

Table 1 Suppl. Predicted target genes of stu-miR856.

miRNA	mRNA sequence ID	Protein ID	Target annotations
stu-miR856	PGSC0003DMT400054750	PGSC0003DMP400036823	StMAPK-10 like
	PGSC0003DMT400018188	PGSC0003DMP400012517	StMAPK-11 like

Table 2 Suppl. Oligonucleotides used for gene cloning and real-time quantitative PCR (qPCR) analysis.

Gene	Forward (F) and reverse (R) sequences of oligonucleotides	Gene length [bp]
Primers for PCR cloning		
<i>StMAPK10</i>	F 5'-GTAGTAGTGTGAGGAATCTTGGTGG-3'	2 107
	R 5'-GGATACAGTTTGCTAAGTCAGGCT-3'	
<i>StMAPK11</i>	F 5'-TGCTCTCTCTCTCTCTCTCTCTCTT-3'	2 283
	R 5'-GCACATCTTGAAGTGTCTCACTGC-3'	
Primers for real-time qPCR		
<i>StMAPK10</i>	F 5'-CGACCAATCTCAAATCTGGA-3'	178
	F 5'-GCCTTCTAAACTGACCTGTTG-3'	
<i>StMAPK11</i>	F 5'-CTTACCACCTTCAAGACGAGA-3'	139
	R 5'-CACGCAGCATCTGATACAG-3'	
<i>eflα</i>	F 5'-ATTGGAAACGGATATGCTCCA-3'	101
	R 5'-TCCTTACCTGAACGCCTGTCA-3'	
stu-miR856	5'-CGCGGCCTTAATAAGATGGTGAAG-3'	-

Table 3 Suppl. Nested PCR primers for miRNA cleavage sites validation by RNA ligase-mediated 5' rapid amplification of cDNA ends.

Target gene	Genomic locust	Outer primer	Inner primer	Size
<i>StMAPK10-like</i>	PGSC0003DMT400054750	CGGACAAAGCCTCTTCAGCA	GCAACATAATCCGTCCAAAGTGC	262 bp
<i>StMAPK11-like</i>	PGSC0003DMT400018188	TGTGGTTGGAGCATCACTGAATG	CCAAAGCCTCTTCAGCAGTTG	239 bp

Table 4 Suppl. Potato micro RNAs (miRNAs) identified by deep sequencing and bioinformatics analysis. LS - length of sequence, NM - number of mismatches; LM - length of mature miRNAs; LP - length of precursor; MFE - minimum folding free energy; MFEI - minimum folding free energy index.

miRNA	stu-miR856
Sequences	CGGCCTTAATAAGATGGTGAAG
Gene ID	AC232102.1
Source	(nr/nt)
LS [nt]	42511
Families	miR856
NM [nt]	5
LM [nt]	22
Strand	minus
LP [nt]	215
Side	3
(G+C)	33.5
MFE	-81.2
MFEI	1.13

Table 5 Suppl. Basic properties and characteristics of two *StMAPK-like* genes in potato.

Gene	<i>StMAPK10-like</i>	<i>StMAPK11-like</i>
Chr	10	7
Genomic locus	PGSC0003DMT400054750	PGSC0003DMT400018188
Position	2532726 - 2538449	52242138 - 52246765
Coding sequence [bp]	1782	1807
Exon number	10	9
Full length [bp]	2107	2283
Amino acid number	593	603
Isoelectric point	9.22	9.37
Relative molecular mass [Da]	67184.24	68234.42

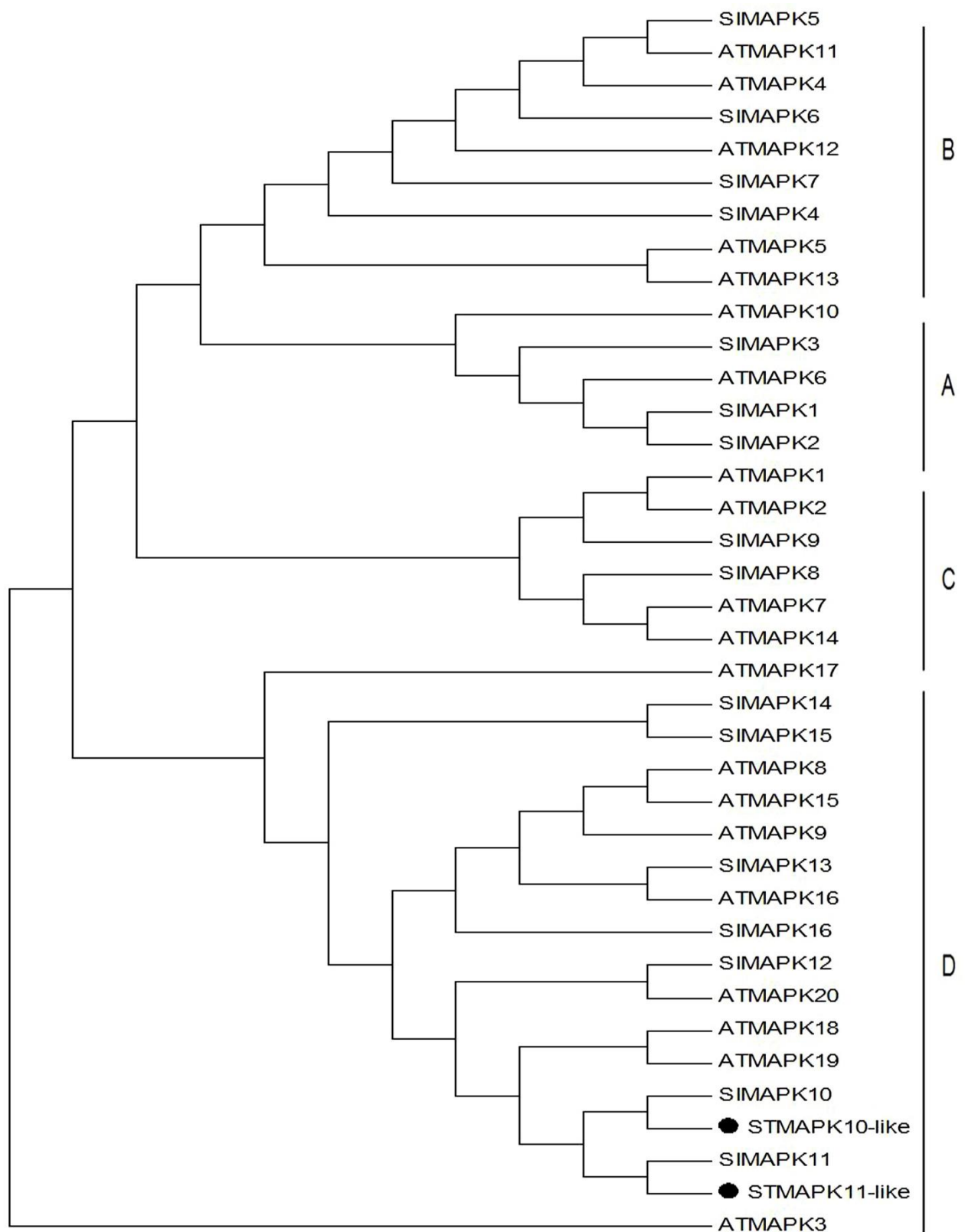


Fig. 2 Suppl. A phylogenetic tree constructed with *ClustalX1.8* using the full-length amino acid sequences of mitogen-activated protein kinase (MAPK) genes from *Arabidopsis*, tomato and potato. The bootstrap analysis was performed using 1 000 replicates in *MEGA 5* to evaluate the reliability of different phylogenetic groups (A to D).

