SUPPLEMENTARY MATERIALs



FIGURE S1 I Expression profile of *ZmGT-3b*. (A) *ZmGT-3b* expression was rapidly and dramatically decreased after inoculation in both the resistant *qRfg1* allele (R-NIL) or the susceptible *qRfg1* allele (S-NIL), which were developed from a QTL *qRfg1* on chromosome 10 that could explain 36.6% of the total variations of maize resistance to *Fusarium graminearum* induced stalk rot (Yang et al., 2010). RCK (SCK) is the primary roots of R-NIL (S-NIL) without inoculation, R6, R18, R48 (S6, S18, S48) was the primary roots of R-NIL (S-NIL) inoculated after 6h,18h and 48h, respectively (Ye et al., 2013). (B and C) *ZmGT-3b* expressed highly in normal seedling roots, and only expressed in a few kinds of young tissues, such as primary roots, ear primordium (2-8μm), embryo at 20 DAP and presheath et al (Chen et al, 2014; Johnston 2014; Maize atlas Stelpflug 2015; Walley 2016).

Supplemental literatures

- Chen J, Zeng B, Zhang M, Xie S, Wang G, Hauck A, Lai J (2014) Dynamic transcriptome Landscape of Maize Embryo and Endosperm Development. Plant physio, 166, 972: 252-264
- Johnston R, Wang M, Sun Q, Sylvester AW, Hake S, Scanlon MJ. Transcriptomic analyses indicate that maize ligule development recapitulates gene expression patterns that occur during lateral organ initiation. Plant Cell. 2014, 26(12):4718-32.
- Stelpflug SC, Sekhon RS, Vaillancourt B, Hirsch CN, Buell CR, de Leon N, Kaeppler SM. An Expanded Maize Gene Expression Atlas based on RNA Sequencing and its Use to Explore Root Development. Plant Genome. 2016, 9(1).

Walley JW, Sartor RC, Shen Z, Schmitz RJ, Wu KJ, Urich MA, Nery JR, Smith LG, Schnable JC,
Ecker JR, Briggs SP. Integration of omic networks in a developmental atlas of maize. Science.
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FIGURE S2 I The decreased *ZmGT-3b* transcript levels, and the maize mature kernel weight and plant height analysis. (A) The transcript levels of *ZmGT-3b* were dramatically decreased in both the roots and leaves of the *GT-KD* seedlings, compared with CK seedlings, with a pair of primers from the third exon (*ZmGT-3b*-qF2: 5'- GGCAGTCGATGCAGAGGATA-3'; *ZmGT-3b*-qR2: 5'-CCTGGTGAGCAAGGTAGTGAG-3') to detect transcript level of the transformed partial cDNA of *ZmGT-3b*. Values are the mean \pm SD (n = 3). (B) The one-hundred-kernel-weight (HKW) of the *GT-KD* plants was similar to that of the CK plants. The mature kernels were harvested and sun-dried under identical conditions. Values are the mean \pm SD (n = 3). (C) The mature *GT-KD* and CK plants grown in the same field had similar plant height. Values are the mean \pm SD (n = 3). CK is the wild type plants (LH244), G3, G6 and G7 were different transgenic maize plants with *ZmGT-3b* knock-down, all the plants were grew in the field under normal condition in Beijing, 2018. 2w/4w was 2/4 weeks and MP was mature plant. Three independent repeats were done in the field. Values are the mean \pm SD (n=3). The asterisk * represents a significant difference at P < 0.05 (according to a paired Student's t-test);

NS, not significant.

A Photocupthocic		R		C		505	
7 THOLOSYILLIESIS	147 0 424 4 074	2 PK	0.504 0.040	BZIP	70 0 440 0 005	EKF	447
Zm00001d014564	0.001 0.000 4.005	Zm00001d018321 8.67	4 0.561 0.913	Zm00001d041604 7.0	0/0 2.419 0.805	Zm00001d026563 3.345 1.392	1.117
Zm00001d010715	0.001 0.003 4.025	Zm00001d029558 Z.32	0 2.606 4.469	Zm00001d020938 2.3	0.787 0.567	Zm00001d053859 6.449 2.913 0	1.992
Zm00001d003767	0.000 0.979	Zm00001d019222 2.63	9 0 469 0 953	Zm00001d012719 2.4	150 0.365 0.565	Zm00001d021089 3.521 2.058 ().485
Zm00001d043299	1000 0.401 1.220	Zm00001d052068 2.03	3 0 320 0 666	Zm00001d015845 1.7	69 2.053 0.834	Zm00001d019475 2.576 3.897 (0.926
Zm00001d018779	140 0.450 0.609	Zm00001d032000 2.55	1 2 739 1 008	Zm00001d046751 1.5	83 1.353 1.093	Zm00001d030513 2.820 0.847 0	0.470
Zm00001d042049	0.440 0.459 0.090	POD	1 2.100 1.000	MYB		Zm00001d016262 2.715 1.094 0	0.268
Zm00001d010134	0.000 0.262	Zm00001d022453 2.65	6 0.836 0.502	Zm00001d038930 2.	839 3.360 1.543	Zm00001d017478 1.905 0.675 0	0.717
Zm00001d006540	220 0.202 1.006	Zm00001d050572 3.33	9 0.898 0.629	Zm00001d018097 3.	078 1.511 0.376	7m00001d020043 1.807 1.545 0	0.535
Zm00001d012146	260 0.592 1.000	Zm00001d022283 2.68	8 0.633 0.406	Zm00001d020569 2.	391 1.298 0.358	Zm00001d005798 1781 0 982 0	580
Zm00001d013140	0.000 0.016	Zm00001d022280 2.84	0 0.510 0.405	Zm00001d035918 3.	814 1.822 0.608	7m00001d043491 1634 3662 1	1 782
Zm00001d019797	010 0 250 4 010	Zm00001d022289 2.65	3 0.523 0.552	Zm00001d041853 2.	876 3.252 1.512	NAC	TUL
Zm00001d022712	110 0.202 0.724	Zm00001d018620 2.11	7 1.017 0.651	Zm00001d008808 3.	027 1.786 0.708	7m00001d011969 2 263 1 340 0	533
Zm00001d023713	135 0 370 1 085	Zm00001d006936 3.29	3 0.373 0.752	Zm00001d012255 2	967 1.455 1.024	Zm00001d023669 2 221 1 261 0	697
Zm00001d049387	000 0 351	Zm00001d029279 2.91	9 0.500 0.473	Zm00001d045560 Z	1/4 3.24/ 1.019	Zm00001d051956 2.741 0.263 0	120
Zm00001d036535	068 0 389 1 504	Zm00001d021533 2.45	2 0.615 0.451	Zm00001d031520 2	67E 1 01E 0 622	Zm00001d023669 2.221 1.261 0.	697
Zm00001d035959	443 0 444 0 219	Zm00001d024734 4.70	6 3.979 0.270	Zm00001d036536 2	100 1 612 0 705	Zm00001d033308 2.329 2.589 1.	298
Zm00001d003853	000 0 264	Zm00001d029280 2.99	7 0.527 0.586	Zm00001d021337 2	002 1 700 0 208	Zm00001d050893 2.020 1.281 0.	391
Zm00001d034283	000 0.423	Zm00001d037359 4.01	4 2.800 0.855	Zm00001d031270 3	784 3 571 0 705	Zm00001d014405 2.254 1.060 0.	435
Zm00001d008706	015 0.622 1.000	Zm00001d009140 3.87	9 0.492 0.295	Zm00001d020405 4	493 10.63 5 716	Zm00001d003052 2.972 0.306 0.	021
Zm00001d019518	035 0 337 2 795	Zm00001d008898 2.60	2 1.114 0.741	Zm00001d053060 1	837 1 581 0 650	DHLH	
Zm00001d033922	102 0 290 3 730	Zm00001d018619 2.00	9 0.360 0.436	Zm00001d046174 1	922 0.910 1.261	Zm00001d039459 3.722 5.468 3	.676
Zm00001d034543	325 0.671 0.537	Zm00001d016177 6.26	5 0.385 0.357	Zm00001d002476 1.	893 1.460 0.801	Zm00001d033407 2.226 0.573 0	.401
Zm00001d005446	044 0 357 3 623	Zm00001d022279 3.49	0 0.523 0.430	Zm00001d004744 1.	867 2.143 1.279	Zm00001d018603 1.741 0.493 0	.568
Dhataquethasia	steppe proteine	Zm00001d047064 11.6	1.800 0.282	WRKY		Zm00001d038863 1.649 2.966 0	.778
Photosynthesis - ar	nienna proteins	Zm00001d04/514 3.40	2 2.207 1.125	Zm00001d012789 5.9	13 4.528 0.560		
Zm00001d021906 0	013 0.398 11.028	Zm00001d022751 2.03	0 0.004 0.249	Zm00001d038761 4.4	49 3.286 0.644		
Zm00001d011285 0	000 0.023	Zm00001d0/22282 3.55	9 0.994 0.340	Zm00001d010805 2.6	16 1.830 0.605	GTIC, CKIL GT	NG-
Zm00001d050403 0	000 0.320	7m00001d006937 2.26	4 0 399 0 632	Zm00001d039531 2.7	04 11.81 4.462	CA CA	-2
Zm00001d006663 0	185 0.252 1.243	CASP	0.000 0.002	Zm00001d038451 2.1	96 2.186 1.736	0 1	-2
Zm00001d032197 0	0.31 0.383 3.164	Zm00001d048728 2.673	3 2.141 1.245	Zm00001d043450 2.3	314 2.324 1.218	Fold changes of FF	PKM
Zm00001d009589 0	000 0.231	Zm00001d022574 1.93	0.972 0.391	Zm00001d043569 1.9	67 1.170 0.765		
Zm00001d033136	018 0.312 4.965	Zm00001d048727 2.43	3 0.199 0.464	Zm00001d002405 1.9	074 1.955 0.819		
Zm00001d015385	0.420 2.592	Zm00001d052433 2.96	0.657 0.197				
Zm00001d033132 0	042 0 405 0 074	Zm00001d038004 2.218	1.385 0.815				
Zm00001d021763 0	000 0 200	Zm00001d019457 2.078	8 0.175 0.259				
Zm00001d046786	127 0 257 0 924	Zm00001d010038 3.143	3 2.418 0.458				
Zm00001d007267	0.357 0.824	Zm00001d007379 1.387	7 3.533 2.495				
Zm00001d021784 0	076 0 409 2 202						
Zm00001d048998	121 0.455 2.149						
Zm00001d020599	020 0 412 5 000						
211000010039040	0.412 0.000						

FIGURE S3 I The differential expression of the photosynthesis, defense-related and TF encoding genes in *GT-KD* seedlings. The relative expression fold of the photosynthesis-related genes (A), defense-related genes (B) and the TF encoding genes (C). The data was from transcriptome sequencing with *ZmGT-3b* knock-down (GT) and CK (LH244) maize seedlings, with (CKi, GTi) or without inoculation (CK, GT). *ZmGT-3b* knock-down significantly down-regulated genes associated with photosynthesis-related functional categories, while significantly upregulated genes that emphasized in functions in plant defense response to various biotic/abiotic stress, such as POD, PR, CASP and a few TF family member encoding genes, such as bHLH, bZIP, MYB, WRKY, ERF, and NAC.



FIGURE S4 I Significant commonalities exist in the transcriptional responses between the *ZmGT-3b* **knockdown (GT) and inoculated control plants (CKi).** *ZmGT-3b* knockdown (GT) induced similar transcriptional reprogramming to the inoculated control plants (CKi), to enhance defense related functional categories and to up-regulate expression of defense-related genes by GO (A) and KEGG (B) analysis with the obtained DEGs. (C)The expression levels of other trihelix TF family members did not show significant changes in the *GT-KD* seedlings.



FIGURE S5 I Comparative transcriptome composition between the various transcriptome pairs. (A) Inoculation induced 1340 genes to be differently expressed in *GT-KD* seedlings (GTi/GT), while 1049 genes were differently expressed in the inoculated two genotypes (GTi/CKi). (B) 254 differentially expressed genes (DEGs) were shared between GT/CK and GTi/CKi, while 462 DEGs were shared between CKi/CK and GTi/GT. Significant commonalities exist in the transcriptional responses between the non-inoculated GT/CK and the inoculated GTi/CKi by GO (C) and KEGG (D) analysis. (E, F) The transcriptional reprogramming between the inoculated and non-inoculated *GT-KD* seedlings (GTi/GT) was much stronger than that of the inoculated and non-inoculated CK seedlings (CKi/CK).



FIGURE S6 I Contents of the mineral elements and expression fold of the related transporter encoding genes in maize seedlings. (A) The contents of mineral elements in CK and *GT-KD* maize seedlings at 7-DAG. Compared with CK seedlings, the content of Al and Fe was significantly decreased, while the content of Cu, K and P was increased in the *GT-KD* seedlings. DW, Dry weight. Values are the mean \pm SD (n=3). The asterisk * represents a significant difference at *P* < 0.05 (according to a paired Student's t-test); NS, not significant. (B) The relative expression fold of the related mineral element transporter encoding genes from the transcriptome sequencing with *ZmGT-3b* knock-down (GT) and CK (LH244) maize seedlings, with (CKi, GTi) or without inoculation (CK, GT).



FIGURE S7 I A proposed model for the involvement of ZmGT-3b in regulating growth and defense response in maize seedlings. Under normal growth conditions, light induces *ZmGT-3b* expression, and ZmGT-3b transcriptionally activates various photosynthesis-related genes, especially *ZmHY5*, to promote photosynthesis and seedling growth; ZmGT-3b synchronically suppresses the expression of various defense-related genes by transcriptionally repressing multiple transcription factor (TF) genes, including *MYBs*, *bZIPs*, *NACs*, *bHLHs*, and *ERFs*. However, *ZmGT-3b* and *ZmHY5* expression dramatically decreases upon pathogen attack. Thus, photosynthetic activity is limited and the repressive effect on TF genes is relieved, thereby inducing the expression of defense-related genes to activate the defense response. Thick lines indicate direct inhibition by pathogens, while broken lines indicate proposed repression. ZmGT-3b and ZmHY5 function collaboratively in regulating the light response and photosynthesis during seedling growth.

Table S1 I The cis-element analysis within 2000bp upstream of ZmGT-3b, ZmHY5 starting codon

ATG.

Table S2 I All the primers used in the experiments.



Table S3. The sequence information of ZmGT-3b used in this research. The image in (A) is the genomic structure information of ZmGT-3b in maize GDB:

https://www.maizegdb.org/gbrowse/maize_v4?name=Chr5:205893484..205894854;h_feat=Zm00001d

017752 T001. The sequence in (B) is the partial genomic sequence from online information, including

NM 001357055.1. The sequence in bold and yellow shade were the cds of ZmGT-3b. The primers

were in bold and red color, the 5'-part of GT-3b was obtained with 5'-

TCCTCCATACGGTCGCAGTAC-3' and 5'- CTGAGGAAGGGAAGTGAAAC-3'; while the partial

cDNA of GT-3b was obtained with 5'-TTCACTTCCCTTCCTCAGAG-3' and 5'-

CAGTTACGATTACGACAGCG-3'. The purple triangle indicates the polyA addition site.