

Supplementary Material

Supplemental Table S1. Conserved motifs predicted by MEME program in PtEXs.

motif	Width	E-value	Motif sequence
1	50	4.1e-781	RTGWQPMSRNWQNWQSNLYLNGQSLSFKVTTS DGRTVVSYNVAPSSWSF
2	41	1.8e-664	HATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFN
3	26	1.8e-438	SDNGGWCNPPRPHFDLAMPFLKIAE
4	50	7.5e-793	GIVPVSYRRVPCRRRGGIRFTINGHSYFNLVLITNVGGAGDVHAVSVKGS
5	15	1.5e-261	NGLSCGACFEIRCVN
6	21	1.5e-210	SGSPSILITATNFCPPNYALP
7	32	5.60E-98	ELFAYGVVDVEFRRIPCRFPGYNLMFKVHEHS
8	28	9.70E-62	DGKWIWARNVLPEDWKPGMTYDSGVQIT
9	8	7.90E-57	QTFEGKQF
10	29	1.60E-51	DDGVNVVVTDYGEDNTDFILSTRAYARM

Supplementary Table S2. TPM values of PtEXs genes in transcriptome sequencing of nine poplar tissues.

[illegible]

<i>PtEXPA20</i>	5.6387	1.28375	3.6212	0.3856	0.07525	4.1132	0	5.7772	2.68995
<i>PtEXPB3</i>	6.74765	6.9824	6.26605	1.9664	1.99285	5.44905	1.3299	8.34675	4.5688
<i>PtEXPA17</i>	5.6207	7.59005	6.1199	2.00295	0.78285	5.9735	5.79455	6.853	3.51815
<i>PtEXPA24</i>	0	0.61075	0.11505	0.05515	0	2.25425	0.3636	1.2403	0.499
<i>PtEXLB2</i>	3.37085	3.848	3.02845	4.6962	4.05775	4.19255	3.86825	4.03695	5.6417
<i>PtEXLB3</i>	0.1837	7.9846	0	0.3054	0	0.0831	4.1475	2.27375	4.7496
<i>PtEXPA32</i>	7.0776	4.63425	5.56275	4.8263	7.69545	8.35875	4.6268	7.7714	5.3472
<i>PtEXPA4</i>	0.93515	0.23025	0	0.08745	0	0	0.75065	0.08535	0
<i>PtEXPA1</i>	0.4998	0	0.17095	0	0	0	0.2852	0.05415	0
<i>PtEXPA13</i>	0	0	0	0	0	0	0	0	0
<i>PtEXPA12</i>	0	0	0	0	0	1.0142	1.06055	0.0695	0
<i>PtEXPA14</i>	2.7896	0.0787	0.13175	0	0	0.09165	1.0624	0.03945	0
<i>PtEXLB1</i>	0.27865	0.20205	3.1513	0.20785	0	0.2921	5.85225	2.0942	0.5947
<i>PtEXLB5</i>	0	4.9367	2.613	3.2479	0	3.3525	6.30125	3.83125	1.27005
<i>PtEXLA2</i>	4.04755	4.84995	1.5976	6.84115	3.61765	4.6709	3.3189	3.90135	6.91395
<i>PtEXPA6</i>	4.8876	0.603	0.3407	0.91245	4.21285	2.50185	0.1104	1.4972	0.63915
<i>PtEXPA8</i>	6.9987	5.39455	3.74755	5.33815	7.95215	7.2564	2.92095	5.0085	6.2822
<i>PtEXPA22</i>	4.1977	6.19065	5.7976	1.06965	0.0631	0.0807	0.0757	6.7203	0.76295
<i>PtEXPA15</i>	5.166	0.7039	0	0	0	0.0642	0.70135	0.5274	0.1555
<i>PtEXPA18</i>	0	0.9607	2.62255	0.05925	0	0	1.18215	2.5502	0.05715
<i>PtEXPA27</i>	7.3889	6.40155	4.2291	3.08545	6.3123	5.29515	2.143	7.0422	4.17595
<i>PtEXPA30</i>	5.52195	8.7086	3.3992	3.8161	3.9579	4.10925	3.30105	4.8975	3.8507
<i>PtEXPA26</i>	9.83135	8.6641	5.694	3.2896	5.21195	7.07055	6.4496	7.86615	4.5251
<i>PtEXPA5</i>	2.8184	2.43445	1.9271	2.1785	3.41605	3.45915	1.3122	2.77135	2.53985
<i>PtEXLA1</i>	3.18435	5.59525	1.50705	7.33715	4.99605	0.5511	7.30765	2.95895	3.03725
<i>PtEXPA31</i>	3.8848	4.98595	3.6256	2.38045	4.94465	7.3377	1.76715	6.3342	2.4432

Supplemental Table S3. List of primer sequences used in qRT-PCR reactions

Gene name	Forward Primer	Reverse Primer	Primer amplification efficiency
UBQ	GTTGATTTTGTCTGGGAAGC	GATCTTGCCCTTCACGTTGT	101%
<i>PtEXLA2</i>	GCTGGATGTGGTGCTTGTTT	TGTCTTGACCCATGCCCTTG	101.9%
<i>PtEXPB3</i>	TGAACTCCCAGTCATTTATCG	TCTAGCCACTCAGTGCCTCC	103.3%
<i>PtEXPA3</i>	ACTCAGGCAGCCCGTCTATT	GGAATCCGTTTATTGTGAACCT	102.5%
<i>PtEXPA12</i>	GCCATTCCAGTACCATCACC	ACAGACACCGCACGAACATC	102.7%
<i>PtEXPA13</i>	TGTAACCCACCTCGTCCTCA	CGGAAACCGTTGATAGTGAA	104.3%
<i>PtEXPA17</i>	TTGATGTGGAAGGGTGAAGG	GTCAGCACCACCGTAGAAGG	105%
<i>PtEXPA18</i>	ATCCTCCTCGTCCTCACTTC	TTCACGCTCACTTTCACAATA	105.6%
<i>PtEXPA19</i>	GGGTCTTGCTACGAGATTAGG	AAAGTGTTGTTGAGGAGGGTT	101.5%
<i>PtEXPA27</i>	AGGGAGGGATTAGATTACCA	GATAGGCTTTGACCGTTGAG	105.3%

amplification efficiency of each primer pair was obtained by combining the dominant equation of the regression between the CT value of amplification and the dilution gradient ($E = (10^{(-1/\text{Slope})} - 1)\%$). As PtEXLA2 and PtEXPA12 were not expressed in 1000×, the amplification efficiencies for these two genes were calculated based on three concentration gradients.