Table 1 Suppl. Primers used in this research.

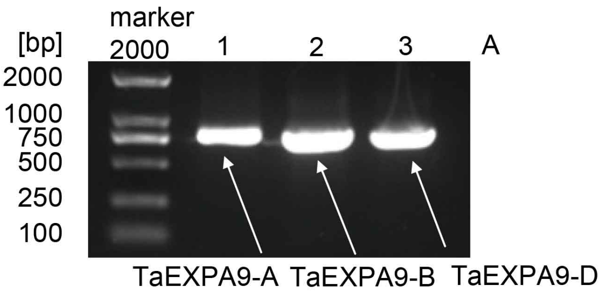
Name	Primer sequences (5’-3’)
TaEXPA9-A	FW: ATGGCCGCCGCAATGC
(RT-qPCR)	RV: CGCACCTCTCCCCCTCGTT
TaEXPA9-B	FW: ATGGCCGCCGCACTGC
(RT-qPCR)	RV: CACCTCTGCCCCTCGTTGAAC
TaEXPA9-D	FW: ATGGCCGCCGCAATGC
(RT-qPCR)	RV: GCGCTGCCCCTCGTTGAA
ACTIN	FW: TCCAATCTATGAGGGATACACGC
(wheat)	RV: TCTTCATTAGATTATCCGTGAGGTC
ACTIN	FW: CCACATGCTATTCTGCGTTTGGACC
(*Arabidopsis*)	RV: CATCCCTTACGATTTCACGCTCTGC
TaEXPA9-A	FW:ATGGCCGCCGCAATGC
(clone the CDS)	RV: CTAGACCCTGAAGTTGTTGCCCTCG
TaEXPA9-B	FW: ATGGCCGCCGCACTGC
(clone the CDS)	RV: TCAGACCCTGAAGTTCTTGCCCTC
TaEXPA9-D	FW: ATGGCCGCCGCAATGC
(clone the CDS)	RV: CTAGACCCTGAAGTTCTTGCCCTCG
TaEXPA9-A	FW: TGACCATGGTAGATCTGATGGCCGCCGCAATGCCACCG
(addition of *Bgl*II)	RV: CCTTTACTAGTCAGATCGACCCTGAAGTTGTTGCCCTCG
TaEXPA9-B	FW: TGACCATGGTAGATCTGATGGCCGCCGCACTGCCACCG
(addition of *Bgl*II)	RV: CCTTTACTAGTCAGATCGACCCTGAAGTTCTTGCCCTC
TaEXPA9-D	FW: TGACCATGGTAGATCTGATGGCCGCCGCAATGCCACCG
(addition of *Bgl*II)	RV: CCTTTACTAGTCAGATCGACCCTGAAGTTGTTGCCCTCG
TaEXPA9-A	FW:GAGAACACGGGGGACTCTAGAATGGCCGCCGCACTGCCACCG
(addition of *Xba*I and *BamH*I)	RV: CCGGGGATCCTCTAGACTAGACCCTGAAGTTGTTGCCCTCG
TaEXPA9-B	FW:GAGAACACGGGGGACTCTAGAATGGCCGCCGCAATGCCACCG
(addition of *Xba*I and *BamH*I)	RV: CCGGGGATCCTCTAGATCAGACCCTGAAGTTCTTGCCCTCG
TaEXPA9-D	FW:GAGAACACGGGGGACTCTAGAATGGCCGCCGCAATGCCACCG
(addition of *Xba*I and *BamH*I)	RV: CCGGGGATCCTCTAGACTAGACCCTGAAGTTCTTGCCCTCG

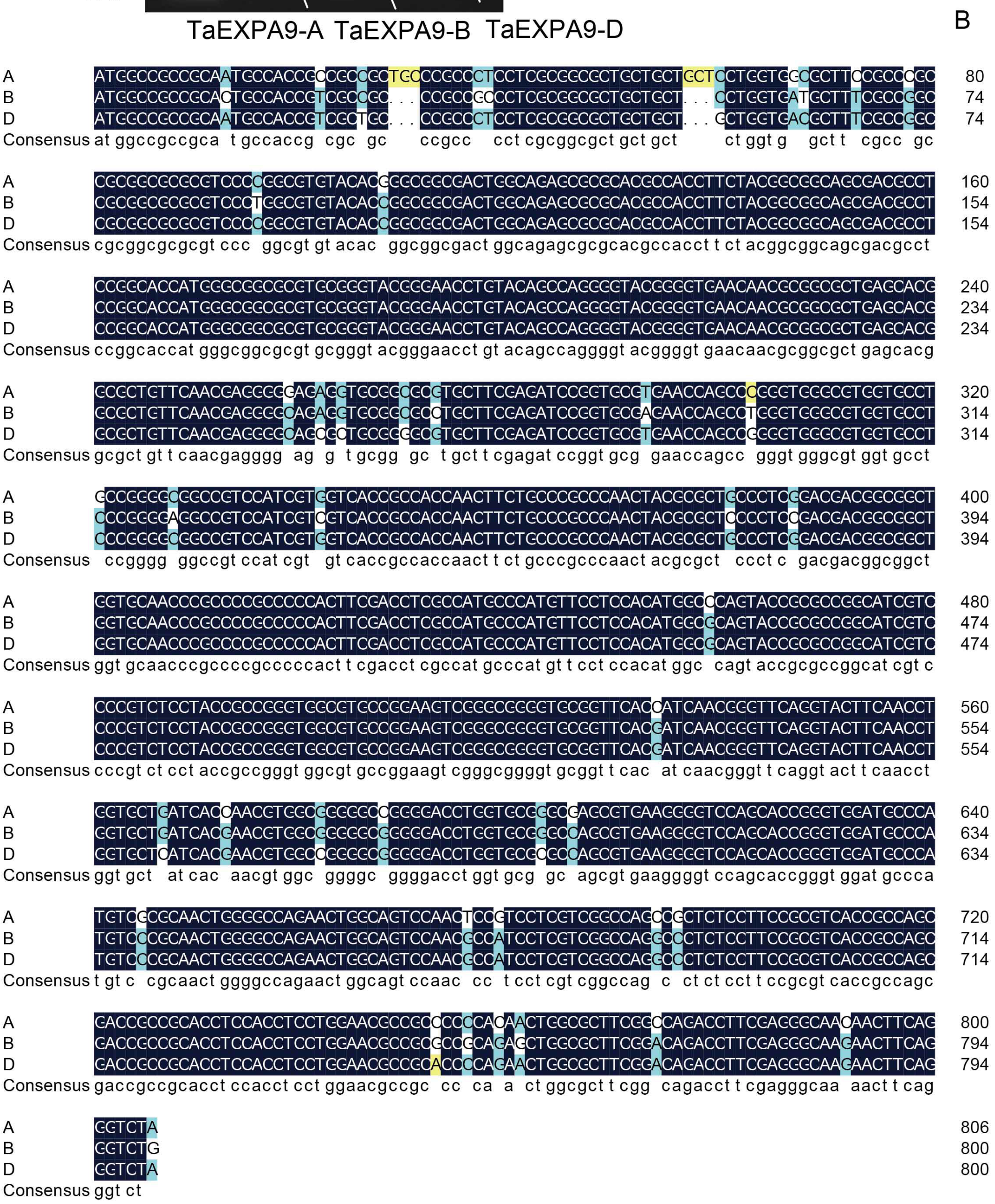
Table 2 Suppl. The physical and chemical properties of *TaEXPA9-A/B/D* proteins predicted by *ExPASy* online site.

Protein	Formula	Molecular mass [kDa]	Isoelectric point	Global hydrophobicity (GRAVY)	Instability index	Aliphatic index
TaEXPA9-A	$C_{1288}H_{1947}N_{367}O_{358}S_{16}$	28.814	9.40	-0.048	43.33	69.96
TaEXPA9-B	$C_{1271}H_{1926}N_{364}O_{358}S_{16}$	28.546	9.51	-0.069	46.23	67.59
TaEXPA9-D	$C_{1274}H_{1935}N_{365}O_{357}S_{16}$	28.590	9.61	-0.039	42.86	69.77

Table 3 Suppl. The number and proportion of amino acids in the TaEXPA9-A/B/D proteins predicted by *ExPASy* online site.

Amino acids	TaEXPA9-A Number of amino acids	Content of amino acid [%]	TaEXPA9-B Number of amino acids	Content of amino acid [%]	TaEXPA9-D Number of amino acids	Content of amino acid [%]
Ala (A)	31	11.6	33	12.4	32	12.0
Gly (G)	30	11.2	30	11.3	30	11.3
Pro (P)	22	8.2	19	7.1	17	6.8
Leu (L)	21	7.8	21	7.1	21	7.5
Ser (S)	19	7.1	21	7.9	20	7.5
Val (V)	19	7.1	17	6.4	17	6.8
Arg (R)	18	6.7	18	6.8	18	6.8
Asn (N)	18	6.7	16	6.0	17	6.4
Thr (T)	13	4.9	13	4.9	14	5.3
Phe (F)	13	4.9	13	4.9	13	4.9
Trp (W)	9	3.4	9	3.4	9	3.4
Tyr (Y)	9	3.4	9	3.4	9	3.4
Cys (C)	8	3.0	8	3.0	8	3.0
Gln (Q)	8	3.0	10	3.8	10	3.8
Met (M)	8	3.0	8	3.0	8	3.0
Asp (D)	7	2.6	7	2.6	7	2.6
IlE (I)	5	1.9	6	2.3	6	2.3
Glu (E)	4	1.5	4	1.5	3	1.1
His (H)	4	1.5	3	1.1	3	1.1
Lys (K)	2	0.7	3	1.1	3	1.1
Pyl (O)	0	0.0	0	0.0	0	0.0
Sec (U)	0	0.0	0	0.0	0	0.0





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B          ATGGCCGCCGCACTGCCACCGTCGCCGC...CCGCCGCCCTCGCGGCGCTGCTGCT...CCTGGTGATGCTTTCGCCGGC   74
D          ATGGCCGCCGCAATGCCACCGTCGCTGC...CCGCCCTCCTCGCGGCGCTGCTGCT...GCTGGTGACGCTTTCGCCGGC   74
Consensus  atggccgccgca tgccaccg cgc gc   ccgcc  cctcgcggcgctgctgct    ctggtg  gctt cgcc gc

A          CGCGGCGCGCGTCCCCGGCGTGTACACGGGCGGCGACTGGCAGAGCGCGCACGCCACCTTCTACGGCGGCAGCGACGCCT   160
B          CGCGGCGCGCGTCCCTGGCGTGTACACCGGCGGCGACTGGCAGAGCGCGCACGCCACCTTCTACGGCGGCAGCGACGCCT   154
D          CGCGGCGCGCGTCCCCGGCGTGTACACCGGCGGCGACTGGCAGAGCGCGCACGCCACCTTCTACGGCGGCAGCGACGCCT   154
Consensus  cgcggcgcgcgtccc ggcgtgtacac ggcggcgactggcagagcgcgcacgccaccttctacggcggcagcgacgcct

A          CCGGCACCATGGGCGGCGCGTGCGGGTACGGGAACCTGTACAGCCAGGGGTACGGGGTGAACAACGCGGCGCTGAGCACG   240
B          CCGGCACCATGGGCGGCGCGTGCGGGTACGGGAACCTGTACAGCCAGGGGTACGGGGTGAACAACGCGGCGCTGAGCACG   234
D          CCGGCACCATGGGCGGCGCGTGCGGGTACGGGAACCTGTACAGCCAGGGGTACGGGGTGAACAACGCGGCGCTGAGCACG   234
Consensus  ccggcaccatgggcggcgcgtgcgggtacgggaacctgtacagccaggggtacggggtgaacaacgcggcgctgagcacg

A          GCGCTGTTCAACGAGGGGGAGAGGTGCGGCGCGTGCTTCGAGATCCGGTGCGTGAACCAGCCCGGGTGGGCGTGGTGCCT   320
B          GCGCTGTTCAACGAGGGGCAGAGGTGCGGCGCCTGCTTCGAGATCCGGTGCGAGAACCAGCCTGGGTGGGCGTGGTGCCT   314
D          GCGCTGTTCAACGAGGGGCAGCGCTGCGGGGCGTGCTTCGAGATCCGGTGCGTGAACCAGCCGGGGTGGGCGTGGTGCCT   314
Consensus  gcgctgttcaacgagggg ag g tgcgg gc tgcttcgagatccggtgcg gaaccagcc gggtgggcgtggtgcct

A          GCCGGGGCGGCCGTCCATCGTGGTCACCGCCACCAACTTCTGCCCGCCCAACTACGCGCTGCCCTCGGACGACGGCGGCT   400
B          CCCGGGGAGGCCGTCCATCGTCGTCACCGCCACCAACTTCTGCCCGCCCAACTACGCGCTCCCCTCCGACGACGGCGGCT   394
D          CCCGGGGCGGCCGTCCATCGTGGTCACCGCCACCAACTTCTGCCCGCCCAACTACGCGCTGCCCTCGGACGACGGCGGCT   394
Consensus   ccgggg ggccgtccatcgt gtcaccgccaccaacttctgcccgcccaactacgcgct ccctc gacgacggcggct

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D          GGTGCAACCCGCCCCGCCCCCACTTCGACCTCGCCATGCCCATGTTCCTCCACATGGCGCAGTACCGCGCCGGCATCGTC   474
Consensus  ggtgcaacccgccccgcccccacttcgacctcgccatgcccatgttcctccacatggc cagtaccgcgccggcatcgtc

A          CCCGTCTCCTACCGCCGGGTGGCGTGCCGGAAGTCGGGCGGGGTGCGGTTCACCATCAACGGGTTCAGGTACTTCAACCT   560
B          CCCGTCTCCTACCGCCGGGTGGCGTGCCGGAAGTCGGGCGGGGTGCGGTTCACGATCAACGGGTTCAGGTACTTCAACCT   554
D          CCCGTCTCCTACCGCCGGGTGGCGTGCCGGAAGTCGGGCGGGGTGCGGTTCACGATCAACGGGTTCAGGTACTTCAACCT   554
Consensus  cccgtctcctaccgccgggtggcgtgccggaagtcgggcggggtgcggttcac atcaacgggttcaggtacttcaacct

A          GGTGCTGATCACCAACGTGGCGGGGGCCGGGGACCTGGTGCGGGCGAGCGTGAAGGGGTCCAGCACCGGGTGGATGCCCA   640
B          GGTGCTGATCACGAACGTGGCGGGGGCGGGGGACCTGGTGCGGGCCAGCGTGAAGGGGTCCAGCACCGGGTGGATGCCCA   634
D          GGTGCTCATCACGAACGTGGCCGGGGCGGGGGACCTGGTGCGCGCCAGCGTGAAGGGGTCCAGCACCGGGTGGATGCCCA   634
Consensus  ggtgct atcac aacgtggc ggggc ggggacctggtgcg gc agcgtgaaggggtccagcaccgggtggatgccca

A          TGTCGCGCAACTGGGGCCAGAACTGGCAGTCCAACTCCGTCCTCGTCGGCCAGCCGCTCTCCTTCCGCGTCACCGCCAGC   720
B          TGTCCCGCAACTGGGGCCAGAACTGGCAGTCCAACGCCATCCTCGTCGGCCAGGCCCTCTCCTTCCGCGTCACCGCCAGC   714
D          TGTCCCGCAACTGGGGCCAGAACTGGCAGTCCAACGCCATCCTCGTCGGCCAGGCCCTCTCCTTCCGCGTCACCGCCAGC   714
Consensus  tgtc cgcaactggggccagaactggcagtccaac cc tcctcgtcggccag c ctctccttccgcgtcaccgccagc

A          GACCGCCGCACCTCCACCTCCTGGAACGCCGCCCCCCACAACTGGCGCTTCGGCCAGACCTTCGAGGGCAACAACTTCAG   800
B          GACCGCCGCACCTCCACCTCCTGGAACGCCGCGCCGCAGAGCTGGCGCTTCGGACAGACCTTCGAGGGCAAGAACTTCAG   794
D          GACCGCCGCACCTCCACCTCCTGGAACGCCGCACCCCAGAACTGGCGCTTCGGACAGACCTTCGAGGGCAAGAACTTCAG   794
Consensus  gaccgccgcacctccacctcctggaacgccgc cc ca a ctggcgcttcgg cagaccttcgagggcaa aacttcag

A          GGTCTA                                                                             806
B          GGTCTG                                                                             800
D          GGTCTA                                                                             800
Consensus  ggtct
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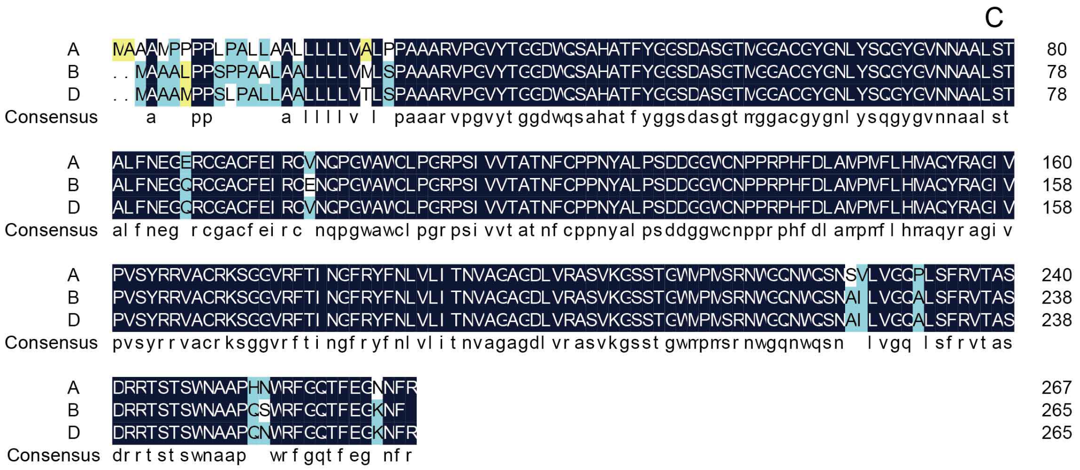
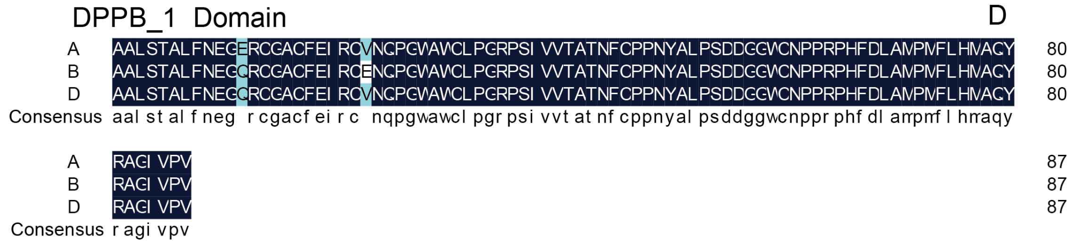
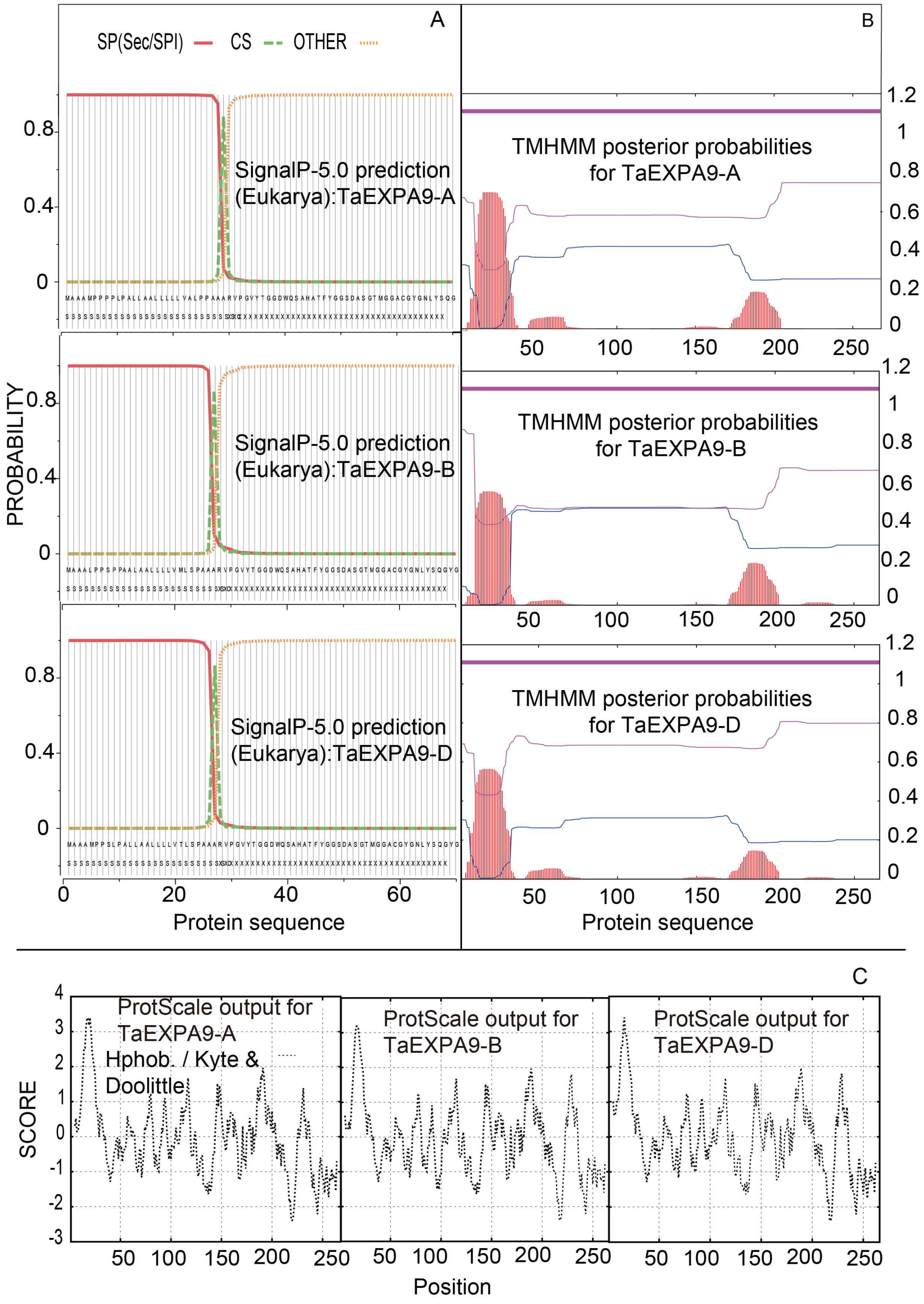


DPPB_1 Domain



Pollen_allerg_1 Domain

Fig. 1 Suppl. Electrophoretic gel diagram and sequence contrast of *TaEXPA9-A/B/D*. *A* - Electrophoresis gel showing the PCR-amplified *TaEXPA9* gene. Lane 1 shows the *TaEXPA9-A* gene; Lane 2 shows the *TaEXPA9-B* gene; and Lane 3 shows the *TaEXPA9-D* gene. *B* - Sequence analysis of *TaEXPA9-A/B/D*. Alignment of the CDS regions of *TaEXPA9-A/B/D*. *C* - Alignment of *TaEXPA9-A/B/D* proteins. *D* - Alignment of the DPPB_1 domain of *TaEXPA9-A/B/D*. *E* - Alignment of the Pollen_allerg_1 domain of *TaEXPA9-A/B/D*.


A
SP(Sec/SPI)
CS
OTHER
SignalP-5.0 prediction (Eukarya):TaEXPA9-A
M A A A M P P P P L P A L L A A L L L L L V A L P P A A A R V P G V Y T G G D W Q S A H A T F Y G G S D A S G T M G G A C G Y G N L Y S Q G
SignalP-5.0 prediction (Eukarya):TaEXPA9-B
M A A A L P P S P P A A L A A L L L L V M L S P A A A R V P G V Y T G G D W Q S A H A T F Y G G S D A S G T M G G A C G Y G N L Y S Q G Y G
SignalP-5.0 prediction (Eukarya):TaEXPA9-D
M A A A M P P S L P A L L A A L L L L V T L S P A A A R V P G V Y T G G D W Q S A H A T F Y G G S D A S G T M G G A C G Y G N L Y S Q G Y G
PROBABILITY
0.8
0.4
0
0
20
40
60
Protein sequence
B
TMHMM posterior probabilities for TaEXPA9-A
TMHMM posterior probabilities for TaEXPA9-B
TMHMM posterior probabilities for TaEXPA9-D
1.2
1
0.8
0.6
0.4
0.2
0
50
100
150
200
250
Protein sequence
C
ProtScale output for TaEXPA9-A
Hphob. / Kyte & Doolittle
ProtScale output for TaEXPA9-B
ProtScale output for TaEXPA9-D
SCORE
4
3
2
1
0
-1
-2
-3
50
100
150
200
250
Position

D

Analysis Report	SeqID:	*TaEXPA9-A*	*TaEXPA9-B*	*TaEXPA9-D*
SVM	LOCALIZATION	RELIABILILY	RELIABILILY	RELIABILILY
Amino Acid Comp.	Extracellular	0.398	0.450	0.471
N-peptide Comp	Extracellular	0.519	0.607	0.642
Partitioned seq.Comp.	Extracellular	0.708	0.751	0.747
Physico-chemical Comp.	PlasmaMembrance	0.680	0.540	0.646
Neighboring seq.Comp	Extracellular	0.871	0.847	0.890
CELLO Prediction				
	Extracellular	2.685*	3.194*	3.396*
	PlasmaMembrane	1.296	0.980	0.826
	Vacuole	0.354	0.257	0.266
	Lysosomal	0.265	0.160	0.163
	Nuclear	0.128	0.118	0.101
	Mitochondrial	0.089	0.092	0.080
	Chloroplast	0.068	0.090	0.073
	Cytoplasmic	0.041	0.044	0.037
	ER	0.036	0.029	0.027
	Golgi	0.016	0.013	0.012
	Peroxisomal	0.013	0.012	0.011
	Cytoskeletal	0.010	0.010	0.009

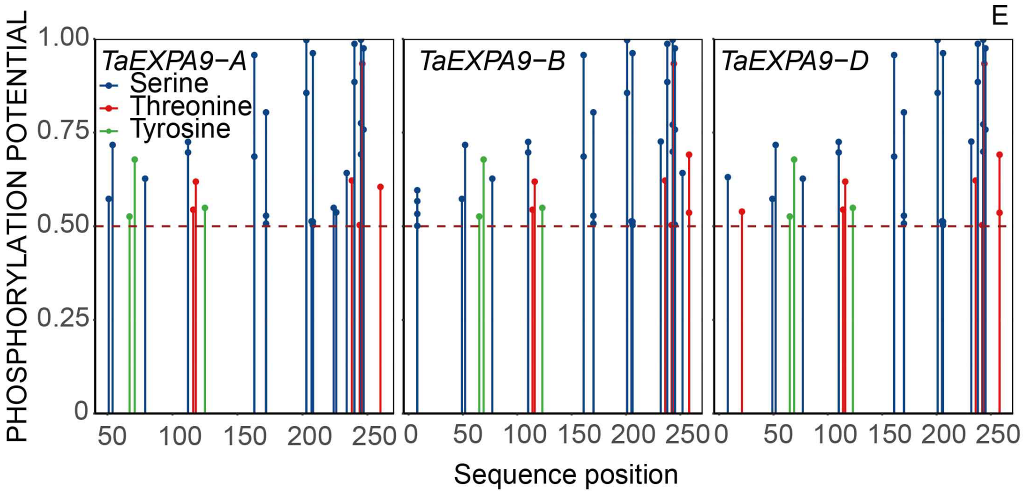
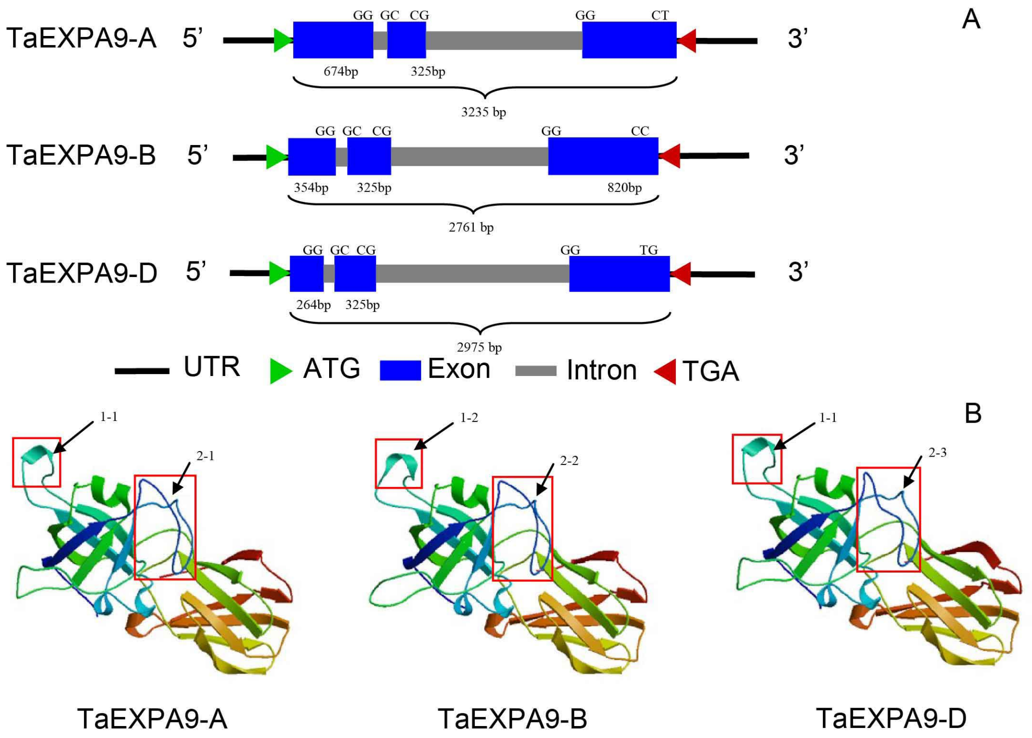
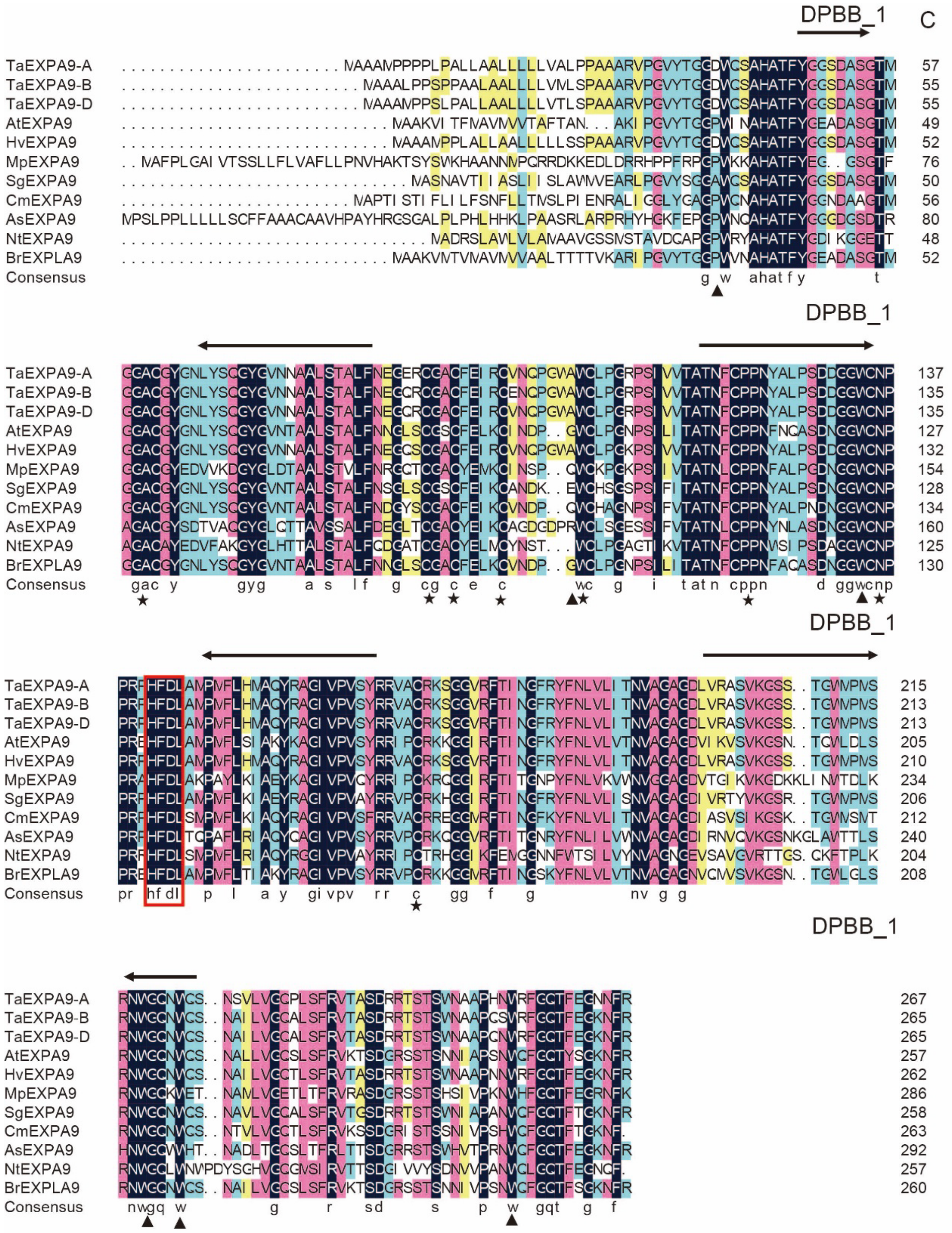


Fig. 2 Suppl. Five bioinformatics analysis of *TaEXPA9-A/B/D*. *A* - The signal peptide sites of *TaEXPA9-A/B/D* proteins predicted by *SignalP 4.1* server. *B* - The transmembrane consatruction analysis of *TaEXPA9-A/B/D* proteins predicted by *TMHMM* server *v.2.0*. *C* - The hydropathicity analysis of *TaEXPA9-A/B/D* proteins predicted by *ExPASy-Prot* scale. *D* - The subcellular localization analysis of *TaEXPA9-A/B/D* proteins predicted by *CELLO v 2.5*. *E* - The phosphorylation sites analysis of TaEXPA9-A/B/D proteins predicted by *NetPhos*.


A
TaEXPA9-A 5'
GG GC CG
GG CT
674bp
325bp
3235 bp
3'
TaEXPA9-B 5'
GG GC CG
GG CC
354bp
325bp
820bp
2761 bp
3'
TaEXPA9-D 5'
GG GC CG
GG TG
264bp
325bp
2975 bp
3'
UTR
ATG
Exon
Intron
TGA
B
1-1
2-1
1-2
2-2
1-1
2-3
TaEXPA9-A
TaEXPA9-B
TaEXPA9-D


C
DPBB_1
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HvEXPA9 ............................MAAAMPPLALLAALLLLLSSPAAARVPGVYTGGDWCSAHATFYGGSDASGTM 52
MpEXPA9 ..MAFPLGAI VTSSLLFLVAFLLPNVHAKTSYSWKHAANNMPGRRDKKEDLDRRHPPFRPGPWKKAHATFYEG..GSGTF 76
SgEXPA9 ....MASNAVTI I ASLI I SLAWMVEARLPGVYSGGAWCSAHATFYGGSDASGTM 50
CmEXPA9 ....MAPTI STI FLI LFSNFLLTMSLPI ENRALI GGLYGAGPWCNAHATFYGGNDAAGTM 56
AsEXPA9 MPSLPPLLLLLSCFFAAACAAVHPAYHRGSGALPLPHLHHKLPAASRLARPRHYHGKFEPGPWNQAHATFYGGGDGSDTR 80
NtEXPA9 ...................................MADRSLAWLVLAMAAVGSSMSTAVDCAPGPWRYAHATFYGDI KGGETT 48
BrEXPLA9 ............................MAAKVMTVMAVMVVAALTTTTVKARI PGVYTGGPWVNAHATFYGEADASGTM 52
Consensus g w ahat f y t
DPBB_1
TaEXPA9-A GGACGYGNLYSQGYGVNNAALSTALFNEGERCGACFEI RCVNCPGWAVCLPGRPSI VVTATNFCPPNYALPSDDGGWCNP 137
TaEXPA9-B GGACGYGNLYSQGYGVNNAALSTALFNEGQRCGACFEI RCENCPGWAVCLPGRPSI VVTATNFCPPNYALPSDDGGWCNP 135
TaEXPA9-D GGACGYGNLYSQGYGVNNAALSTALFNEGQRCGACFEI RCVNCPGWAVCLPGRPSI VVTATNFCPPNYALPSDDGGWCNP 135
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SgEXPA9 GGACGYGNLYSQGYGVNTAALSTALFNSGLSCGSCFEI KCANDK..EWCHSGSPSI FI TATNFCPPNYALPSDNGGWCNP 128
CmEXPA9 GGACGYGNLYSQGYGVNTAALSTALFNDGYSCGACFEI KCVNDP..GWCHAGNPSI FVTATNFCPPNYALPNDNGGWCNP 134
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BrEXPLA9 GGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFELKCVNDP..GWCLPGNPSI LI TATNFCPPNFACASDNGGWCNP 130
Consensus gac y gyg a s lf g cg c e c wc g i tat n cppn d ggwcnp
DPBB_1
TaEXPA9-A PRFHFDLAMPMFLHMAQYRAGI VPVSYRRVACRKSGGVRFTI NGFRYFNLVLI TNVAGAGDLVRASVKGSS..TGWMPMS 215
TaEXPA9-B PRFHFDLAMPMFLHMAQYRAGI VPVSYRRVACRKSGGVRFTI NGFRYFNLVLI TNVAGAGDLVRASVKGSS..TGWMPMS 213
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CmEXPA9 PRFHFDLSMPMFLKI AQYKAGI VPVSFRRVACRREGGMRFTI NGFKYFNLVLI TNVAGAGDI ASVSI KGSK..TGWMSMT 212
AsEXPA9 PRFHFDLTQPAFLRI AQYQAGI VPVSYRRVPCRKQGGVRFTI TGNRYFNLI LVWNVAGAGDI RNVQVKGSNKGLAWTTLS 240
NtEXPA9 PRFHFDLSMPMFLRI AQYRGGI VPVAYRRI PQTRHGGI KFEMGGNNFVTSI LVYNVAGNGEVSAVGVRTTGS.GKFTPLK 204
BrEXPLA9 PREHFDLAMPMFLTI AKYRAGI VPVSYRRVPCRKKGGMRFTI NGSKYFNLVLVTNVAGAGNVQMVSVKGSN..TGWLGLS 208
Consensus pr hf dl p l a y gi vpv rr c gg f g nv g g
DPBB_1
TaEXPA9-A RNWGQNWQS..NSVLVGQPLSFRVTASDRRTSTSWNAAPHNWRFGQTFEGNNFR 267
TaEXPA9-B RNWGQNWQS..NAI LVGQALSFRVTASDRRTSTSWNAAPQSWRFGQTFEGKNFR 265
TaEXPA9-D RNWGQNWQS..NAI LVGQALSFRVTASDRRTSTSWNAAPQNWRFGQTFEGKNFR 265
AtEXPA9 RNWGQNWQS..NALLVGQSLSFRVKTSDGRSSTSNNI APSNWQFGQTYSGKNFR 257
HvEXPA9 RNWGQNWQS..NAI LVGQTLSFRVTASDRRTSTSWNAAPNNWRFGQTFEGKNFR 262
MpEXPA9 RNWGQKWET..NAMLVGETLTFRVRASDGRSSTSHSI VPKNWHFGQTFEGRNFK 286
SgEXPA9 RNWGQNWQS..NAVLVGQALSFRVTGSDRRTSTSWNI APANWQFGQTFTGKNFR 258
CmEXPA9 RNWGQNWQS..NTVLVGQTLSFRVKSSDGRI STSSNI VPSHWQFGQTFTGKNF. 263
AsEXPA9 HNWGQVWHT..NADLTGQSLTFRLTTSDGRRSTSWHVTPRNWQFGQTFEGKNFR 292
NtEXPA9 RNWGQLWNWPDYSGHVQGQGMSI RVTTSDGI VVYSDNVVPANWQLGQTFEGNQF. 257
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Consensus nwgq w g r sd s p w gqt g f

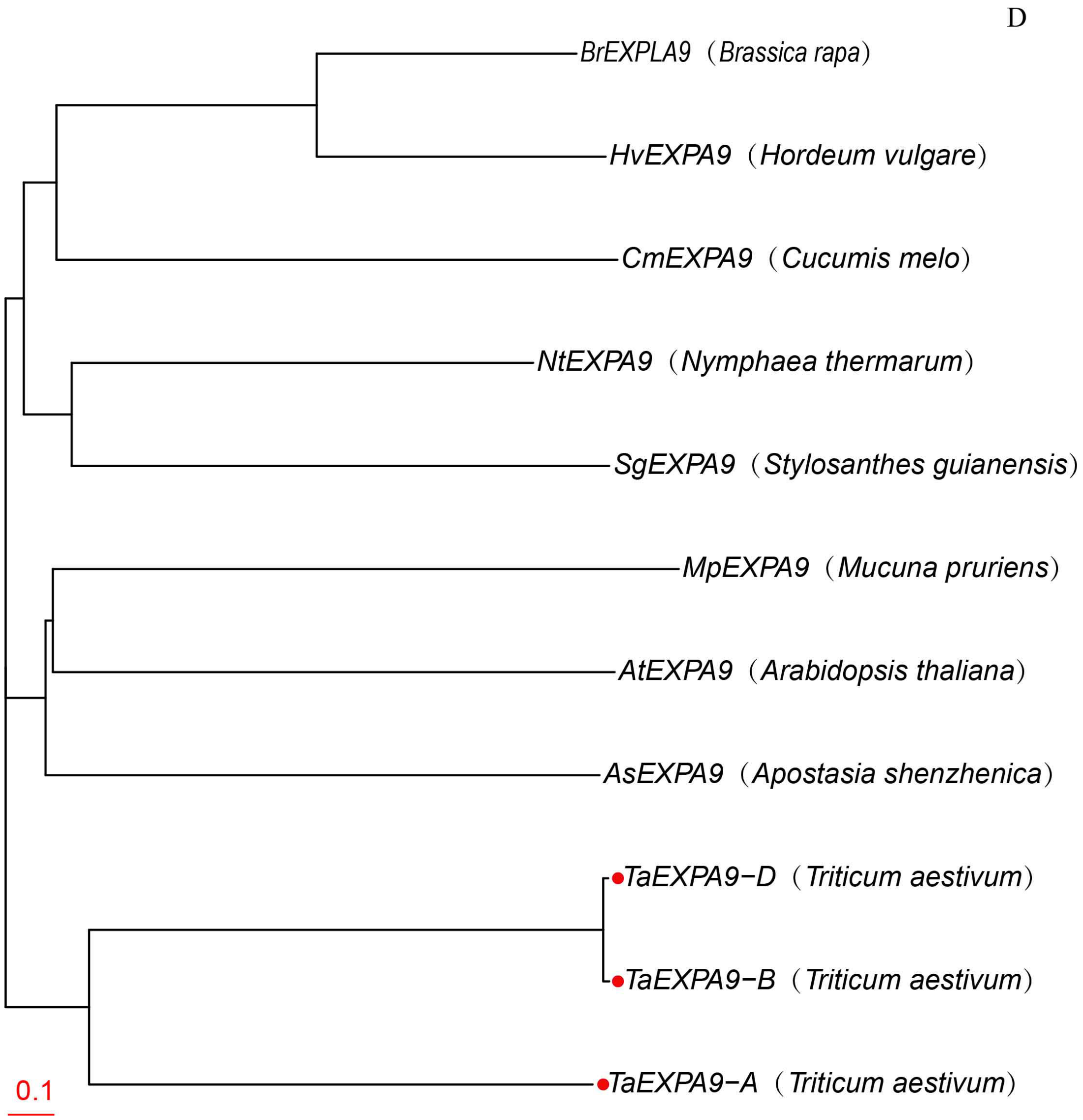
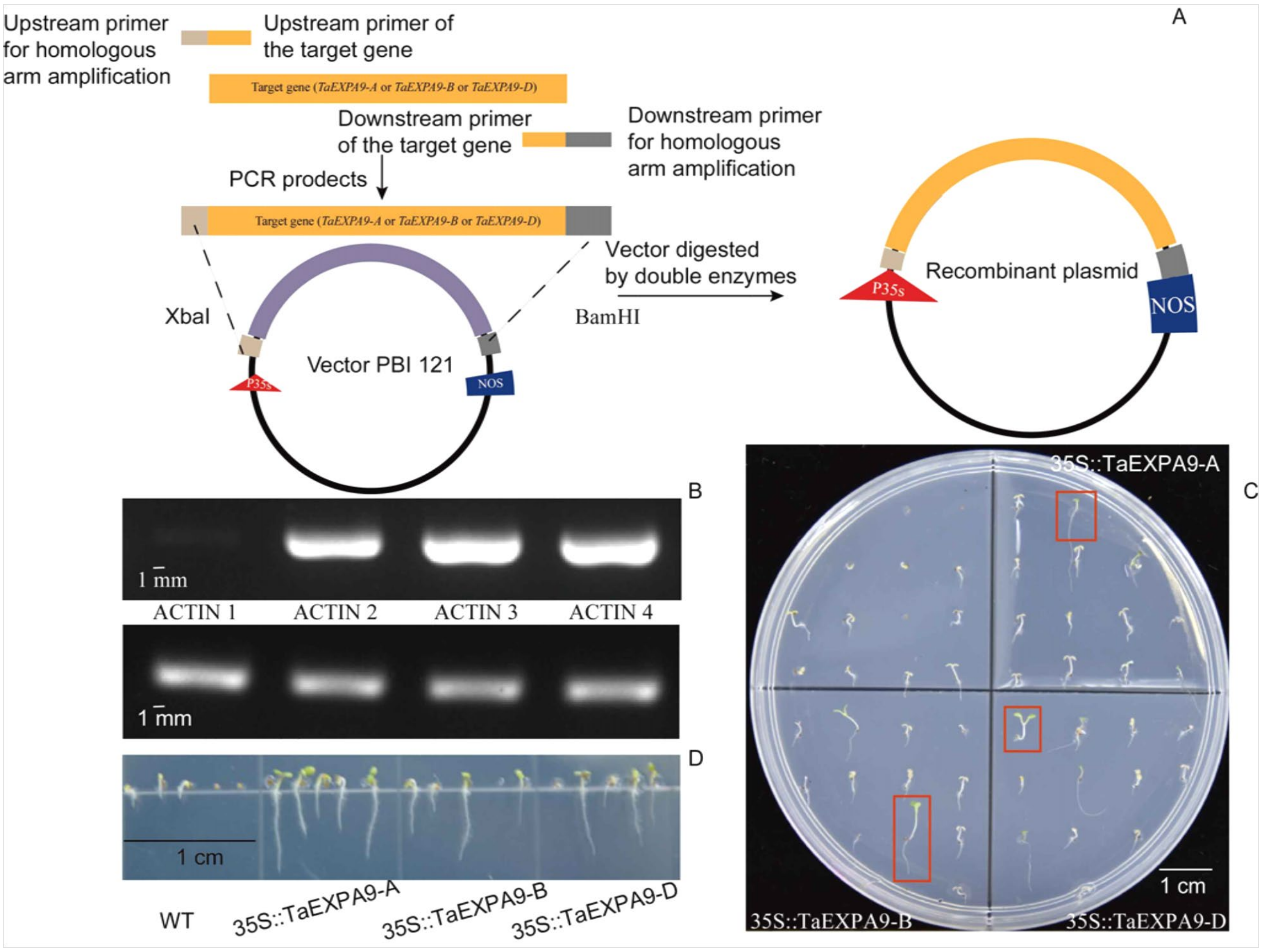
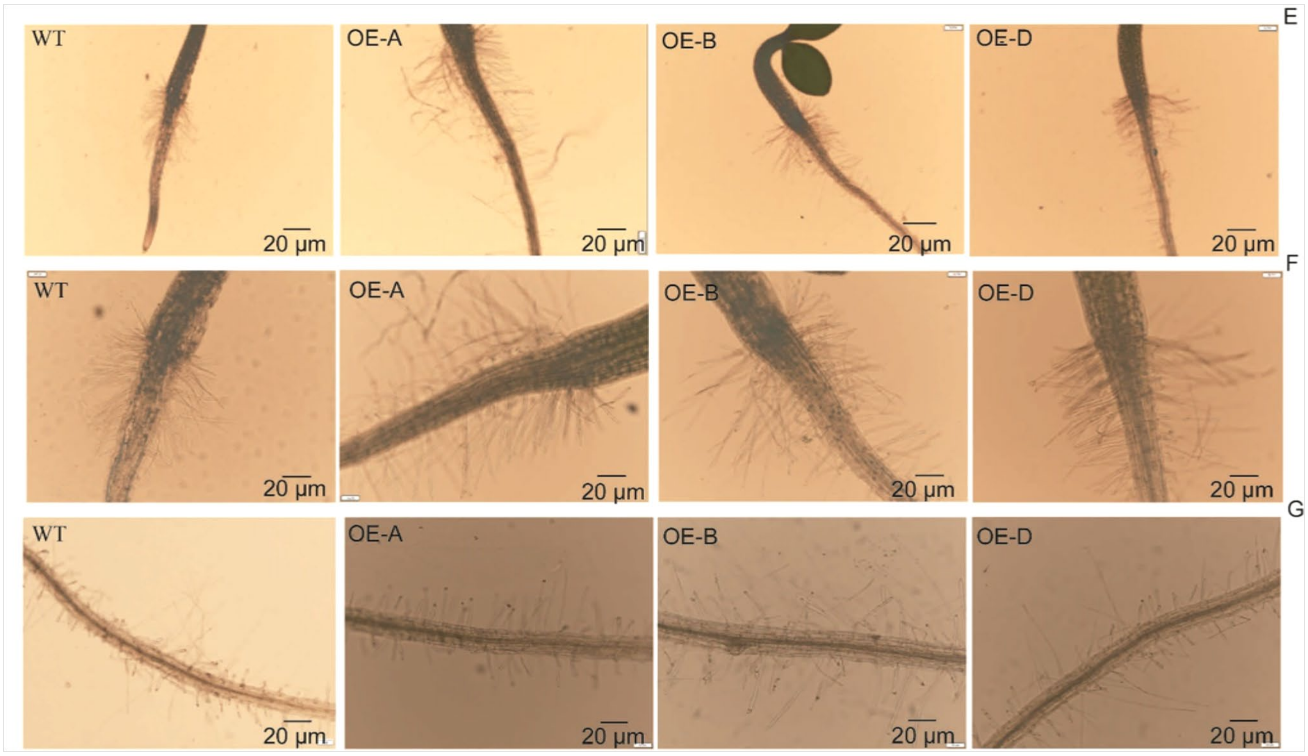


Fig. 3. Suppl. Gene structure and tertiary structure model of *TaEXPA9-A/B/D*. Comparative analysis and phylogenetic construction of *EXPA9* and *EXPLA9* proteins. *A* - Structure of *TaEXPA9-A/B/D*. *B* - The tertiary structure model of *TaEXPA9-A/B/D* proteins predicted by *ExPASy-SWISS-MODEL*. The dark blue region is the signal peptide region, the green region is the catalytic region, the yellow and red areas were cellulose binding areas, the red boxes represent the difference area. *C* - Alignment analysis of the amino acid sequences of TaEXPA9-A/B/D with EXPA9 and EXPLA9 proteins in eight other plant species. AtEXPA9 (*Arabidopsis thaliana*), HvEXPA9 (*Hordeum vulgare*), MpEXPA9 (*Mucuna pruriens*), SgEXPA9 (*Stylosanthes guianensis*), CmEXPA9 (*Cucumis melo*), AsEXPA9 (*Apostasia shenzhenica*), NtEXPA9 (*Nymphaea thermarum*), BrEXPLA9 (*Brassica rapa*). The dark blue represents 100 % identity, the pink represents 75 % identity, and the blue-green represents 50 % identity, as defined by *ClustalX*. The *black arrows* indicate two conserved domains: DPDD_1 domain. (★) indicates eight C (cysteine) residues. (▲) indicates six W (tryptophan) residues in the C-terminal region. The *red box* denotes the HFD (His-Phe-Asp) motif in the central region of the sequence (for interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article). *D* - The genetic relationship of expansin protein sequences in different species was analyzed. Phylogenetic tree of TaEXPA9-A/B/D with the above ten proteins.


A
Upstream primer for homologous arm amplification
Upstream primer of the target gene
Target gene (TaEXPA9-A or TaEXPA9-B or TaEXPA9-D)
Downstream primer of the target gene
Downstream primer for homologous arm amplification
PCR prodects
Target gene (TaEXPA9-A or TaEXPA9-B or TaEXPA9-D)
XbaI
Vector PBI 121
P35s
NOS
Vector digested by double enzymes
BamHI
Recombinant plasmid
P35s
NOS
B
1 mm
ACTIN 1
ACTIN 2
ACTIN 3
ACTIN 4
1 mm
C
35S::TaEXPA9-A
35S::TaEXPA9-B
35S::TaEXPA9-D
1 cm
D
1 cm
WT
35S::TaEXPA9-A
35S::TaEXPA9-B
35S::TaEXPA9-D


E
WT
OE-A
OE-B
OE-D
20 μm
F
WT
OE-A
OE-B
OE-D
20 μm
G
WT
OE-A
OE-B
OE-D
20 μm

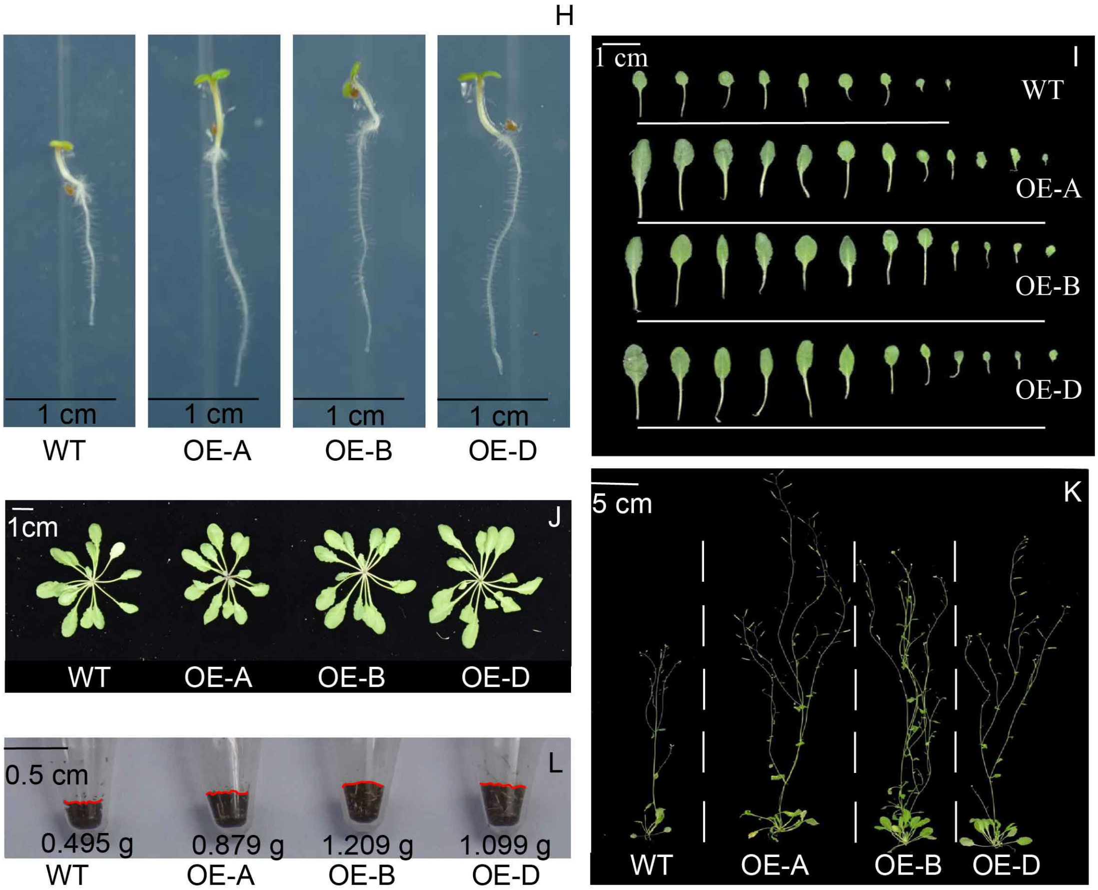


Fig. 4. Suppl. Identification and phenotypic observation results of *A. thaliana* overexpressing *TaEXPA9-A*, *B,* and *D*. WT, OE-A, OE-B, and OE-D represent wild-type and overexpressed *TaEXPA9-A/B/D A. thaliana*, respectively. *A* - Structure of the expression vector. *B* - The expressions of *TaEXPA9-A*,*B,* and *D* in transgenic lines as determined by RT-PCR. *C* - Screening of resistant transgenic plants. The green plants selected in the *red box* are overexpressed plants showing resistance, which can be used for subsequent phenotypic observation tests. *Scale bars* 1 cm. *D* - Observation on hypocotyl of *A. thaliana*, *scale bars* 1 cm. Observation on lateral root of *A. thaliana*. Magnification 10×10 and 10×40, *scale bars* 20 µm (*E*, *F*). *G* - Observation on root hair length of *A. thaliana*. *Scale bars* 20 µm. *H* - Observation on root length of *A. thaliana*. Magnification, 10×10, *scale* bars 1 cm. Observation on leaf number and rosette diameter of *A. thaliana*. *Scale bars* 1 cm (*I*, *J*). *K* - *A. thaliana* plants height. *Scale bars* 5 cm. *L* - *A. thaliana* seed yield (per plant). *Scale bars* 0.5 cm.