

Supplementary Material

Figure S1. Phylogenetic tree showing relationships between homologues of *OsYUC9*, *OsYUC11* and *OsYUC12* from rice, sorghum and maize. The tree is rooted using *OsYUC8*. The tree was produced in MEGA5.2 [25] using the Neighbour-Joining method [26]. MUSCLE [27] was used for multiple sequence alignment. The bootstrap consensus tree was inferred from 500 replicates [28]. Evolutionary distances were computed using the Poisson correction method [29]. All ambiguous positions were removed for each sequence pair. Highlighted sequences are encoded by genes expressed in endosperm during early caryopsis development.

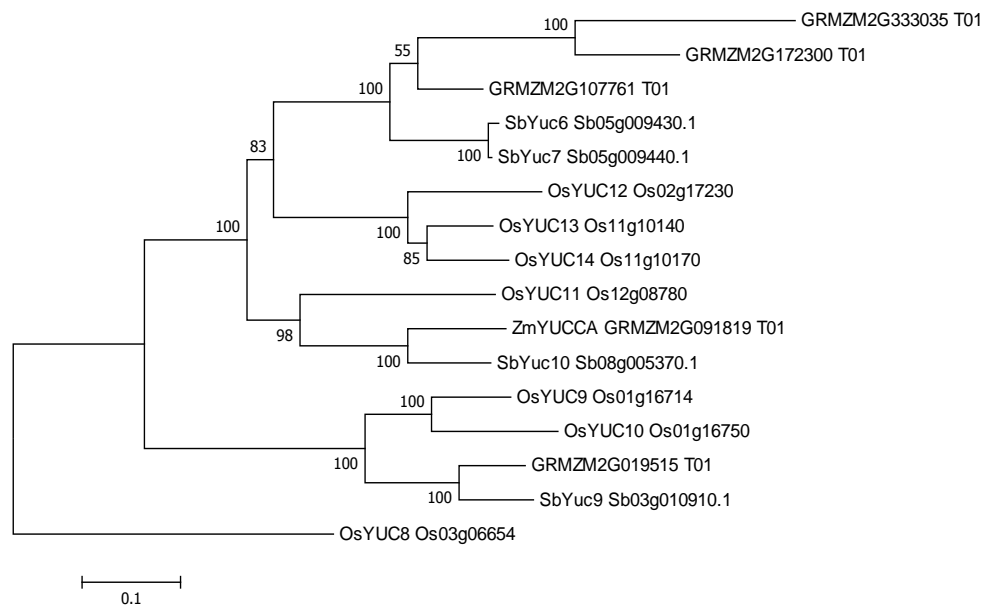


Figure S2. Expression of maize orthologue of *OsYUC12*, (*GRMZM2G107761_T01*) during grain development using RMA normalized data from Genome-wide atlas of transcription during maize development [13] accessed as accession ZM37 from PLEXdb.

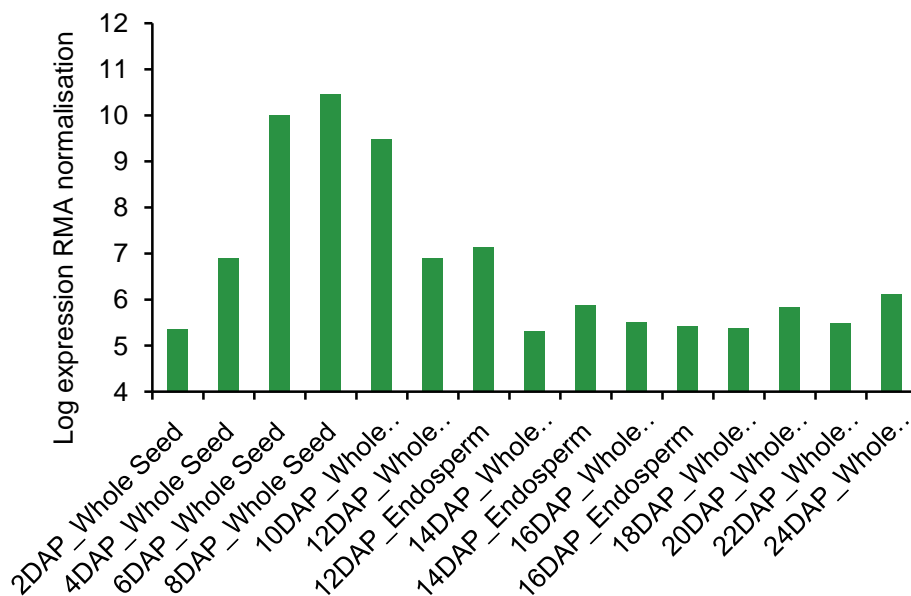


Figure S3. Multiple sequence alignment of INVINH/PMEI protein sequences used for the phylogenetic tree in Figure 2. The alignment was carried out using MUSCLE [22]. CLUSTAL multiple sequence alignment by MUSCLE (version 3.8) The sequences shown below as **A**, **B** and **C** are contiguous.

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Os08g04760 -----MVKPIGSLAIAAVVPELLA-----ALCLVSVCTGGDARWCAVPVSMTEQAQDAVC--GTAHMLK
Os08g04710 -----MNTIPLPLRLLVAVSL-----AVAGVAGDDEKTCPGAPTM---TVESACRNVS--GTQAMYD
Os08g04740 -----MNTIPLFSLPLLVAVSLI-----VAGAGAGDETTTCPGAPSM---TVESACRNVS--HTQAMYD
Os08g04670 -----MEKTTFAVLSLSLLLAG-----GGGADACEDYDV---PMSAAVAFERASTGRAMSE
Os08g04700 -----MEKPAAVFAVLSMGSATAT-----LLLLLAGGGVADACSDWDVPSMSAAVQORAS--TGRTISQ
Os08g04650 -----MERSATVFVALTLVAGS-----VVVVVVVDACDGVPRM-----SAVEACKQAS--VGPAMSR
Os08g04660 -----MSVALTISLTLTAASLLA-----GVADGCDGVPRM-----SAVDACKQAS--TAGVMWQ
Os08g04690 -----MTRASATGFLAAVAMALA-----VAAVVVDGCDNVPSM-----SMDDACKLAS--TSQPLLA
Os08g04680 -----MNKRDAIVFLVLAAMAVVV-----IVVDACDGVPRM-----SMSLEDTCKAFG--TAAAPT
Os04g36770 -----MAARLVFSLLLTVACSHA-----ALAAAASSS-----AVEDTCAKATASGSRKDLAP
Os08g25070 -----MTTAMASSSRGVTVPFLMILPFLF-----VVAALPAEIVTVGGD-----ILLPCKTVGGG-STYFDVQ
Os12g03510 -----MVSSHGIVNAFFLFAVAL-----VAAHQAGHAANADS-----FMGACKIVAGSSSGVSVT
Os11g03740 -----MSSINGVSLFLLAVLL-----PASQLAAGIDS-----ALYGACTVAGN-SGVVSVT
Os11g03750 -----MASSNNGVSLFLLAVLLI-----AASQLAAGINS-----AVYGACTIAG-SGSLIGVT
Os07g14130 -----MADHQTLSAVFLLVLP-----HAACMMAKPSSST-----LLQDKCLYAA--GDRFSYD
Os02g46360 -----MRRLLVFPVLLMLGLSTC-----ESSVLQDCKSVAAG-HKYVTYN
Os04g49730 -----MKLVRSFSLVFLVLSLL-----LTSSTTSRAS-----LVDDACKSPAAS-HADIGYA
Os04g49720 -----MAFLRALSLPVLFTLLLL-----AASTSDAS-----ILEETCKSLAGN-HTAIDYP
Os05g20570 -----MGPAHGHLVLLVAVALLSAGF-----LPHAVAKGGVAPP-----AVADIC-----SRTFFPD
Os01g14940 -----MARSLAHATLLLVAVVVA-----AAACWTTAAGENE-----EVARIKCK-----TSYPE
Os03g61530 -----MAAASLRLVVVAAVAIS-----LRGAAATAV-----TVEDAC-----RHRTRHEA
Os01g20970 -----MASSPYHAAGVAVLAILL-----AAPAEAGAPTAAPLANY-----SLEDACK-----KTGPHYG
Os05g29740 -----MASSSVLVVVAACLAIA-----LVCLANVAPASCARATAALPHASIAETCSF-----VDDHK
Os02g01300 -----MATLCSGVCFLFVIMVIA-----SSPAVAAAGED-----IVETCKQCSRS-NPNVNYT
Os03g40900 -----MFLALVILLAVAAGSQPAATSTPATVSPAPAVS-----VVAAPAGELCGGAGARRDQREFFVRGCC-----ARTLYPR
Os08g12600 -----MATVLVLMVSTGGLSPPCAAAAKEEKPVVVL-----PPAAAPGEAFPAEAAA-----FVRSCETALP--AERDASS
Os08g12160 -----MSRSSSMATVILVLMVVSAGLSPPCAAAAKEEKPVVVL-----PPAAAPGEAFPSADAAA-----FVRSCDTALQ--ADRDGSS
Os08g12230 -----MSRSSSMATVILVLMVVSAGLSPPCAAAAKEEKPVVVL-----PPAAAPGEAFPSADAAA-----FVRSCDTALQ--ADRDGSS
Os08g12520 -----MSRSSMAAVFLVVLIAINVCLSPQGATAAPEGELHKLNLLEL-----PPPLPPGKEPSTEAYR-----FTQVQDFGTSTFEQMIGA
Os08g19780 -----M-----TAVLLQEPSPFAIYQ-----FSRTICRIP-----KDPYKI
Os03g43820 -----MDLGQFVSTKVSSIFTMASSPSLALSFLVLLVLATFTTTTTLATNML-----PPSAPALSPASSAAAKE-----FLRATCT-----SKSELPE
Os10g10700 MEQVHLRSLNFTPNPIVVLQPQNTQPPYNSLLNLSLKFPLCISTAKPATASSSRNNGASSSHDRLLRLRRRTTVVVGSGDSQGGHFAAPPVAPFAAVALFRASC-----ASTLYRL
Os10g10630 -----MPSSRAGFRHVLLVLMFFAAAV-----AARGADAASFVTTTRFCGAAAAASFCLSRC-----ATTVYPA
Os10g10560 -----MAAASATQATAEAAA-----PCSTTKTESTSSSS-----FLRARC-----ATTRYPD
Os10g10620 -----MAPLPPRAISLVFLFLFT-----AASATRRLDDAGQPTAASSATAFLRSR-----ATTRYPD
Os10g36500 -----MARSLSLLLVACFLVAGATAAR-----PAPSTSGAAIIS-----FVRSWC-----AGTKYPA
Os04g01570 -----MAITRRHPPLLLFLAVAAA-----ATIAGASQSTRPRPAVSPAAAADFVRRSC-----RATRYPQ
Os06g49760 -----MSRSSLAMALLLAAFAA-----AATANSGAAPAASD-----FIRKSC-----RATQYPA
Os08g24160 -----MALLLLAFAA-----AATANGAAPAASN-----FIRKLC-----RATQYPA
Os12g37480 -----MASSPPLVACVLLAAVVFTAVAPPAGAVCVPRNGKAAPGKPGMSAPPKK-----LTPAPPTTPPKAKFILPGGGDLVKALC-----AKTDYPV
Os08g01670 -----MASSMAPAAMAAILLLALLMPATLCSRSGPPSSKHGH-----GGHAKRAPPASPVVVPVAPQAAALVRATC-----NSTAYYD
Os12g18560 -----MASMAPSAMVILVLLVVLPSSTLCSRAGPSSKHGHGG-----HAKRVPPASVPPPPPPPPAPAALVRATC-----NSTSYD
Os02g46290 -----MHPITATLLAAA-----IAPGLTVGSPS-----LINETC-----TATSNYG
Os02g01310 -----MSIRFPMESRSSSSSVVMCCVLMIM-----IAAAAHAQEAEACASPM-----SIEEACRGASET-HHAVAYD
Os05g05640 -----MKASSLAAVAAV-----VAAACSGRAPVAEA-----TIESTCGAAAKG-DRVDVVG
Os03g01020 -----MRMSKALAAVVAISVLS-----AAAMGVDA-----TVESTCSDAAAS-DKRVHLA
Os02g33130 -----MRPSSLALVIVAT-----AILTLSGAAHA-----DVQGTCKAAAGI-DSRISYK
Os02g33380 -----MAQRASRRPAAAAAAVVVA-----VVLAVSGVGA-----TPETACRAAAEE-DRVDYD
Os02g33390 -----MLMMMKPYTAALLAVVA-----VLGVVAVDA-----TVVTTCRAAADA-DARVDYD
Os08g42890 -----MARPAAAVTVLLAVVVV-----SVAASLPSAVVGDAR-----FVARTCK-----RTNHT
Os01g02070 -----MADAG-----FIADTCKN-----KTHNA

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(A)

Figure S4. Comparison of expression of all cell wall invertases during grain development using RMA normalized data from Expression data for reproductive development in rice [20] accessed as accession OS5 from PLEXdb. Data represent the mean of 3 samples \pm standard error.

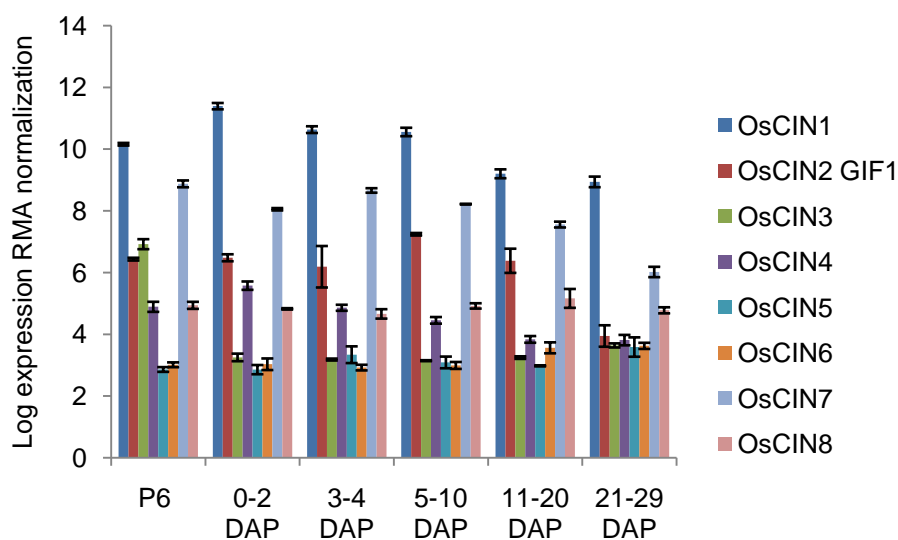


Table S1. Genes with a pairwise mutual coexpression rank <50 with each of the bait genes, *OsINVINH3*, *OsIAA29* and *OsYUC12*. Pearson correlation coefficients (PCC) are shown. Genes listed in order of increasing mutual co-expression rank. Cysteine rich proteins are coloured yellow, ZmEBE homologues are coloured red, INVINH/PMEI homologues are coloured green, putative transcriptional regulators are coloured blue.

Transcript ID	PCC <i>OsYUC12</i>	PCC <i>OsIAA29</i>	PCC <i>OsINVINH3</i>	Product Description
Os12g13960.1	0.8738	0.9242	0.9658	LTPL33 [37]
Os02g07628.1	0.8669	0.9171	0.9448	DEF5 [37]
Os11g45360.1	0.8901	0.8848	0.9293	DEFL15 [37]
Os01g70680.1	0.8909	0.8474	0.9399	DEF1 [37]
Os02g07624.1	0.8217	0.9411	0.9280	DEF4 [37]
Os11g18140.1	0.8363	0.9109	0.9132	ZmEBE 1 homologue
Os04g49720.1	0.8391	0.8957	1.0000	OsINVINH3
Os06g17480.1	0.8499	0.8796	0.9102	OsHAP3D [34]
Os05g07850.1	0.8366	0.8900	0.9073	Leucine-rich repeat receptor-like kinase [39]
Os11g14880.1	0.8300	0.8920	0.9009	LTPL32 [37]
Os11g11430.1	0.8189	1.0000	0.8957	OsIAA29 [40]
Os01g28810.1	0.8250	0.9185	0.8727	expressed protein (nuclear)
Os04g12639.1	0.7898	0.9329	0.8954	ZmEBE 1 homologue
Os08g35670.1	0.8177	0.8742	0.8963	OsRR33 [35]
Os12g12230.1	0.8682	0.8561	0.8678	DEFL43 [37]
Os02g15710.1	0.8613	0.8141	0.8996	plastocyanin like (extracellular)
Os08g16650.1	0.7807	0.9250	0.8677	hypothetical protein (nuclear)
Os02g54960.1	0.7439	0.9141	0.8948	ZmEBE 1 homologue
Os02g07550.1	0.7717	0.8823	0.8725	DEFL1 [37]

Table S1. *Cont.*

Transcript ID	PCC <i>OsYUC12</i>	PCC <i>OsIAA29</i>	PCC <i>OsINVINH3</i>	Product Description
Os09g11790.1	0.8456	0.8099	0.8935	DEFL14 [37]
Os11g03870.1	0.8439	0.8172	0.8885	LTPL31 [37]
Os01g26320.1	0.8027	0.8249	0.8926	ZmEBE 1 homologue
Os08g42890.1	0.7936	0.8257	0.9268	INVINH/PMEI homologue
Os01g12030.1	0.8342	0.8226	0.8387	endoglucanase GH9 (plasma membrane)
Os01g67800.1	0.7783	0.8638	0.8234	retrotransposon protein, putative,
Os12g27940.1	0.8283	0.8332	0.8282	low glutelin content-like (extracellular)
Os02g17230.1	1.0000	0.8189	0.8391	<i>OsYUC12</i>
Os02g07600.1	0.7703	0.8390	0.8661	DEF3 [37]
Os03g39170.1	0.7341	0.8901	0.8410	frigida, putative, expressed
Os05g48560.1	0.7671	0.8302	0.8339	expressed protein
Os10g19925.1	0.7100	0.8584	0.8487	DEFL68 [37]
Os08g04740.1	0.7645	0.8646	0.8193	INVINH/PMEI homologue
Os11g41880.1	0.8008	0.7907	0.8628	Homologue of OBERON1/OBERON2 nuclear PHD finger proteins
Os02g38940.1	0.7604	0.8958	0.8108	cytochrome P450 71D8 (P450 CP7)
Os11g11530.1	0.7693	0.8206	0.8549	ZmEBE 1 homologue
Os07g41290.1	0.7223	0.8968	0.8302	DEFL13 [37]

Table S2. Primers used for qRT-PCR.

Gene ID	L primer	Tm °C	R primer	Tm °C	Product size
Os02g42314	CTGCGAGCTGAAACACTTTG	59.78	TTCTCGCTGCACCTCCTTAT	59.98	105
Os04g49720	GGCCATCGACTACCCCTACT	60.35	CCGCCTCGGTGATCCT	60.76	107
Os11g11430	CAACTATTCCATGTCACCATTTG	59.26	ATGGGACATCACCAAGGAAG	59.78	131
Os02g17230	GAGTTATCGACGTGCTCGAA	59.03	TGCTTTACCATTCCTTTAGCC	59.35	147
Os07g41290	TTGCTACGCACATGTTGAGG	60.87	TGCCTGCAATACTGAGATGC	59.98	123
Os11g14880	CTCATCGCCAGGTTTTGG	60.19	GATGCCAGGCTGATCAATTT	60.04	103
Os11g18140	AGATCGCGTGGGTTGATAAT	59.42	ACAGTGGAAACTGGCCTGA	59.25	112
Os06g17480	GTCGGCCCAACTATGAGTA	59.96	TGCTAATCGATCGACAGACG	59.97	115