A novel rice *fragile culm 24* mutant encodes a UDP-glucose epimerase that affects cell wall property and photosynthesis

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Primer sequence (5' to 3')
ACACGTTTGTACGTTCGTTTCG
GCCGACAAACACTCTCATTGG
GTCCGACTCACCTCCCTCTTGC
CCTCATCCTCTCCACGCTCTCC
CAGCAATAAGATGCTACAAGAA
GAAAACGAAATAAACAAACTCC
AGCCACCGACCAAATAATCAG
GGACGGCGGAAGTATCTCAAT

Supplemental Table S1. Primers for map-based cloning of Osfc24.

Primer name	Primer sequence (5' to 3')	Purpose	
Promoter-UGE2-F	ATTGAAAGATGAAGACAGGGGAC		
Promoter-UGE2-R	GAATGTGGGGGGGGGGAGGAGGAGTAG	Promoter cloning of OsUGE2	
CDS-UGE2-F	CCTGAATCCCTCCTCCTACTCT	CDS region cloning of OsUGE2	
CDS-UGE2-R	CCCGGGAAGAGAAAACATGAGCATCGGT		
Q-OsUGE1-F	TACTGCTCCGATACTTCAACCC		
Q-OsUGE1-R	CCATCCGCTAGATCAACAACAT		
Q-OsUGE2-F	TATGGATACGGGTCACTTGACTC		
Q-OsUGE2-R	ACCAGTCCATATCCGTTGTGAC		
Q-OsUGE3-F	TGGAACAGGAAAGGGAACATC		
Q-OsUGE3-R	TCGTGGACCAATAACCAAAGG	Q-PCR of OsUGEs	
Q-OsUGE4-F	TCGCTACTCCTGACATTGGTT		
Q-OsUGE4-R	TGATCGCCCTAATTCTGCTC		
Q-OsPHD1-F	CTGTGACAATAAGCCTCTTTCCAG		
Q-OsPHD1-R	GCTCCCAACCAATCTCAGAAC		
Mse I-UGE2-F	TGGTGATGCGGAGATT	Amplify the fragment covered the	
Mse I-UGE2-R	CGTTATGCTTGGCAGAGT	mutation site of Osfc24	
GFP-UGE2-F	CAGTGGTCTCACAACATGGCGGTGGAGAAGACGGT	Subcellular localization of OsUGE2	
GFP-UGE2-R	CAGTGGTCTCATACAGTGGAAGTGGCCGTTGCCGT		
28a-OsUGE2-F	CGGGATCCATGGCGGTGGAGAAGACG	Recombinant expression of OsUGE2	
28a-OsUGE2-R	CCCAAGCTTGTGGAAGTGGCCGTTGC	in <i>E. coli</i> .	

Supplemental Table S2. Primers for functional studies of OsUGE2.

Primer name	Primer sequence (5' to 3')
Q-SUS1-F	CATCTCAGGCTGAGACTCTGA
Q-SUS1-R	CAAATTCAATCGACCTTACTT
Q-SUS2-F	GAGGCTGATGACCTTGACTGG
Q-SUS2-R	CCCTCCATTACTTGGATGTGCT
Q-SUS3-F	GTGAGACACGCCGCTACCTGGAGA
Q-SUS3-R	CCCTGAAATCAACTAAACCCT
Q-SUS4-F	TGAACTGGCGAAGACTGTACC
Q-SUS4-R	CAATGGCAATGAAGCACTGAG
Q-SUS5-F	CAGGTTAGCCGGGCAGAAG
Q-SUS5-R	CATTGTACACAAATCTCACGCAAG
Q-SUS6-F	CGAACAACCAGCACAACCTAC
Q-SUS6-R	GGAGCAGTGGTCCAAGTAAGT
Q-CESA1-F	GGCATGGTGGCGGGTATAT
Q-CESA1-R	AGGCGACGGCTTTCTGAGT
Q-CESA3-F	GTGTAGATAGAAACACGAAAGGTG
Q-CESA3-R	CAATGGGCACCCACACGT
Q-CESA4-F	CCATCGTCTACCCGTTCACC
Q-CESA4-R	TCCAGCCCAGCAATCATCTT
Q-CESA5-F	CCTTGTTAATACCCCCTACC
Q-CESA5-R	AATCCAAACCACACTCCTCC
Q-CESA6-F	GAAGGCAAAACAGCACACCCA
Q-CESA6-R	CCAAGTAAGCTCAGCGATGA
Q-CESA7-F	TTAACGGGGTTCAAGATGC
Q-CESA7-R	ATGGTGTTGGTGTAGGCGA
Q-CESA8-F	TGGTCGGTGTTGTTGCTGG
Q-CESA8-R	ATGGTCGGAGTGCGGTTTT
Q-CESA9-F	TACAAGAACGGCAACCTCA
Q-CESA9-R	AAGAACAAACTCGCAAACG
Q-UBQ-F	CCAGGACAAGATGATCTGCC
Q-UBQ-R	AAGAAGCTGAAGCATCCAGC

Supplemental Table S3. Primers for qRT- PCR of OsSUSs and OsCESAs.

Supplemental Figure Legends

Supplemental Figure S1. Leaf green-color quantification of *Osfc24* mutant. (A) Leaf phenotype at heading stage. (B) Color quantification. Error bars represent mean \pm SD (three biological replicates) with Student's *t*-test for significant difference, $n \ge 10$ leaves in were measured in each replicate. The rate (%) calculated by subtraction of values between the WT and *Osfc24* divided by the WT value. Scale bar indicates 2 cm in (A).

Supplemental Figure S2. Genetic complementation test of rice brittleness mutant *Osfc24* by *pFC24F*. (A) Plant height; (B) Tiller number; (C) Breaking force; (D) extension force of 2^{nd} internode at heading stage (E) Cell wall compositions of mature plants of wild type (WT) and *pFC24F*. Error bars represent mean \pm SD (three biological replicates) with Student's t-test for significant difference, $n \ge 20$ plants in (A-D) were measured in each replicate.

Supplemental Figure S3. Protein sequence alignment of the UGE protein family in rice and *Arabidopsis*. Green asterisk represents the mutated amino acid site.

Supplemental Figure S4. Prediction of OsUGE2 protein domain by TMHMM2.0 program.

Supplemental Figure S5. Transcriptional analysis of *OsUGEs* and *OsPHD1* genes in stems tissues of the *Osfc24* mutant. *Ubiquitin* gene used as internal standard. Error bars represent mean \pm SD (three biological replicates). ***P* < 0.01 by Student's t-test.

Supplemental Figure S6. UGE activity in stem tissues of the *Osfc24* mutant. Error bars represent mean \pm SD (three biological replicates). ***P* < 0.01 by Student's t-test. The rate (%) calculated by subtraction of values between the WT and *Osfc24* divided by the WT value.

Supplemental Figure S7. Stomatal conductance and transpiration rate in the Osfc24

mutant. Values represent means \pm SD, n = 12. ***P* < 0.01 by t-test.

Supplemental Figure S8. Transcriptional analysis of *OsCESAs* in young root tissues of the WT under Yariv treatment. (A) Germinated seeds were treated with β -glucosyl Yariv reagent (50 μ M) for 5 days. (B) Fold of change on *OsCESAs* after Yariv treatment. *Ubiquitin* gene used as internal standard. Error bars represent mean \pm SD (three biological replicates). ***P* < 0.01 by Student's t-test.

Zhang et al., Supplemental Figure S1





Zhang et al., Supplemental Figure S2

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+ 50 uM Yariv