

Figure S1. The phylogenetic relationships of expansin proteins between sweetpotato and Y22.

(a): The phylogenetic relationships between IbEXP1, IbEXP2, IbEXPL1 and Y22 expansin proteins. (b): The expression heatmap of the Y22 expansin genes (RPKM > 1).

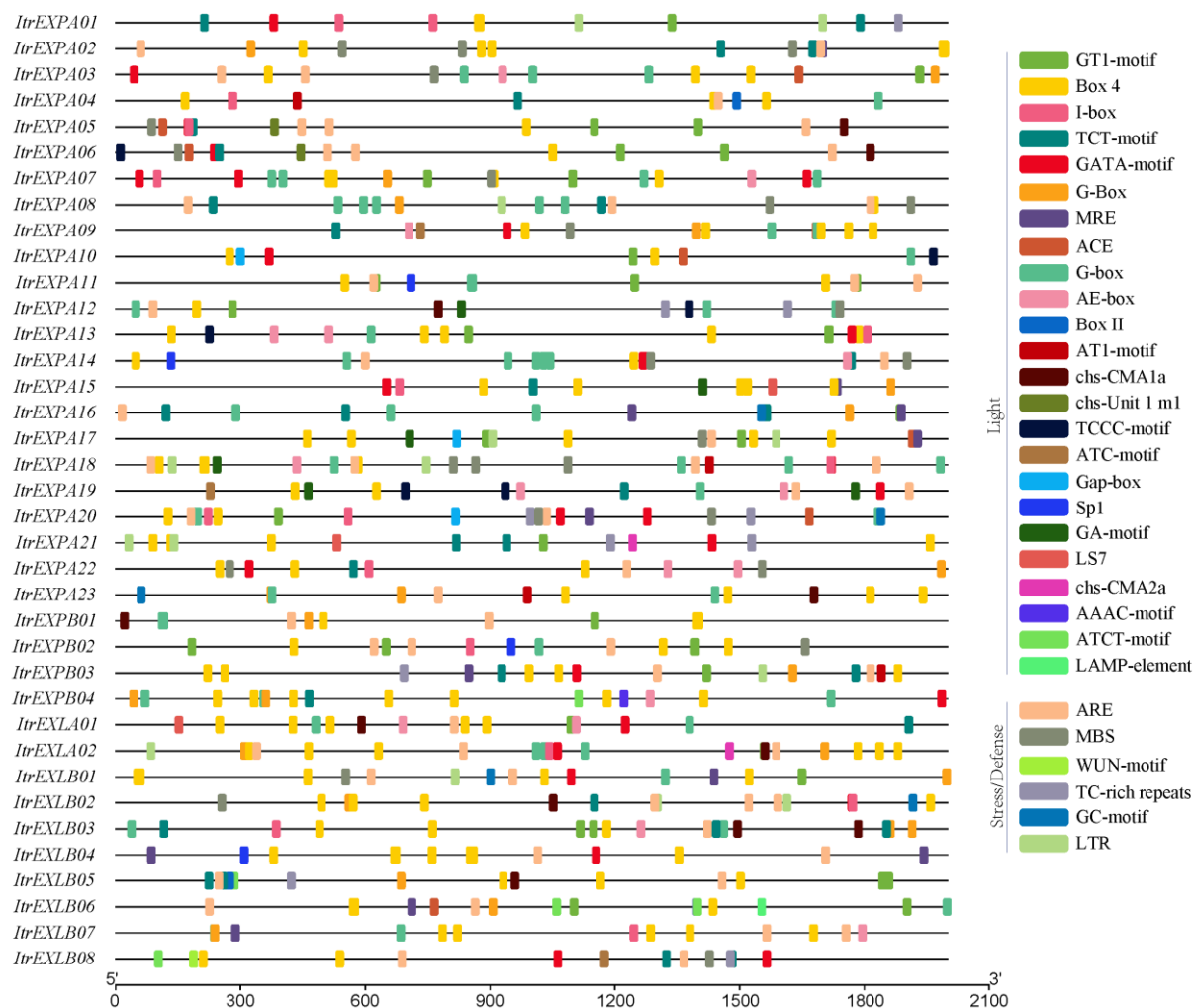


Figure S2. Potential light and stress/defense *cis*-elements in the promoter region of expansin genes. Left part showed the locations of *cis*-elements in the promoter regions, right part showed the *cis*-element types and their symbols.

Table S1. The primer pairs of selected genes for qRT-PCR.

Gene Name	Primer Name	5'-3' sequence	Products
<i>ItrEXPA10</i>	F-PA10	CTCGCCGTCCAAGCCAGAAT	120bp
	R-PA10	CCCATACCCACAAGCACCAC	
<i>ItrEXPA13</i>	F-PA13	GCCCTCCGAACTATGCTTTGC	167bp
	R-PA13	CCTTATGCCTCCTTTCCTCACAC	
<i>ItrEXPA03</i>	F-PA03	TACGCCTTGCCTAATGACAATG	177bp
	R-PA03	CTAGGTTGAAGAAACGGTGGC	
<i>ItrEXPA15</i>	F-PA15	TGTGGAGCCTGCTTTGAGATC	166bp
	R-PA15	GCATGGCGAGATCAAAATGCG	
<i>ItrEXPA09</i>	F-PA09	ATCCAACGCATACCTAACGG	116bp
	R-PA09	CGAAAGTCTGCCCAAATCTCCAA	
<i>ItrEXPA08</i>	F-PA08	CAACACTTCGACATGGCTCAG	164bp
	R-PA08	CCAACGTTAGTCACCAACACC	
<i>ItrEXPB02</i>	F-PB02	AGTGCATTTTCGACCTCAGCGG	185bp
	R-PB02	CCACCAAGAGTGAAAGCCAGAA	
<i>ItrEXPB03</i>	F-PB03	ATGCTCGGGAAAGGCAGTGAC	127bp
	R-PB03	CTGGTCAGCTTTGCCGGAAGA	
<i>ItrEXLA02</i>	F-LA02	CTGCGTCCACCAAACCAAAGTC	116bp
	R-LA02	CTGCGGCAGCAAGATGTCCT	
<i>ItrEXLB05</i>	F-LB05	GGAGCTTGTGGGTTTGGTGAC	151bp
	R-LB05	TCCTCGTACCTTCCTCGTTGC	
<i>ItrEXLB08</i>	F-LB08	GTCTTGCAGTTCTCATAGGGAC	127bp
	R-LB08	CTATCTGTGCCATTGTCATCGG	

Table S2. The expansin genes of *I. nil* and *I. triloba*.

<i>I. nil</i>		<i>I. triloba</i>	
Gene Name	Gene ID	Gene Name	Gene ID
<i>IniEXPA01</i>	gene-LOC109162042	<i>IlbEXPA01</i>	gene-LOC115998052
<i>IniEXPA02</i>	gene-LOC109166240	<i>IlbEXPA02</i>	gene-LOC116025128
<i>IniEXPA03</i>	gene-LOC109189038	<i>IlbEXPA03</i>	gene-LOC116020824
<i>IniEXPA04</i>	gene-LOC109193479	<i>IlbEXPA04</i>	gene-LOC115999375
<i>IniEXPA05</i>	gene-LOC109154062	<i>IlbEXPA05</i>	gene-LOC116000481
<i>IniEXPA06</i>	gene-LOC109154072	<i>IlbEXPA06</i>	gene-LOC115999911
<i>IniEXPA07</i>	gene-LOC109154073	<i>IlbEXPA07</i>	gene-LOC116007517
<i>IniEXPA08</i>	gene-LOC109181060	<i>IlbEXPA08</i>	gene-LOC116003819
<i>IniEXPA09</i>	gene-LOC109173867	<i>IlbEXPA09</i>	gene-LOC116013951
<i>IniEXPA10</i>	gene-LOC109186551	<i>IlbEXPA10</i>	gene-LOC116020110
<i>IniEXPA11</i>	gene-LOC109154973	<i>IlbEXPA11</i>	gene-LOC116019994
<i>IniEXPA12</i>	gene-LOC109154972	<i>IlbEXPA12</i>	gene-LOC115998007
<i>IniEXPA13</i>	gene-LOC109157987	<i>IlbEXPA13</i>	gene-LOC116030898
<i>IniEXPA14</i>	gene-LOC109159018	<i>IlbEXPA14</i>	gene-LOC116017466
<i>IniEXPA15</i>	gene-LOC109148147	<i>IlbEXPA15</i>	gene-LOC116003780
<i>IniEXPA16</i>	gene-LOC109186601	<i>IlbEXPA16</i>	gene-LOC115999171
<i>IniEXPA17</i>	gene-LOC109192973	<i>IlbEXPA17</i>	gene-LOC116011772
<i>IniEXPA18</i>	gene-LOC109173472	<i>IlbEXPA18</i>	gene-LOC116022872
<i>IniEXPA19</i>	gene-LOC109149167	<i>IlbEXPA19</i>	gene-LOC116027442
<i>IniEXPA20</i>	gene-LOC109152686	<i>IlbEXPA20</i>	gene-LOC116026901
<i>IniEXPA21</i>	gene-LOC109183517	<i>IlbEXPA21</i>	gene-LOC116001114
<i>IniEXPA22</i>	gene-LOC109168111	<i>IlbEXPA22</i>	gene-LOC116012277
<i>IniEXPA23</i>	gene-LOC109188880	<i>IlbEXPA23</i>	gene-LOC115998240
<i>IniEXPA24</i>	gene-LOC109167477	<i>IlbEXPA24</i>	gene-LOC116003784
<i>IniEXPA25</i>	gene-LOC109177514	<i>IlbEXPA25</i>	gene-LOC116030964
<i>IniEXPA26</i>	gene-LOC109188155	<i>IlbEXPA26</i>	gene-LOC116028302
<i>IniEXPA27</i>	gene-LOC109153624	<i>IlbEXPA27</i>	gene-LOC116030858
<i>IniEXPA28</i>	gene-LOC109153727	<i>IlbEXPB01</i>	gene-LOC116008214
<i>IniEXPA29</i>	gene-LOC109191378	<i>IlbEXPB02</i>	gene-LOC116017748
<i>IniEXPA30</i>	gene-LOC109153593	<i>IlbEXPB03</i>	gene-LOC116014045
<i>IniEXPA31</i>	gene-LOC109153631	<i>IlbEXPB04</i>	gene-LOC116014258
<i>IniEXPB01</i>	gene-LOC109188048	<i>IlbEXPB05</i>	gene-LOC116014428
<i>IniEXPB02</i>	gene-LOC109186602	<i>IlbEXPB06</i>	gene-LOC116014343
<i>IniEXPB03</i>	gene-LOC109186593	<i>IlbEXLA01</i>	gene-LOC116019640
<i>IniEXPB04</i>	gene-LOC109193325	<i>IlbEXLA02</i>	gene-LOC116029340
<i>IniEXPB05</i>	gene-LOC109193328	<i>IlbEXLB01</i>	gene-LOC116028927
<i>IniEXPB06</i>	gene-LOC109193326	<i>IlbEXLB02</i>	gene-LOC116002815
<i>IniEXPB07</i>	gene-LOC109193320	<i>IlbEXLB03</i>	gene-LOC115997228
<i>IniEXLA01</i>	gene-LOC109161325	<i>IlbEXLB04</i>	gene-LOC116001079
<i>IniEXLB01</i>	gene-LOC109174806	<i>IlbEXLB05</i>	gene-LOC116001309
<i>IniEXLB02</i>	gene-LOC109177426	<i>IlbEXLB06</i>	gene-LOC116028391

Table S2. The expansin genes of *I. nil* and *I. triloba* (continued).

<i>I. nil</i>		<i>I. triloba</i>	
Gene Name	Gene ID	Gene Name	Gene ID
<i>IniEXLB03</i>	gene-LOC109174872	<i>IlbEXLB07</i>	gene-LOC116001078
<i>IniEXLB04</i>	gene-LOC109185131	<i>IlbEXLB08</i>	gene-LOC116002898
<i>IniEXLB05</i>	gene-LOC109185314	<i>IlbEXLB09</i>	gene-LOC116030832
<i>IniEXLB06</i>	gene-LOC109174855	<i>IlbEXLB10</i>	gene-LOC116030871
<i>IniEXLB07</i>	gene-LOC109174854		

The expansin genes were identified by the same pipeline as that used for Y22.

Table S3. The duplication type of expansin genes in Y22 genome.

Subfamily	Gene Name	Gene Id	Code	Type of duplication
EXPA	<i>ItrEXPA01</i>	Itr.Sc0000011.164	4	WGD or segmental
EXPA	<i>ItrEXPA02</i>	Itr.xfSc0000576.12	4	WGD or segmental
EXPA	<i>ItrEXPA03</i>	Itr.Sc0000007.290	4	WGD or segmental
EXPA	<i>ItrEXPA04</i>	Itr.Sc0000051.50	4	WGD or segmental
EXPA	<i>ItrEXPA05</i>	Itr.Sc0000046.34	4	WGD or segmental
EXPA	<i>ItrEXPA06</i>	Itr.Sc0000046.36	3	Tandem
EXPA	<i>ItrEXPA07</i>	Itr.xfSc0000007.14	4	WGD or segmental
EXPA	<i>ItrEXPA08</i>	Itr.xfSc0000007.15	3	Tandem
EXPA	<i>ItrEXPA09</i>	Itr.Sc0000078.10	4	WGD or segmental
EXPA	<i>ItrEXPA10</i>	Itr.Sc0000001.78	2	Proximal
EXPA	<i>ItrEXPA11</i>	Itr.xfSc0000049.46	4	WGD or segmental
EXPA	<i>ItrEXPA12</i>	Itr.Sc0000003.235	4	WGD or segmental
EXPA	<i>ItrEXPA13</i>	Itr.Sc0000003.134	4	WGD or segmental
EXPA	<i>ItrEXPA14</i>	Itr.Sc0000025.53	4	WGD or segmental
EXPA	<i>ItrEXPA15</i>	Itr.Sc0000014.125	4	WGD or segmental
EXPA	<i>ItrEXPA16</i>	Itr.Sc0000087.3	4	WGD or segmental
EXPA	<i>ItrEXPA17</i>	Itr.Sc0000013.190	4	WGD or segmental
EXPA	<i>ItrEXPA18</i>	Itr.xpSc0079065.36	4	WGD or segmental
EXPA	<i>ItrEXPA19</i>	Itr.xpSc0079065.38	3	Tandem
EXPA	<i>ItrEXPA20</i>	Itr.xpSc0079065.39	3	Tandem
EXPA	<i>ItrEXPA21</i>	Itr.xpSc0079065.40	3	Tandem
EXPA	<i>ItrEXPA22</i>	Itr.xfSc0000000.33	4	WGD or segmental
EXPA	<i>ItrEXPA23</i>	Itr.xfSc0001203.1	1	Dispersed
EXPB	<i>ItrEXPB01</i>	Itr.xfSc0000185.16	4	WGD or segmental
EXPB	<i>ItrEXPB02</i>	Itr.Sc0000024.30	4	WGD or segmental
EXPB	<i>ItrEXPB03</i>	Itr.xfSc0000047.33	4	WGD or segmental
EXPB	<i>ItrEXPB04</i>	Itr.xfSc0001448.1	1	Dispersed
EXLA	<i>ItrEXLA01</i>	Itr.Sc0000050.70	4	WGD or segmental
EXLA	<i>ItrEXLA02</i>	Itr.Sc0000020.14	4	WGD or segmental
EXLB	<i>ItrEXLB01</i>	Itr.xpSc0079072.22	4	WGD or segmental
EXLB	<i>ItrEXLB02</i>	Itr.xfSc0000061.14	4	WGD or segmental
EXLB	<i>ItrEXLB03</i>	Itr.xfSc0000061.13	3	Tandem
EXLB	<i>ItrEXLB04</i>	Itr.xfSc0000239.16	1	Dispersed
EXLB	<i>ItrEXLB05</i>	Itr.Sc0000071.6	4	WGD or segmental
EXLB	<i>ItrEXLB06</i>	Itr.xfSc0000002.83.1	4	WGD or segmental
EXLB	<i>ItrEXLB07</i>	Itr.xfSc0000002.86	3	Tandem
EXLB	<i>ItrEXLB08</i>	Itr.xfSc0000002.103	4	WGD or segmental

Comparative genomic analysis revealed that the WGT occurred in an ancient ancestor of *Ipomoea* [23, 24], therefore the "WGD" in this table was the WGD or WGT.

Table S4. Collinearity result of expansin genes between *C. canephora* and Y22 genome.

Location	<i>C. canephora</i> Genes	<i>I. trifida</i> Genes				
		iter=1	iter=2	iter=3	iter=4	iter=5
chr1	gene-GSCOC_T00028253001	<i>ItrEXPA15</i>	<i>ItrEXPA12</i>		<i>ItrEXPA10</i>	
chr1	gene-GSCOC_T00016583001		<i>ItrEXPA13</i>	<i>ItrEXPA17</i>		
chr2	gene-GSCOC_T00028856001					
chr2	gene-GSCOC_T00028854001					
chr2	gene-GSCOC_T00029906001	<i>ItrEXPA03</i>	<i>ItrEXPA10</i>		<i>ItrEXPA12</i>	
chr4	gene-GSCOC_T00035723001	<i>ItrEXPA04</i>				
chr5	gene-GSCOC_T00042204001	<i>ItrEXPB02</i>				
chr6	gene-GSCOC_T00023514001		<i>ItrEXPA22</i>		<i>ItrEXPA15</i>	<i>ItrEXPA12</i>
chr6	gene-GSCOC_T00042971001		<i>ItrEXPA18</i>			
chr7	gene-GSCOC_T00039583001					
chr7	gene-GSCOC_T00036829001		<i>ItrEXPA11</i>			
chr8	gene-GSCOC_T00027140001			<i>ItrEXLB03</i>		
chr8	gene-GSCOC_T00027139001			<i>ItrEXLB03</i>		
chr8	gene-GSCOC_T00027142001	<i>ItrEXLB06</i>		<i>ItrEXLB03</i>		
chr8	gene-GSCOC_T00027143001	<i>ItrEXLB07</i>		<i>ItrEXLB03</i>		
chr8	gene-GSCOC_T00000261001	<i>ItrEXLB08</i>				
chr8	gene-GSCOC_T00037639001	<i>ItrEXLB08</i>				
chr8	gene-GSCOC_T00030309001					
chr8	gene-GSCOC_T00027141001			<i>ItrEXLB02</i>		
chr9	gene-GSCOC_T00041034001	<i>ItrEXLA02</i>				
chr10	gene-GSCOC_T00024595001		<i>ItrEXPA09</i>			
scaffold_368	gene-GSCOC_T00003973001					

All of the identified expansin genes of *C. canephora* are shown in this table; the term 'iter' was the software parameter.

Table S5. The protein sequences of different conserved motifs.

Motif	Length	Motif Consensus	PFAM Domain
1	21	ALSTALFNNGLSGACYEVKC	DPBB_1
2	15	WIPMSRNWGQNWETN	Pollen_allerg_1
3	15	AGIVPVEYRRVPCKK	DPBB_1
4	23	AHATFYGGSDASGTMGGACGYGN	DPBB_1
5	27	DNGGWCNPPRPHFDLSMPAFLKIAQYR	DPBB_1
6	29	KGGIRFTINGHRYFNLVLVTNVGGAGDVH	
7	29	LSFRVTTSDGRTVTSYNVAPANWQFGQTF	
8	21	GPGSITVTATNFCPPNYALPN	DPBB_1
9	11	LYSQGYGTNTA	
10	15	TDFILSYTAFGKMAK	DPBB_1
11	21	KENALCSEKGVKVVITDEGEG	DPBB_1
12	21	KILDSSSNPNYLAIVILNQGG	Pollen_allerg_1
13	21	SSKNAIPADWKAGVTIDTGIQ	
14	8	VSIKGSRT	
15	34	WKEAHATYYGPPEGTIGGACGFEEYKQTYSPYTA	DPBB_1