

WT:	MEVVLHEGDAKDWWYKGEAANLILSYTGSSPSMLGKVLRVKILKDKGQAPAPNCIVFSS	60
<i>Osipk1_1</i> :	MEVVLHEGDAKDWWYKGEAANLILSYTGSSPSMLGKVLRVKILKDKGQAPAPNCIVFSS	60
<i>Osipk1_2</i> :	MEVVLHEGDAKDWWYKGEAANLILSYTGSSPSMLGKVLRVKILKDKGQAPAPNCIVFSS	60
<i>Osipk1_3</i> :	MEVVLHEGDAKDWWYKGEAANLILSYTGSSPSMLGKVLRVKILKDKGQAPAPNCIVFSS	60

WT:	HEEHLWGKIPGLLESVKNDCLPQAYATIVMSQHLGANHVDGGVVRVRSKNFFELAGKNVL	120
<i>Osipk1_1</i> :	HEEH-----VKNDCLPQAYATIVMSQHLGANHVDGGVVRVRSKNFFELAGKNVL	109
<i>Osipk1_2</i> :	HEEHLWGKIPGCWNLLKMLACHKFMQLL-----	89
<i>Osipk1_3</i> :	HEEHLWGKIPGVGIC-----	75

WT:	DNRPAWRVNASAIDAGADSALLISDHTLFSGNPRGSSCIAVEIKAKCGFLPSSEYISKEN	180
<i>Osipk1_1</i> :	DNRPAWRVNASAIDAGADSALLISDHTLFSGNPRGSSCIAVEIKAKCGFLPSSEYISKEN	169
<i>Osipk1_2</i> :	-----	89
<i>Osipk1_3</i> :	-----	75
WT:	SIKKQVTRYKMHQHLKPHLGEISKTSYDPLDLFSGSKERIHMMAIKSFFSTPQNNFRIFV	240
<i>Osipk1_1</i> :	SIKKQVTRYKMHQHLKPHLGEISKTSYDPLDLFSGSKERIHMMAIKSFFSTPQNNFRIFV	229
<i>Osipk1_2</i> :	-----	89
<i>Osipk1_3</i> :	-----	75
WT:	DGSLVFGMGGGADSVHPNETEKLEDLSKVTGLQLSDFIELLSEAFKSGVLGKLLATQ	300
<i>Osipk1_1</i> :	DGSLVFGMGGGADSVHPNETEKLEDLSKVTGLQLSDFIELLSEAFKSGVLGKLLATQ	289
<i>Osipk1_2</i> :	-----	89
<i>Osipk1_3</i> :	-----	75
WT:	KLDDHDIEGAIHLYYNIISQPCLVCKSITDTELLRKYSTLHSLPLDKSEKIVRDPLISAT	360
<i>Osipk1_1</i> :	KLDDHDIEGAIHLYYNIISQPCLVCKSITDTELLRKYSTLHSLPLDKSEKIVRDPLISAT	349
<i>Osipk1_2</i> :	-----	89
<i>Osipk1_3</i> :	-----	75
WT:	AKDCSLMISFRPQSGTTDSEYDSVFLDSVNQSYDYKAYFIDLVDKPLDKMVHYFKLDQK	420
<i>Osipk1_1</i> :	AKDCSLMISFRPQSGTTDSEYDSVFLDSVNQSYDYKAYFIDLVDKPLDKMVHYFKLDQK	409
<i>Osipk1_2</i> :	-----	89
<i>Osipk1_3</i> :	-----	75
WT:	IVNFYTRNGEVGGDPRDPPKGCGR	445
<i>Osipk1_1</i> :	IVNFYTRNGEVGGDPRDPPKGCGR	434
<i>Osipk1_2</i> :	-----	89
<i>Osipk1_3</i> :	-----	75

Figure S1. The predicted protein of mutant line is shown together with its WT one using the Clustal Omega Multiple Sequence Alignment (<https://www.ebi.ac.uk/Tools/msa/clustalo/>).

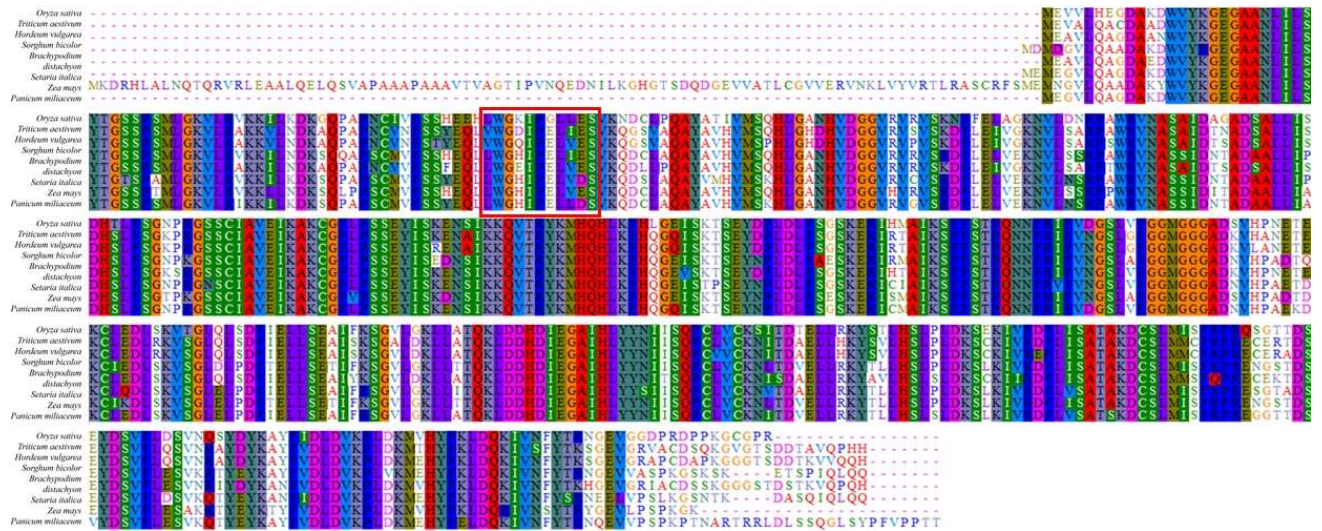


Figure S2. Multiple sequence alignment of IPK1s. All the data are from RAP-DB (<http://rapdb.dna.affrc.go.jp/>) and Gramene (<http://www.gramene.org/>). Analysis of IPK1 sequences from nine organisms using BioEdit software. Identical amino acid residues are boxed in same color. Short lines indicate gaps introduced during alignment. The mutant site of OsIPK1 is marked by a red box.

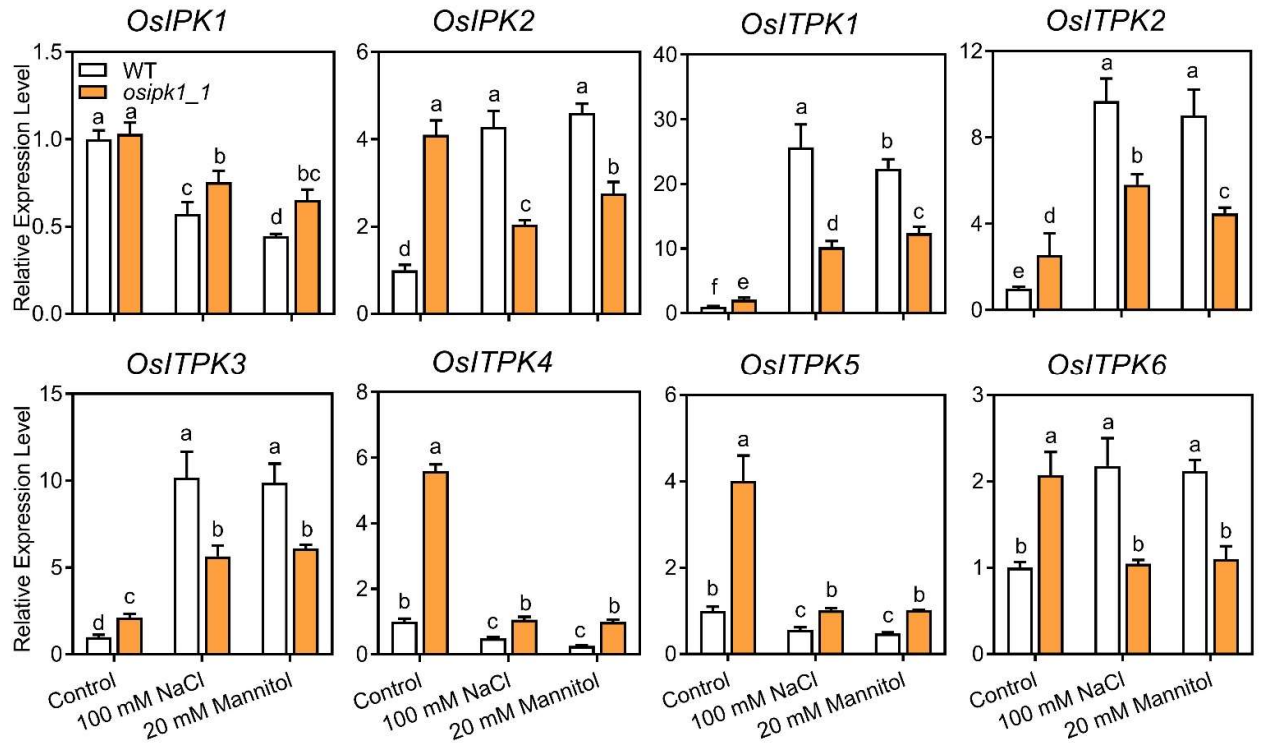


Figure S3. Relative expression level of phytic acid biosynthesis genes in Xidao #1 (WT) and its *OsIPK1* mutant line *osipk1_1*. All analyses were performed with three replicates. Error bars represent standard error. The different letters show the significant difference at a probability of $p < 0.05$.

Table 1. Primers used in this study.

Primer Name	Primer Sequence (5'→3')
C1-F	GGCAGGCAAGATCCCAGGATTGT
C1-R	AAACACAATCCTGGGATCTTGCC
HygR-F	AGAAGAAGATGTTGGCGACCT
HygR-R	GTCCTGCGGGTAAATAGCT
P1-F	GGCAAGGTTCTGCGAGTC
P1-R	CCGCCATCAACATGATTGG
qRT-OsIPK1F	TGTGTTTCTACAAGTGTGCATG
qRT-OsIPK1R	CAGATCACAGATTCACAGCAAG
qRT-OsIPK2-F	TTTGAAAGAGGAAACTTCACCG
qRT-OsIPK2-R	GAATCCCATGGTTTAAAGGGG
qRT-OsITPK1F	CCAGGACGATATTAAGAACA
qRT-OsITPK1R	GGAAGTCAGTGAACGATT
qRT-OsITPK2-F	GGCGAGGAAGAAGGGAATTAAT
qRT-OsITPK2-R	AAATGGGCCTTGTCTGCAA
qRT-OsITPK3-F	AGTTATCTCTTGCTTATGA
qRT-OsITPK3-R	CCAACAATGTAGACCTTA
qRT-OsITPK4-F	CCGACCCAGCGTTTGAAC
qRT-OsITPK4-R	TTGCTTGGCTTCATTGATTATTGTT
qRT-OsITPK5-F	AATCCTTTCTCCTAACTCCTTTC
qRT-OsITPK5-R	TCTCTTGGCTGCTCTAACTA
qRT-OsITPK6-R	GCGACAACATTCATACTAAT
qRT-OsITPK6-R	CTAAGTGACAAGCAACCT
qRT-OsPOX8.1-F	CTGCTCCAAAGTGAACATAATAATTAAGTAAAG
qRT-OsPOX8.1-R	CCCAGCCTTATTCCCAAATTT
qRT-OsPOX22.3-F	CAGCTGCTCCAAGGTGAAGTC
qRT-OsPOX22.3-R	AGATTTGCTTCCAGCAACGAA
qRT-OsP5CS-F	GCTGACATGGATATGGCAAAAC
qRT-OsP5CS-R	GTAAGGTCTCCATTGCATTGCA
qRT-OsRab16D-F	CGGGTAAACAATAAAGTCGTGATG
qRT-OsRab16D-R	GCGCACTTACATACAGTGCTACGT
qRT-OsGDSL-F	TCATCGTACAGCAGTTCAT
qRT-OsGDSL-R	TTGTTGGTCGAGCTTGAG
qRT-OsbZIP23-F	GGAGCAGCAAAAGAATGAGG
qRT-OsbZIP23-R	GGTCTTCAGCTTCACCATCC
qRT-OsSNAC1-F	CATGGTCCCGTTCTGAGGTG
qRT-OsSNAC1-R	CACACGTTGCAGCATCGATC
qRT-DREB1A-F	AGGACTTCTTCCGGCGCCGCCT
qRT-DREB1A-R	TCGTTCGTTCGTCGGTGCCTGGGGT
qRT-OsActin-F	TGGCATCTCTCAGCACATTCC
qRT-OsActin-R	TGCACAATGGATGGGTCAGA