



Article

Disruption of *OsPHD1*, Encoding a UDP-Glucose Epimerase, Causes JA Accumulation and Enhanced Bacterial Blight Resistance in Rice

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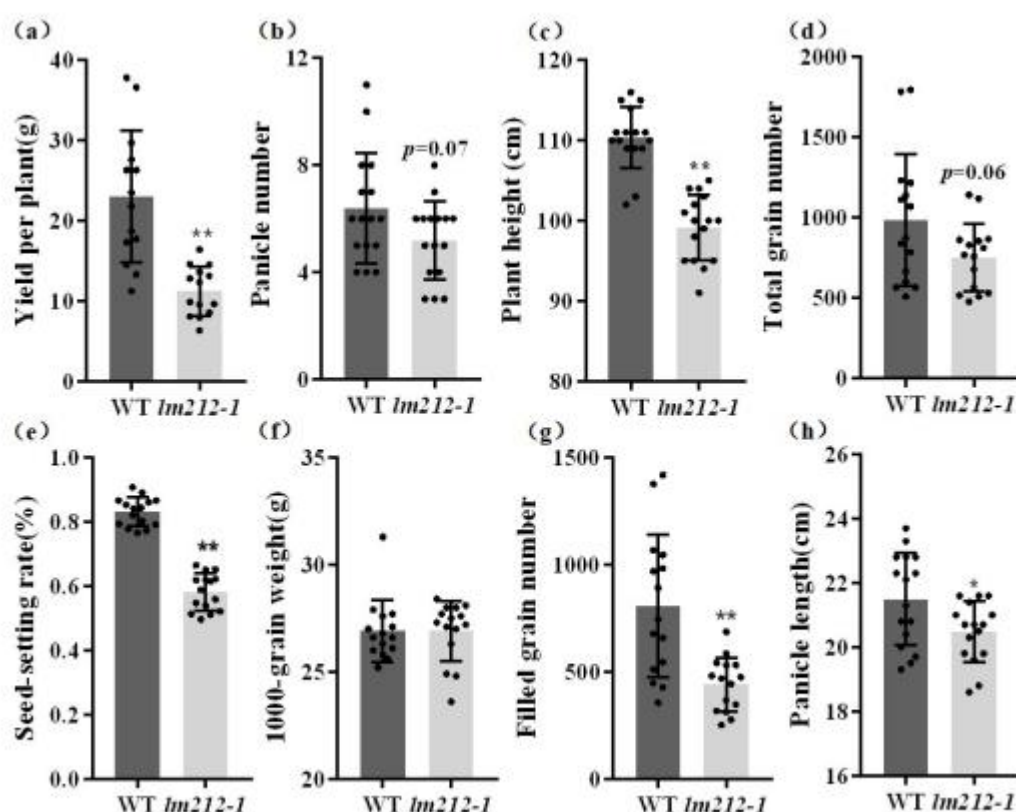


Figure S1. Several agronomic traits of WT and *lm212-1* mutant. ** $p < 0.01$ by student's t -test. Data are means \pm SD of sixteen biological replicates.

Table S1. List of primers and their uses.

Primer name	Sequence(5'-3')	purpose
LD1-F	TATCGACAAGTCATCTGGTG	mapping
LD1-R	GTTTCCTTGCATTACAGGTG	
LD9-F	CATTGTATATGCCCTTGTGC	
LD9-R	GCCAACAGGCAGTAATGTAT	
LD12-F	AAGGCGCTAAAAGAAACCTA	
LD12-R	GTGCAGGAAACGATTGAGAT	
LD13-F	CCTGCAGCATATATAGAGTA	
LD13-R	TGGTTTCCTTTCATATTCCG	
COM-F	TCTAGAGTCGACCTGCAGCAGGACAGTCCAGC AACGAG	complementation
COM-R	AAGCTTGCATGCCTGCAGGAGTGACGGCGTC TTGCTT	
OE-F	ATCCTCTAGAGTCGACATGGGCGGCGCCGCCG TC	overexpression
OE-R	ATGCCTGCAGGTCGACTCAACTGTCAAGACCA AGGAATTCTG	
GUS-F	GCAGGCATGCAAGCTTAACCTACTACTCCACC TGCCA	GUS
GUS-R	CTCAGATCTACCATGGCGCGCGGGCGGGCGGTG GT	
GFP-F	CGGGCTGCAGGAATTCATGGGCGGCGCCGCCG TCTC	GFP
GFP-R	GCTTGATATCGAATTCAGTGTCAAGACCAAGG AATTCTGTGA	
OsUBQ10-F	TGGTCAGTAATCAGCCAGTTTGG	qPCR
OsUBQ10-R	GCACCACAAATACTTGACGAACAG	
OsPR10-F	CAGTGGTCAGTAGAGTGATCAG	
OsPR10-R	GGGTAAAGCTTCATGGTGTAGA	
OsPAL1-F	GACCCTGTATTTTCTTCGTTCCG	
OsPAL1-R	AGTAGCAATACTTTCACCCCAA	
OsWRKY45-F	CGTCGACCAGATTCTCCACACCT	
OsWRKY45-R	CTCGCTCTGCACCTCCGACCC	
OsPO-C1-F	ATAGCAATGTGTACGTGGAGAT	
OsPO-C1-R	ATTCCATGCACATACAGATGGA	
OsSGR-F	AGGGGTGGTACAACAAGCTG	
OsSGR-R	GCTCCTTGCGGAAGATGTAG	
OsNYC1-F	CATGCAACACCAACAAAAGG	
OsNYC1-R	GACCATTCAGGAGAAGCAG	
OsNYC3-F	TCTATCTAGGTGCCAAAGGC	
OsNYC3-R	ATTCTGGCACCTGCTGTTTC	
OsNOL-F	CCACGAAAGGTATAGGATATG	
OsNOL-R	TCAAGTCAGTCACCGCAGAT	
OsCOI1a-F	TACCTTCCTATCTATCCCTGGG	
OsCOI1a-R	TAGTAGCTTATTCGGGCACAAT	
OsCOI1b-F	TAAGGAGTTGTTGCTTCAGTGA	
OsCOI1b-R	CATGAGATCGTGACCAGTCTTA	
OsCOI2-F	TGCTACCAACAATAGTGTCTT	

OsCOI2-R	CTTCAAAACTTTCAGCCTTCGA
OsJamyb-F	GTTGATGATAGCGGAGACTACA
OsJamyb-R	TCTTCAAATCTTGTGACTCCGA
OsMYC2-F	GGGTTTTGTTATCTCCTCTCCT
OsMYC2-R	AGAATAGGAGGAGAGGAAAGGT
OsRERJ1-F	GGATAGTGTCCAAATGAAGCAG
OsRERJ1-R	CCAAAACGCATGACTCCATATA
OsHHLH148-F	CACAGACATCTCATGTGCAAAA
OsHHLH148-R	CTTGCTCCATCACAAGCTTTTA
OsJAZ13-F	ACACGTCAGCTTTAATCCCATA
OsJAZ13-R	AGGAATAATCGTGCCTGTACA
OsJAZ12-F	ACCCAAAGAGTTCTTTCACTGA
OsJAZ12-R	TGGAGACAGTTGTACTTGTACA
OsJAZ11-F	TGAGCCGAAGAACTGAAGATA
OsJAZ11-R	ACAGACACGTGGAAATCAAATG
OsJAZ10-F	CGCAAGAGGATTGATTCACCTT
OsJAZ10-R	TTCCCATCAATTCAATCTCCCT
OsJAZ9-F	AGAATTGAGAGCTCGATCGATT
OsJAZ9-R	AATCAACTCAAGGCCGTTAATG
OsJAZ8-F	ATGAATGCAAATGCTCCATACC
OsJAZ8-R	GCTTTATTGTCATCTCTTGCC
OsJAZ6-F	GAGCCAATGAATCAATGCTCAA
OsJAZ6-R	CATCGGATCATCTCCTAACACA
OsJAZ5-F	ATTACTGTTGATTGGTCCCCT
OsJAZ5-R	CGATCGATCAACACTAAACAGG
OsCEBiP-F	TTCATCAATCAGCGATACCTCA
OsCEBiP-R	CTGGTTTGTATGATGAGCGATG
OsCERK1-F	TGAACAACCTGTATGAGAACCA
OsCERK1-R	ATGTACAATTTCCAGTGTGC
OsRLCK185-F	ACTGGGTCGAATTAGGTACATG
OsRLCK185-R	ATTTGCATGATCAATCACGAGG
OsBSK1-F	ACCTGGCATATACACCTCCA
OsBSK1-R	TGTCAAGTGCAAGGGTAGGA
OsLysM-RLK10-F	GTTAGCGAATCAAAAGGACTGG
OsLysM-RLK10-R	GATCAATCAGTTCGTCAAGAGC
OsPUB44-F	ATGCCTTACTGAAACCAAACC
OsPUB44-R	ATTCATAGCAAACCCCGAGTAG
OsSERK2-F	GGCTATGGAATCATGCTTCTTG
OsSERK2-R	CAATCGAGCAACATCACATCAT
OsMGD-F	TTTTCATACCATCGCCAGAAAC
OsMGD-R	TAGGACAAAGGCAAATTTACAG
Os09g0423600-F	ACCAGGTATTCGTCACTGATTT
Os09g0423600-R	AGTATGTCATCTTCCACAAGGG
Os11g0158400-F	AGAACGGAGAAGCATAATTCCT
Os11g0158400-R	GGCTCTTCCAAAATAGCAATGT
Os04g0416900-F	GGTTATTCTGGACAAGATGGGA
Os04g0416900-R	GATCTCATTGCCAGTTAAGCAG
Os02g0539100-F	CTGAACCTGGTATCATCATGGGA
Os02g0539100-R	ATTGTTGATGTGTTTGACCAGG

Os03g0268300-F	GCATTCTTCAAGGGTGCATATT
Os03g0268300-R	CAGCTCCATCTTAAGACCAGAT
Os03g0214400-F	ATAAGTTCAGGCGAGTGATAGG
Os03g0214400-R	AATCTTGTGGCAATAAATCCGG
Os01g26920-F	GTTCTCGGGGTGTCTGATGATA
Os01g26920-R	CCAACAATCAGCAAATCGTTCT

Table S2. Genetic analysis of the *lm212-1* mutant.

Cross combination	F ₁ phenotype	Segregation in F ₂		χ^2
		Wild type	Mutant type	
<i>lm212-1</i> × ZhongHui8015	Wild type	586	214	0.64