

Table 1. Suppl. The list of primers used for amplification of *CIMPKs*.

Primer	Description	Sequence (5'-3')
5PR-AAP	5'RACE abridged anchor primer	GGCCACCGCGTCGACTAGTACGGGIIGGGIIGGGIIG
5PR-AUAP	5' RACE abridged universal amplification primer	GGCCACCGCGTCGACTAGTAC
CIMPK1-5PR1	5' RACE primer for CIMPK1, outer	GCGCAGAACCTGATACAGAAAATA
CIMPK1-5PR2	5' RACE primer for CIMPK1, nested	GAAAATACTGGCAATGTTCTTCG
CIMPK5-5PR1	5' RACE primer for CIMPK5, outer	ATAGCAATGTTCTCGCTCAGTTC
CIMPK5-5PR2	5' RACE primer for CIMPK5, nested	ATGCCAATAATGTTTCATGATCC
CIMPK3-5PR1	5' RACE primer for CIMPK3, outer	CTGAAACAGAAAATACTGGCAATG
CIMPK3-5PR2	5' RACE primer for CIMPK3, nested	CATAATATCTTCAGCGCAATCAC
CIMPK4-5PR1	5' RACE primer for CIMPK4, outer	CTGAAACAGAAAATACTGGCAATG
CIMPK4-5PR2	5' RACE primer for CIMPK4, nested	CATAATATCTTCAGCGCAATCAC
CIMPK1F	gene specific primer, forward	CGATCTCGATAGCGTGTAGG
CIMPK1R	gene specific primer, reverse	GTCCATCAGATGCGAGGATTA
CIMPK5F	gene specific primer, forward	CTGTCGATCTGTCTCCGTCA
CIMPK5R	gene specific primer, reverse	TAATGCCCTGTGCCAACTCAG
CIMPK3F	gene specific primer, forward	GCCTACTTCTCTCCTCAGAAAGG
CIMPK3R	gene specific primer, reverse	CTTTCTCCACCTTCATGTTCATC-
CIMPK4F	gene specific primer, forward	GCACGTACAACATAGACAACATGA
CIMPK4R	gene specific primer, reverse	TTGTATAACTCAAGTGGCAGAAC

Table 2 Suppl. The list of primers used in qRT-PCR for detection of *CIMPK* gene expression.

<i>CIMPK</i> gene	Forward primer (5'-3')	Reverse primer (5'-3')	Product size [bp]	Annealing temp [°C]
CIMPK-GS1	GCCTGCTGATGGAACGTGATT	CGGATCAAAGGTCAAGCATT	179	60
CIMPK-GS5	CGGTGCGCAATATACACATCG	CGGTGCGCAATATACACATCG	205	60
CIMPK-GS3	TGGCAGACCCCTGTTGAAAT	TATCTTCAGCGCAATCAGC	226	60
CIMPK-GS4	CGAAGCGGATCTGGAATTAA	CGGGCTCATATACGGATGTT	202	60

Table 3 Suppl. The fold change of *MAPK* genes expression (log2-based ratio) in *Arabidopsis* (the *Genevestigator* database) under various treatments at a particular time period (3 h). More than 0.5 fold upregulated genes were assigned 1, less than -0.5 fold downregulated genes were assigned -1, others are assigned as 0. DEGs - differentially expressed genes. For *CIMPKs*, 1 represents the up-regulated gene compared with the control, -1 represents the down-regulated gene and 0 represents no significant changes according to the RT-PCR results.

Stress treatments		<i>AtMPK1</i>	<i>AtMPK2</i>	<i>AtMPK3</i>	<i>AtMPK6</i>
Cold	log2 based ratio	-0.48283	-0.46618	0.98377	0.20875
	DEGs	0	0	1	0
Drought	log2 based ratio	0.31490	-0.21030	-0.40224	-0.14692
	DEGs	0	0	0	0
Salt	log2 based ratio	0.08080	0.18556	-0.32103	0.88528
	DEGs	0	0	0	1
SA	log2 based ratio	-0.21630	-1.06326	-0.07127	-1.11362
	DEGs	0	-1	0	-1
ABA	log2 based ratio	-1.47326	-1.66735	-1.66784	0.03613
	DEGs	-1	-1	-1	0
MeJA	log2 based ratio	-0.56321	-0.47638	-0.32618	-0.33562
	DEGs	-1	0	0	0
Mannitol	log2 based ratio	0.78633	0.16537	0.12699	1.19672
	DEGs	1	0	0	1
Wounding	log2 based ratio	-0.19368	-0.19638	0.82619	-0.04327
	DEGs	0	0	1	0
		<i>CIMPK3</i>	<i>CIMPK4</i>	<i>CIMPK5</i>	<i>CIMPK1</i>
Cold	0	0	0	0	0
	0	1	1	1	1
Drought	0	1	0	0	0
	0	1	0	0	1
Salt	0	1	0	0	0
	0	1	0	0	1
SA	0	1	0	0	1
	0	1	0	0	1
ABA	0	1	0	0	1
	0	1	0	0	1
MeJA	1	1	0	0	1
	0	0	0	0	1
Mannitol	0	0	0	0	1
	0	1	1	0	0
Wounding	0	1	1	1	0

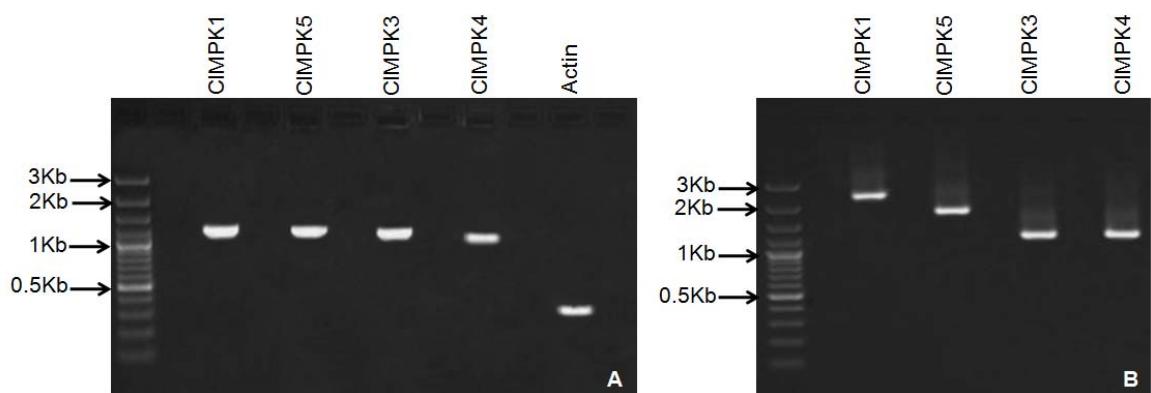


Fig. 1 Suppl. The amplified products of ClMPKs. *A* – The full-length cDNA amplified product of *ClMPKs* obtained through a reverse-transcriptase PCR amplification using gene specific primers. *B* – The full-length genomic DNA fragment of *ClMPKs* obtained through PCR using specific primers designed based on the 5' and 3' termini of the full-length transcripts of *ClMPKs*.

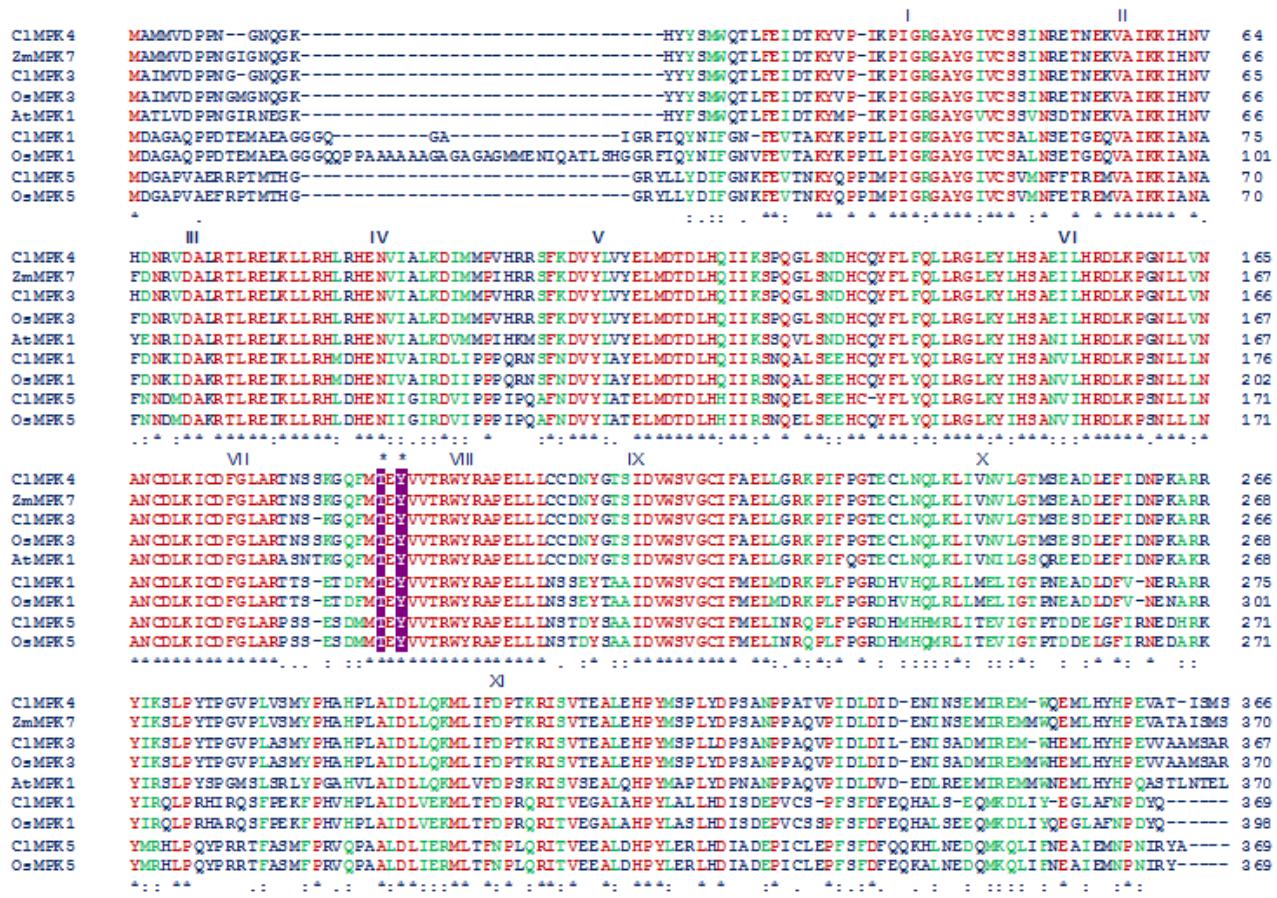
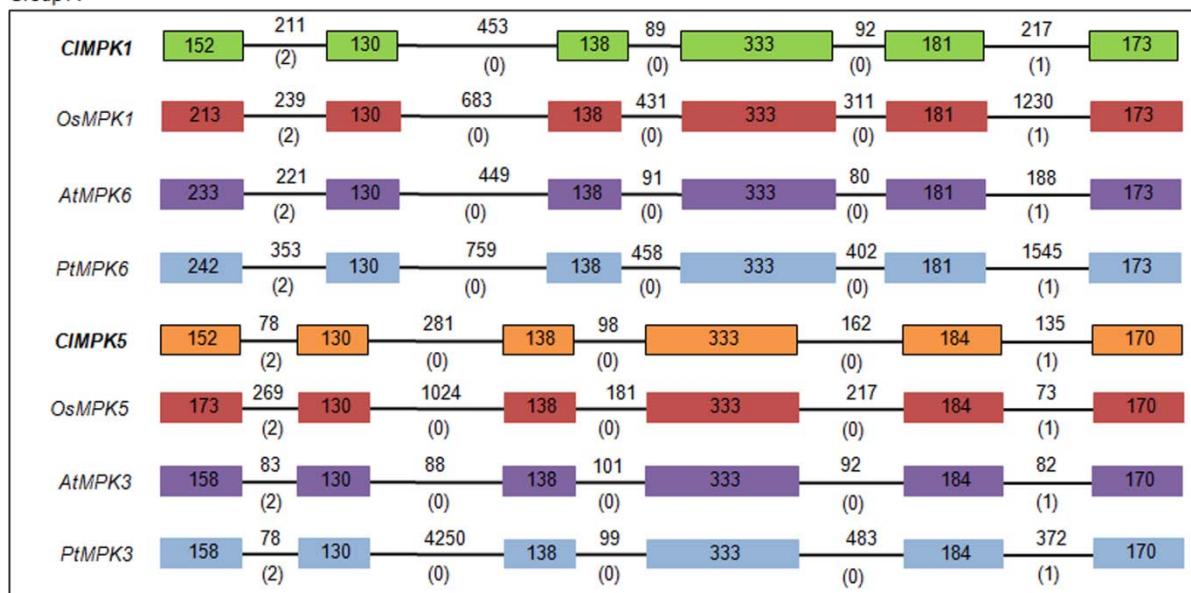


Fig. 2 Suppl. The alignment of deduced amino acid sequences of four ClMPKs with closely related MAPKs from other plant species. Eleven protein kinase subdomains are marked in *roman numerals* and the activation T-loop with the characteristic threonine (T) and tyrosine (Y) amino acid residues indicated by asterisks. Zm - *Zea mays*, Os - *Oryza sativa*, At - *Arabidopsis thaliana*.

Group A



Group C

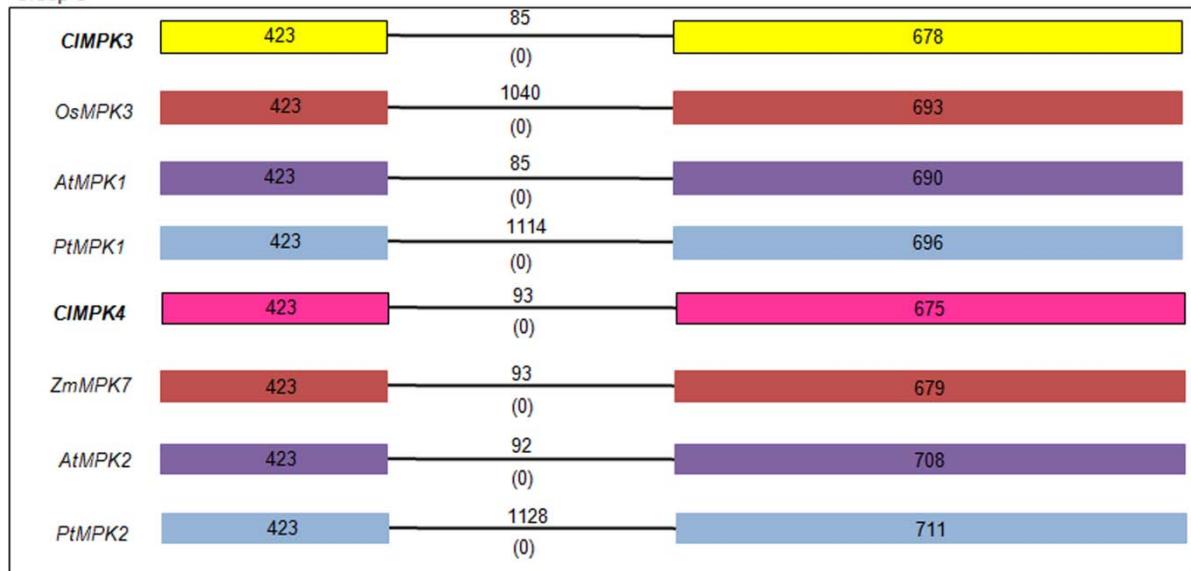


Fig. 3 Suppl. Graphical representation of the isolated turmeric MPKs (*CIMPK1*, *CIMPK5*, *CIMPK3* and *CIMPK4*) gene structures and their comparison with corresponding orthologs from rice (*OsMPKs*), *Arabidopsis thaliana* (*AtMPKs*) and poplar (*PtMPKs*). Exons are represented by *closed boxes* and introns by *solid lines*. The individual exons and intron lengths were given in base pairs. Numbers within brackets correspond to the intron phase.