmGLK1-3*, and *ZmUBIpro:ZmG2-2* rice plants after 10 d of drought stress followed by 6 d of recovery. Data are presented as the mean \pm SD from 3 biological replicates. **C)** The RWC of WT, *ZmUBIpro:ZmGLK1-2*, *ZmUBIpro:ZmGLK1-3*, and *ZmUBIpro:ZmG2-2* rice leaves after 0, 7, and 10 d of drought stress. Data are presented as the mean \pm SD.

10 d of PE treatment (Supplemental Fig. S1B). We also monitored changes of RWC in rice seedlings during PE treatment. The results showed that the transgenic plants retained significantly higher RWC compared to the WT. Specifically, RWC values were 11.7% to 19.1% and 9.5% to 19.7% higher in *ZmUBIpro:ZmGLK1-2* and *ZmUBIpro:ZmGLK1-3* rice plants, respectively, compared to the WT (Supplemental Fig. S1C). These results together indicated that overexpression of *ZmUBIpro* and rice genes significantly improve the tolerance to drought and osmotic stress.

ZmL1 and ZmG2 regulate stomatal closure and drought stress response
 To further investigate the physiological mechanism underlying the elevated drought tolerance conferred by *ZmL1* and *ZmG2*, we evaluated the effects of drought treatment on stomatal traits of rice seedlings in the pots. The rosette chamber, since stomata are the main channels for gas exchange and water respiration in plants, serving as the dominant pathway to photosynthesis under drought. We therefore first measured

stomatal conductance and photosynthesis-related parameters under control conditions using a LICOR 6400 T portable photosynthesis system. The results revealed significantly higher stomatal conductance (g_m) and photosynthesis rate (P_n) in rice seedlings (0.118–0.139 and 0.16–0.131, respectively) compared to the WT (0.083) under control conditions; while the transgenic plants also performed higher photosynthesis rates, intercellular CO₂ concentrations (C_i), and transpiration rates (Supplemental Fig. 5), as the plants grew in the field (Luo et al. 2009). In contrast, after 7 d of drought treatment, g_m and P_n in rice plants displayed sharply decrease (stomatal conductance: 0.06–0.073 and 0.057–0.059, respectively), whereas that of WT remained relatively stable under drought conditions (0.087; Supplemental Fig. 5B). The photosynthesis rates, C_i , and transpiration rates showed correspondingly declines in rice plants during water deprivation (Supplemental Fig. 5, C, and D). We next compared the stomatal traits between WT and *ZmUBIpro:ZmGLK1-2* or *ZmUBIpro:ZmGLK1-3* rice plants under

both control and drought conditions. Transgenic plants presented higher stomatal density in the leaves but had significantly shorter stomata compared to the WT regardless of conditions (Fig. 2). In contrast, surprisingly, the stomata were prominently wider in the transgenic plants compared to the WT under control conditions (Fig. 2D), whereas under drought stress, the stomatal widths were significantly decreased in transgenic plants to a lower level than WT, consistent with the stomatal aperture data (Fig. 2E).

Considering the relative low light intensity in the growth chamber could lead to the stomatal closure, we further conducted a pot experiment in the greenhouse. To guardly hit to exclude the influence of low light as expected, the results

showed consistency with the chamber experiment (Fig. 1).

All plants were severely impaired due to the rapid loss of water during the 10 d drought duration (Supplemental Fig. S3; Fig. 3). After re-watering for 7 d, we observed the higher survival rate in the transgenic plants (Fig. 3B), as well as the significantly higher

RWC of leaves than WT either during the drought or the recovery stage (Fig. 3C). Moreover, we monitored the dynamics of photosynthesis rate and stomatal conductance throughout the duration of drought and thereafter (Fig. 3D).

In transgenic plants performed higher photosynthesis rate and stomatal conductance under sufficient water

drought deeper, of which : and
: rice plants presented lower photosynthesis
rate and the stomatal conductance compared to the WT
Fig. 3, D and E. These results together clearly indicated

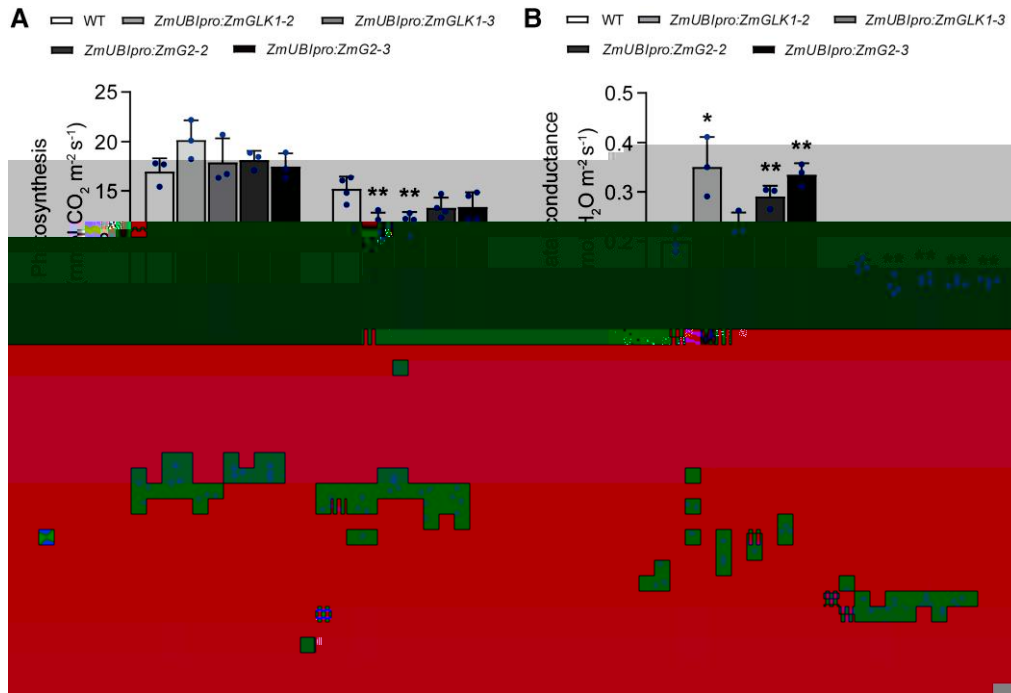


Figure 4. Exogenous B application reduced the photosynthesis rate and stomatal conductance in rice plants overexpressing ZmL1 or Zm2 compared to the WT. **A)** Photosynthesis rates, **B)** stomatal conductance, **C)** and **D)** transpiration rates of 3-week-old WT, ZmL1, Zm2, ZmL1+Zm2, ZmL1+Zm2+ZmGLK1-2, ZmL1+Zm2+ZmGLK1-3, ZmL1+Zm2+ZmG2-2, and ZmL1+Zm2+ZmG2-3 rice plants 3 h before or 3 h after B treatment. D data are shown as the mean \pm SD from 3 biological replicates. * $P < 0.05$, ** $P < 0.01$. Student's *t* test.

the WT and transgenic plants mimicked the results obtained from the drought stress treatments, which indicated the utilization of rapid stomatal closure response to water deficit stress conferred by ZmL1 and Zm2 is B mediated.

ZmL1 and Zm2 regulate stomatal closure

To further understand the molecular mechanisms regulated by ZmL1 under drought stress, we next compared the expression levels of several genes associated with stomatal movement in WT, ZmL1, Zm2, ZmL1+Zm2, ZmL1+Zm2+ZmGLK1-2, ZmL1+Zm2+ZmGLK1-3, ZmL1+Zm2+ZmG2-2, and ZmL1+Zm2+ZmG2-3 rice plants under control and drought stress conditions. Under control conditions, several key genes are highly expressed in the transgenic plants compared to the WT but profoundly downregulated in response to drought stress. These comprised genes encoding proteins associated with guard cell K⁺ and Cl⁻ channels (3, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000).

Gene ontology (GO) transcriptome analysis was also conducted in WT, ZmL1, Zm2, ZmL1+Zm2, ZmL1+Zm2+ZmGLK1-2, ZmL1+Zm2+ZmGLK1-3, ZmL1+Zm2+ZmG2-2, and ZmL1+Zm2+ZmG2-3 rice plants 3 h after B treatment to investigate the global effects of ZmL1 and Zm2 introduced by B, especially

on stomatal movement. WT plants clearly showed distinct expression patterns compared to the transgenic plants, as demonstrated by the clear separation in the principal component analysis (PCA; Fig. 6A). Specifically, after B treatment, 70 and 775 genes were significantly upregulated in ZmL1 and Zm2 plants, respectively, compared to the WT, of which 48 genes were upregulated both transgenically (Fig. 6B). Gene ontology (GO) term enrichment analysis revealed that the upregulated differentially expressed genes (DEGs) in ZmL1 and Zm2 plants included multiple biological processes but primarily the B and water deprivation pathways (Fig. 6, C and D). Next, we performed DNA affinity purification (seq) (DAP-seq) analysis to identify genes directly regulated by the ZmL1/2 TFs. This analysis revealed 6,601 and 6,565 putative binding sites of ZmL1 and Zm2 in the rice genome, respectively, with more than half of the identified sites being bound by both ZmL1 and Zm2 (Supplemental Fig. S9). Of the 3,835 binding sites shared by ZmL1 and Zm2, 17.4% were located to promoters, 8.5% to exons, and 5.6% to intergenic regions (Supplemental Fig. S9B). Motif analysis demonstrated that the most enriched core motifs found in the ZmL1 and Zm2 binding regions were CCTCT and TTCT (Supplemental Fig. S9, C and D). Fifty genes were identified from the DAP-seq data as potential targets of ZmL1 and Zm2 in rice. We also identified from the RNA-seq data 100 RNAs differentially expressed

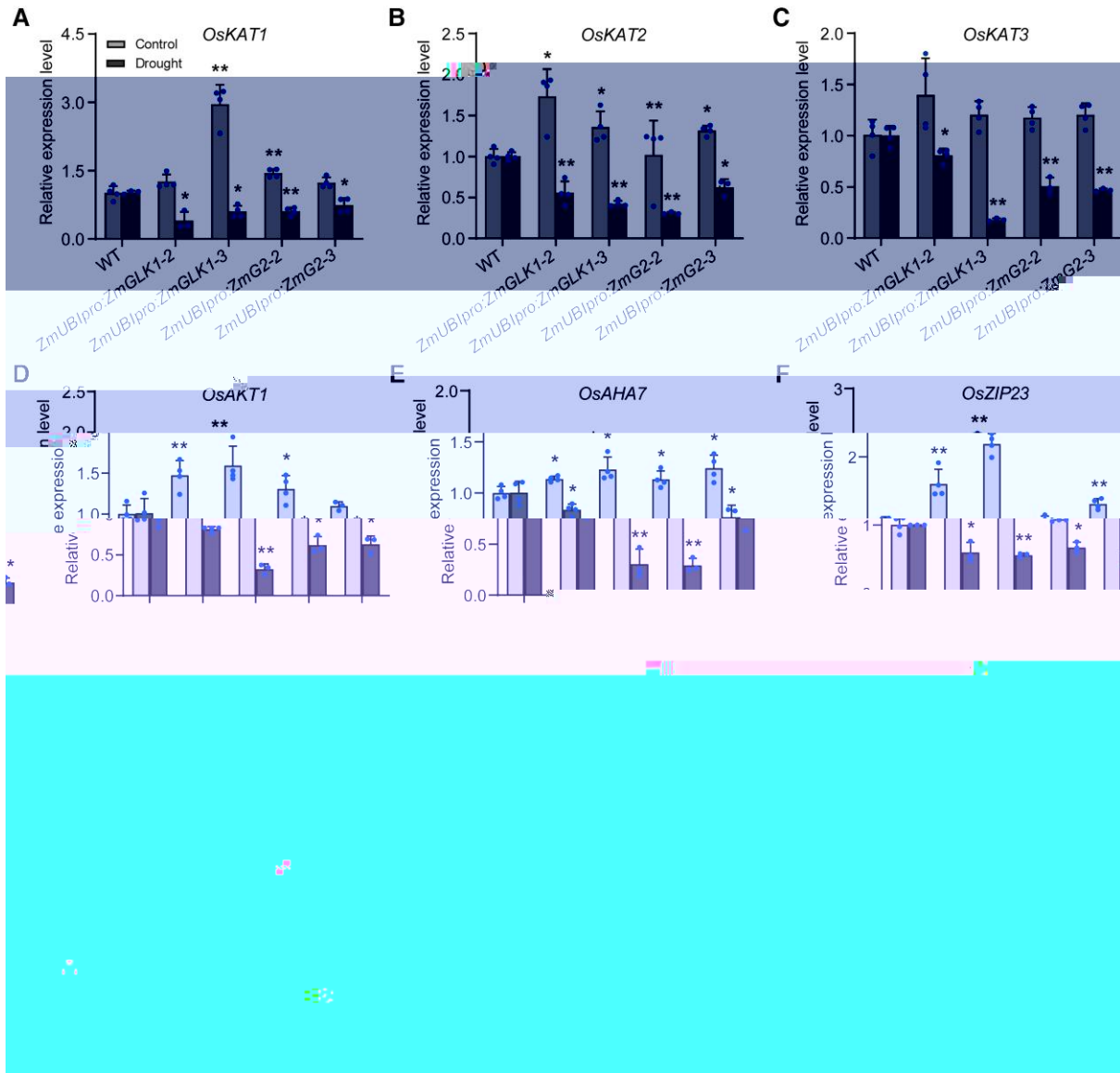


Figure 5. Relative expression levels of genes evolved stomatal movement and stomatal aperture. WT, ZmUBIpro-ZmGLK1-2, ZmUBIpro-ZmGLK1-3, and ZmUBIpro-ZmG2-2 rice under normal conditions and after 7 d of drought stress. Expression levels of (A) *OsKAT1*, (B) *OsKAT2*, (C) *OsKAT3*, (D) *OsAKT1*, (E) *OsAHA7*, (F) *OsZIP23*, (G) *ZmL1*, and (H) *Zm2* gene expression levels were measured by RT-qPCR in the leaves of 3-week-old rice plants grown in soil under normal conditions or drought stress for 7 d. Data are presented as the mean \pm SD from 3 biological replicates. * < 0.05, ** < 0.01 Student's test.

plants overexpressing *ZmL1* or *Zm2* (Fig. 6B; Supplemental Table S1). We observed upregulated DE genes were associated to abiotic stress tolerance and showed strong biological processes. The DE pathway analysis simultaneously. Therefore, these genes were identified as putative target genes of ZmL1 and Zm2 in rice, including rice genes

and *ZmL1* (Fig. 7, A to D). The gene expression from RNA-seq data of these genes is prominently higher in *ZmL1* and *Zm2* rice plants (Fig. 7, E to H). Further reverse transcripto-

quantitative-PCR (RT-qPCR) analysis verified that these genes were highly induced in *ZmL1* and *Zm2* rice under drought stress conditions (Fig. 7, I to L). These putative target genes may contribute to enhanced drought tolerance by enabling rapid stomatal movement to suffer from water deficit.

Discussion

L1 TFs have long been regarded as some of the most important regulators of chloroplast biology and photosynthetic organelle formation; they have been identified in Arabidopsis, tomato (Liu, et al. 2011), and maize

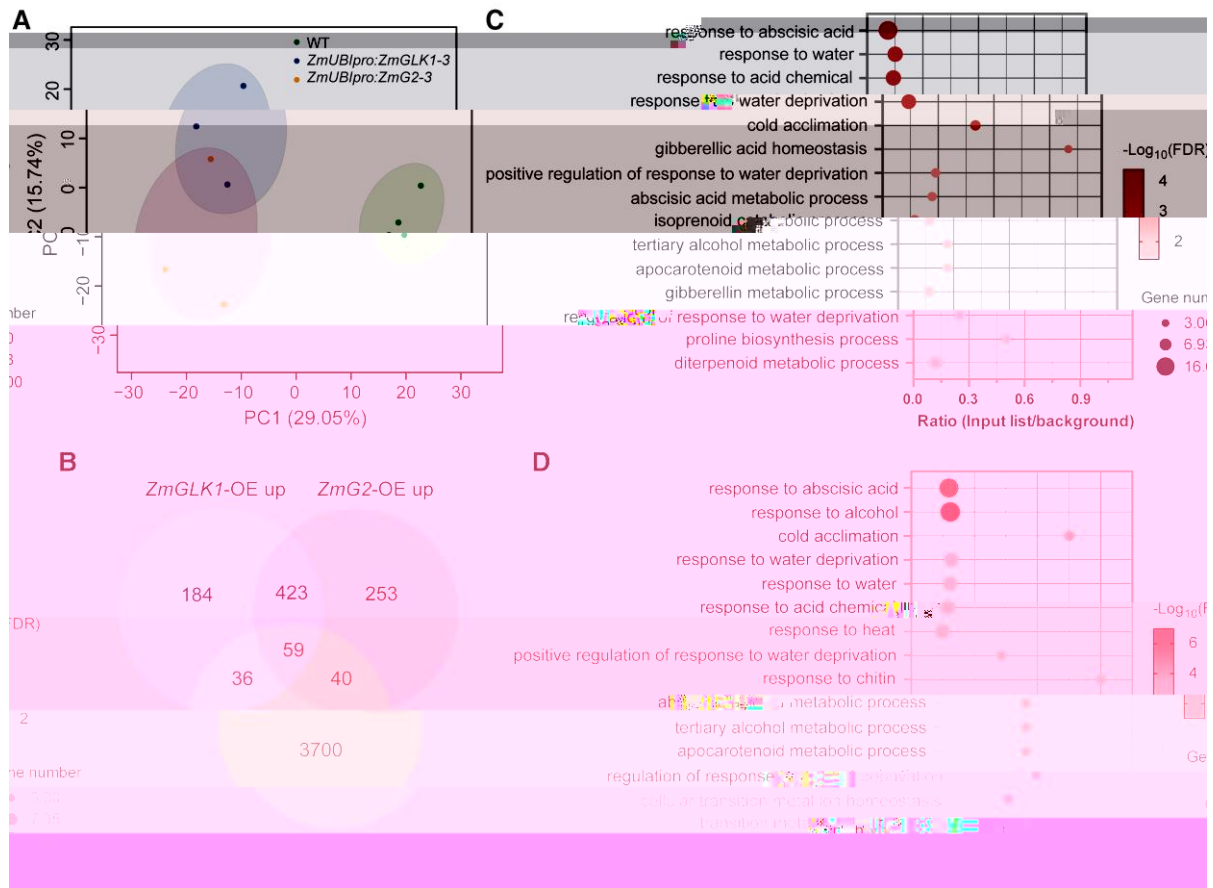


Figure 6. Transcriptomic analysis of WT, ZmGLK1-OE, and ZmG2-OE rice plants 3 h after B treatment. **A)** PCA of gene expression in WT, ZmGLK1-OE, and ZmG2-OE rice plants based on RNA-seq data. **B)** Unique and overlapping DEs upregulated in ZmGLK1-OE and ZmG2-OE rice plants compared to the WT and unique overlapping DEs downregulated in ZmGLK1-OE and ZmG2-OE rice plants. DEs were defined based on $|\log_2(\text{fold change})| > 1$ and $p < 0.05$ by DESeq2 R package. **C, D)** Functional categories for DEs upregulated in ZmGLK1-OE (**C**) and ZmG2-OE (**D**) rice plants compared to the WT. Bubble size indicates the number of DE counts in the corresponding GO category; bubble density corresponds to the $-\log_{10}$ false discovery rate (FDR) value; and the radius indicates the ratio of DEs in each GO category to all genes in the category.

Ross et al. 2001; Waters et al. 2009; Poell et al. 2011). In rice, ectopic expression of maize *ZmGLK1* and *ZmGLK2* promotes a protodermal status in the leaf anatomy, creating chloroplasts and mitochondria development in rice vascular sheath cells (Wang et al. 2017). In previous study by our lab, it is revealed that rice plants overexpressing maize *ZmGLK1* and *ZmGLK2* have increased biomass and yield as a result of improved photosynthetic capacity and reduced photo-inhibition under high and fluctuating light conditions (Liu et al. 2020).

In the present study, we uncovered that overexpression of maize *ZmGLK1* and *ZmGLK2* in rice enhanced drought tolerance by promoting stomatal closure. Specifically, the plants were more resistant under standard, well-watered conditions, as observed smaller stomatal size but higher stomatal density and stomatal aperture in rice plants overexpressing *ZmGLK1* or *ZmGLK2* compared to the WT plants (Fig. 2, B and E). These results were consistent with earlier studies showing that *ZmGLK1* overexpression led

to increased stomatal conductance in leafy rice (Liu et al. 2020), rice hairy root rice (Chen et al. 2021), and rice roots (Nagesh et al. 2016). In contrast, under drought stress, the stomata of *ZmGLK1* or *ZmGLK2* overexpressing rice plants rapidly closed (Fig. 3B and 3E), improving drought tolerance by preventing water loss. Previous studies in rice have reported that small, high density stomata close quickly, thus promoting resilience to drought stress (Cao et al. 2019; Cao et al. 2023); these prior results were consistent with those of the present study. Notably, differences in stomatal status between control and drought stressed plants as a result of *ZmGLK1* or *ZmGLK2* overexpression were directly caused by regulation of genes involved in stomatal movement, mainly *SLAC1* and *OST1* (TPase) (Liu et al. 2020; Fig. 5). Upregulation of *SLAC1* and *OST1* in rice plants by *ZmGLK1* or *ZmGLK2* overexpression under normal conditions is like the previous study in rice roots showing that *ZmLs* positive regulation of *SLAC1* and *OST1* genes and stomatal movement (Nagesh et al. 2016); thus, this rapid

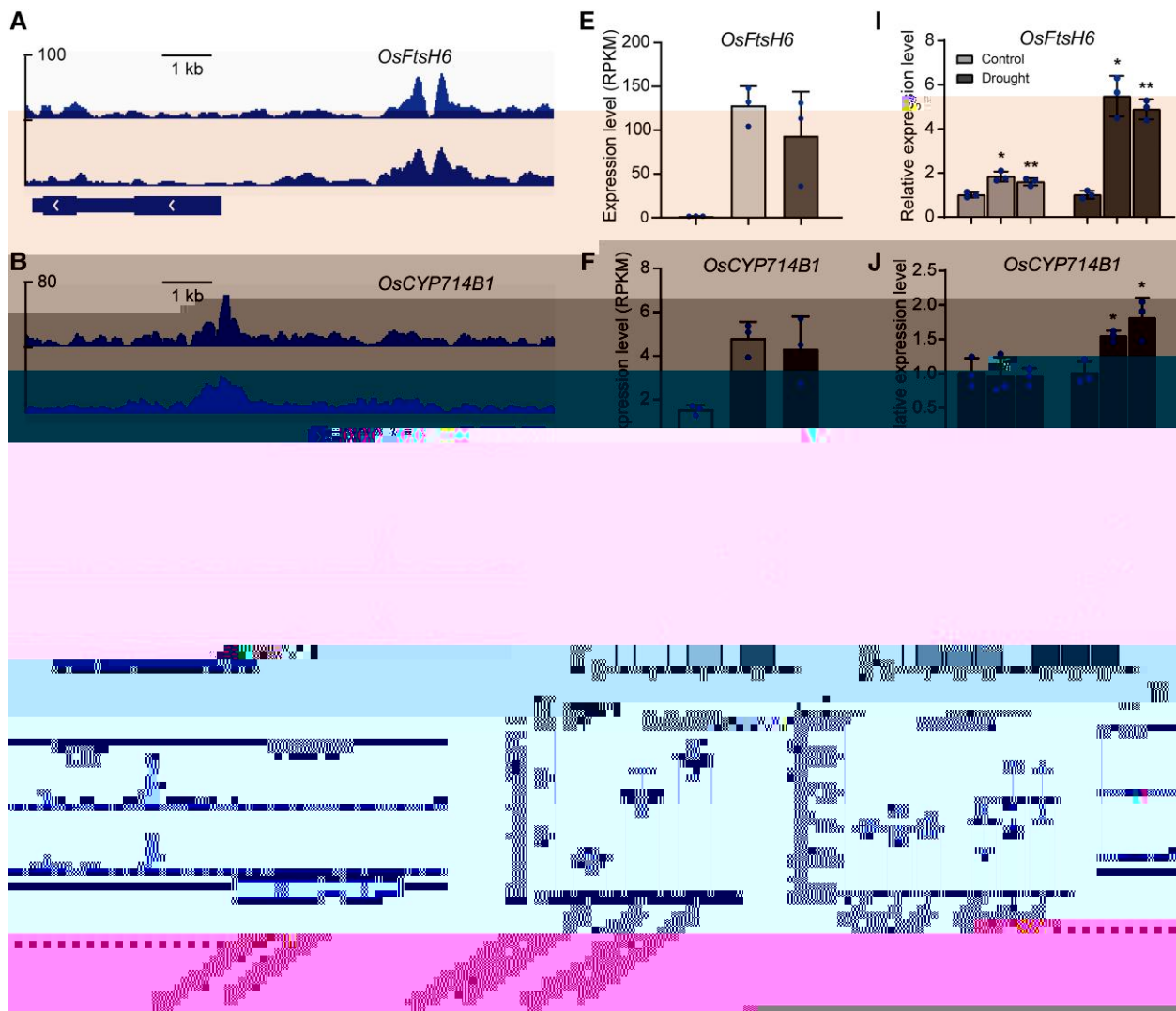


Figure 7. Putative *Zm L1* and *Zm2* target genes. **A to D)** DNase-seq indicated that *Zm L1* and *Zm2* preferentially bound to the promoters of **A)**, **B)**, **C)**, and **D)**. **E to H)** Expression levels of **E)**, **F)**, **G)**, and **H)** WT, rice, and rice overexpressing lines were determined with RNA-seq analysis. Gene expression was calculated as RPKM. **I to L)** Relative expression levels of **I)**, **J)**, **K)**, and **L)** WT, rice, and rice overexpressing lines under drought stress were determined with RT-qPCR. Data are presented as the mean \pm SD from 3 biological replicates. * < 0.05, ** < 0.01 Student's *t*-test.

stomatal closure of transgenic plants resulted directly from a significant reduction of the expression levels of those genes under drought conditions.

Notably, we verified that the regulation of rapid stomatal closure response to water deficit is B-mediated, supported by the exogenous application of B-induced faster stomatal closure.

Lines compared with the WT (Fig. 4B), which mimicked the effects of drought stress. Our results are consistent with the previous study that suggested the fastest stomatal closure requires a high B sensitivity (Cáceres-Sobrado et al. 2019). Our results also implied that *Zm L1*s may function in the B biosynthesis pathway, as indicated by the higher B accumulation (Supplemental Fig. S5) along with the abundant expression

of several key genes involved in B biosynthesis. B biosynthesis starts with the epoxidation of exanthol and this xanthophyll precursor therefore plays an important role in B biosynthesis. We previously discovered that *Zm L1*s increase levels of xanthophylls, including exanthol and lutein (Lee et al. 2020), which may lead to the improved B biosynthesis pathway. Moreover, a study in rice probably showed that *L1*s directly activate the expression of *BSS1*, and *L1-WR10* to either epoxidatively regulates B synthesis (Kim et al. 2019), suggesting a possible regulatory role of *Zm L1*s in the B synthesis pathway. We also proposed that the GlcA esters conferred by *Zm L1*s as mentioned above may contribute to the rapid stomatal

closure. This has been demonstrated by model simulations and experimental data that major C₄ crops are capable of more rapid stomatal closure compared to C₃ crops in response to water deficit, resulting in the high water use efficiency (WUE) (McAusland et al 2016; Wang et al 2011; Oxe et al 2007). Notably, previous studies have demonstrated that slower stomatal closure rates are associated with reduced responsiveness to B and sugars compared to asperms (Lima et al 2019; Cardo Sobrinho et al 2007), while the rapid transport of ions and osmolytes between guard cells and subsidiary cells in grass species contributes to the fast stomatal movement (Chen et al 2017).

Stomatal conductance and leaf senescence

Leaves were detached from control or drought treated plants and immediately cut into 3 × 3 mm pieces, excluding the veins. Samples were directly fixed in 2.5% (v/v) glutaraldehyde, 0.1 M phosphate buffer, pH 7.0 and then fixed with 1% osmium tetroxide. After washing twice with 0.1 M phosphate buffer, samples were dehydrated gradually in each alcohol series (30%, 50%, 60%, 70%, 80%, 90%, and 100%) for 15 min each, followed by incubating in tertiary butanol for 35 min. The samples were dried using a critical point dryer, pasted on the sample stubs, and then coated with gold. Stomata were observed and photographed using a SU 8010 scanning electron microscope (Hitachi, Japan). The size, number, and aperture sizes of stomata were calculated using image software.

Protein extraction of exogenous ABA

The uppermost expanded leaves of control and drought stressed rice seedlings were detached and flash frozen in liquid nitrogen. Ground samples (100 mg each) were extracted with a 60% (v/v) methanol extraction buffer standard at 4 °C overnight. Samples were centrifuged, and the resulting supernatant was extracted again. The combined extracts were purified on a C₁₈ silica column and dried in a rotary evaporator. After resolving methanol and passing through a 0.2-µm filter, BSA was quantified on a PLCE-MS/MS system as described by Liu et al. (2017).

Exogenous ABA treatment

Forty-day-old rice seedlings in pots were sprayed with 100 µM ABA solution containing 0.5% (v/v) Tween-20 as a surfactant until the leaves were moist. The volume of ABA solution applied is consistent between seedlings. 2.5 h after treatment, leaf exchange parameters and stomatal traits were evaluated as described above.

RNA extraction and RT-qPCR

The uppermost fully expanded leaves were harvested from 3-week-old rice seedlings in pots under normal conditions or drought stress for 7 d. Samples were flash frozen in liquid nitrogen and ground to powder, and the total RNA was extracted with TRzol reagent in vitro. RNA purity and quantity were evaluated using a NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific, USA). After DNase treatment, cDNA was synthesized from 1 µg of total RNA per sample using the Revert-First Stranded cDNA Synthesis kit (Thermo Fisher Scientific, USA). RT-qPCR was performed using the OD S-BR reagent with the ROTOR OBO on a B-QuantiStudio 6 Flex instrument (Applied Biosystems, USA). Relative transcript levels were calculated with the $2^{-\Delta\Delta CT}$ method (Livak and Schmittgen, 2001) with 3 biological replicates for each treatment using the untreated control. Primers are listed in Supplemental Table S1.

RNA sequencing

At 3 h after exogenous ABA treatment, leaves were collected from 3-week-old rice seedlings in pots. Total RNA was extracted with TRzol reagent and the RNA purity was assessed with the NanoDrop 2000 Bioanalyzer (Bio-Techologies, USA). RNA-seq libraries were constructed from WT, *gla1*, and *gla2* rice plants using the TruSeq Stranded mRNA LT Sample Prep kit (Illumina, USA) with 3 biological replicates per line. The resulting libraries were sequenced on the Illumina HiSeq 2500 sequencing platform. After removing the adaptor sequences and low-quality reads, clean reads were mapped to the rice cv. Nipponbare reference genome using HIS-TOP (Li et al., 2015) and Bowtie (Langmead et al., 2009). Gene expression levels were calculated as reads per kilobase of transcript per million mapped reads (RPKM) using cuffdiffs. DE genes were detected with the DESeq2 R package. The thresholds for classification as a DE gene were the transcript levels compared to the WT were < 0.05 and $|\log_2(\text{fold change})| > 1$.

DAP sequencing analysis

The full-length coding sequences of *gla1* and *gla2* were amplified from cDNA of the maize accession B73. Each sequence was recombined to the p-rHLO vector using LR Clonase II in vitro. The rHLO Zm L1 and rHLO Zm 2 proteins were generated using 500 µg each of the p-rHLO Zm L1 and p-rHLO Zm 2 plasmids

considered significant ($P < 0.05$). Figures were generated with GraphPad Prism 8.0 and Adobe Illustrator CS3.

Accession numbers

Raw sequence data generated in this study have been deposited in the NCBI BioProject database under accession number PRJN1018861 for RNA-seq and PRJN1019016 for D-P seq. The sequence data from this article can be found in the EBI/EMBL database under the following accession numbers: EBI/EMBL: F318580 and EBI/EMBL: F318579.

Acknowledgments

We would like to thank Prof. Jonathan Lacey from Oxford University for kindly providing the rice seeds.

Author contributions

W.Z. and J.L. conceived and designed the experiments. J.L., S.W., H., and R. performed most of the experiments. Z.L. and R.P. performed the D-P seq experiment. P.W. critically commented and edited the manuscript. The manuscript was prepared by J.L., J.L., and W.Z. All authors discussed and commented on the manuscript.

Supplemental data

The following materials are available in the online version of this article.

Supplemental Figure S1. Enhanced tolerance of rice plants to drought stress induced by 0% PE 6000.

Supplemental Figure S2. Overexpression of *ZmL1* or *ZmL2* resulted in decreased stomatal conductance and photosynthetic parameters response to drought.

Supplemental Figure S3. Dynamic changes of soil water content during the drought stress-free recovery experiment.

Supplemental Figure S4. Genome-wide summary of the regulatory network downstream of *ZmL1* and *ZmL2* based on D-P seq data.

Supplemental Figure S5. Changes in chlorophyll content in WT, *ZmL1*, and *ZmL2* rice leaves under normal conditions and after 7 d of drought stress.

Supplemental Figure S6. Relative expression levels of biosynthetic genes in the leaves of WT, *ZmL1*, and *ZmL2* rice plants under normal conditions and after 7 d of drought stress.

Supplemental Table S1. Relative change of gene expression level of 50 overlapping genes from RNA-seq and D-P seq analyses.

Supplemental Table S2. Primers used for RT-qPCR.

Funding

This study was supported by grants from the National Key Research and Development Program of China

(2016 FD030010). W.Z. was supported by the Innovation Program of the Chinese Academy of Agricultural Sciences and the Elite Youth Program of the Chinese Academy of Agricultural Sciences. J.L. was supported by the National Natural Science Foundation of China (3160137).

The authors declare that they have no conflict of interests.

Data availability

The data underlying this article are available in the article and its online supplementary material.

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