

Supplementary Materials: Interspecies and Intraspecies Analysis of Trehalose Contents and the Biosynthesis Pathway Gene Family Reveals Crucial Roles of Trehalose in Osmotic-Stress Tolerance in Cassava

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MeTPS1	1	MISKQLLTERYAPCQGLDVMSCKLQASSQNKNNCTLVTHKTGLESLLLDVRVKFTELFAN	60
MeTPS2	1	MPGNKYNGTPTVTPRTRLERLLLNRELKRFNR-----FFNPSDE---LDDGLKEAELFAN	51
MeTPS3	1	MPGNQYNGNSTPYPSRTQRLRLRERELKKSSRASHSNEVTDNHGGTEPCEHDLRLRERDNS	60
MeTPS4	1	MPGNQYNSNSTPYPSRTQRLRLRERELKKSSRSSHSNEATDNHGGIEPCEHDLRLREGDDS	60
MeTPS5	1	MVSRSCMNFLLDLASGNLLEIP-----HTPRSIPRVMTV	33
MeTPS6	1	MVSRSCNLNLDLASGNLLEIP-----HTPRSIPRVMTV	33
MeTPS7	1	MMSRSCINLLDLASGDMNLNLP-----RTPRSIPRVMTV	33
MeTPS8	1	MMSKSCINFLDLSSGDMNLNFS-----RTPRSIPRVMTV	33
MeTPS9	1	MMSRSYTNLLDLASGNFPVMGQP-----REKKRLPRVMTV	35
MeTPS10	1	MVSRSYSNLLDLASGESPTFG-----RERKRLPRVATV	33
MeTPS11	1	MVSRSYSNLLDLASGESPSFG-----RMTRRIPRIMTV	33
MeTPS12	1	MVSRSYSNLLDLASGESPSFG-----RMSRRIPRIMTV	33
GG1/GP1			
MeTPS1	61	DSVTKETETHGPHLEDTSLEEVDVNCERPR RPKQRL LVVANS LPVSAIRK GQ--DSWKLEI	118
MeTPS2	52	DSVLNKDENCQPFNEETFSEGVDSER-- LHKQRL LVVAN RLPVSAVR KGE--DSWQLEM	107
MeTPS3	61	NNSYIDQYVEGAIAATRQLAEGCEKQDGR PLRQRL LVVAN RLPVSAVR RGE--DSWSLEI	118
MeTPS4	61	NNCYIEQDLEGAIAATKTLAEGCEYQDAR PLRQRL LVVAN RLPVSAVR RGE--DSWSLEI	118
MeTPS5	34	PGIISDLGYPY---GSNDEDSEIA-SS ICRERK IIIVAN MLPLQAK DPG-TAKWCFW	88
MeTPS6	34	PGIISDLGYPY-----SNDGDSENA-SS ICRERI IIIVAN MLPLHAK DPG-TAKWFFW	85
MeTPS7	34	PGIFSDTDGDG-----SNDGDSAP-SS GCGKKQ IIIVAN FLPLHAQ KDLN-SSKWSFSF	85
MeTPS8	34	EGIFSNTDSG-----SNDGDTNVP-SAR CYKKK IIIVAN FLPLHAQ KDLE-TSKWSFSF	85
MeTPS9	36	PGVISELDDQ-----ANSVASDVP-SS LVQDRI IIIVAN QLPVKAK RRPD-NKGWGFW	87
MeTPS10	34	AGVLSELEDEN-----SNSVGSAP-SS VSQERM IIIVAN QLPLRVH QSPDGNGEWCFW	86
MeTPS11	34	AGIISDLDDDP-----SASVCSDPSSSS IQKDRI IIIVAN QLPIRAQ RKSDGSKSWIFTW	87
MeTPS12	34	AGIISDLDDDP-----TDSVCSDPSSSS VQDRRI IIIVAN QLPIRAQ RKSDGSKSWIFTW	87
URI			
MeTPS1	119	SVDGLVN PL---LGVKEFEARWIGWAGVNPDEIGQKALSTALAEKKCIPVFLDEHIVHQ	175
MeTPS2	108	SVGGLVS AL---LGVKEFDARWIGWAGVNPDEIGQKALTALAEKRCIPVFLDEDIVHQ	164
MeTPS3	119	SAGGLVS AL---LGVKEFEARWIGWAGVNPDEIGQKALTALAEKRCIPVFLDEEIVHQ	175
MeTPS4	119	SAGGLVT AL---LGVKEFEARWIGWAGVNPDEIGQKALTRALAEKRCIPVFLDEEIVHQ	175
MeTPS5	89	DEDSLFL QLKDGFS-PETEVYVGLSKADIDATDQEEVSQKLEDFNCVPTFLPQDLQRK	147
MeTPS6	86	DEDSLFL QLKDGFS-PETEVYVGLSKADIKASEQEEVSQKLEDFNCVPTFLPQDLQKK	144
MeTPS7	86	DEDSLIL QMKDGFS-INTEVVYVGLSKVDVDTSEQEEVSQKLEEFNCVPTFLPPDLHKK	144
MeTPS8	86	DEDSLIL QMKDGFS-DNTEIVYVGLSKVDVDASEQEEVSQKLEEFNCVPTFLPPDLHKK	144
MeTPS9	88	DEDSLIL QLKDGLP-EDMEVYVGLSRVEVDLSEQDDVSQLLDRFKCVPAPFLPPDILSK	146
MeTPS10	87	DEDSLIL QLKDGLP-EDMEVYVGLSKVEVDLSEQDDVAQTLLSEFKCVPAPFLPPDILSK	145
MeTPS11	88	DENSLIL QLKDGGLDDIEVYVGLCLREDIHPSEQDEVSQILLETFCVPTFLPPDLFSR	147
MeTPS12	88	DENSLIL QLKDGGLDDIEVYVGLCLREDIHPSEQDEVSQILLETFCVPTFLPPDLFSR	147

Figure S1. Cont.

		GP2	GG2		
MeTPS1	176	YNGYCNVNLWPLFHYLGLPQEDRLPTTRSFQSQFDAYKKANQMFADVNRHYE-EGDVV	234		
MeTPS2	165	YNGYCNVNLWPLFHYLGLPQEDRLATTRSFQSQFDAYKKANQMFADVNRHYE-EGDVV	223		
MeTPS3	176	YNGYCNVNLWPLFHYLGLPQEDRLATTRSFQSQFAAYKKANQMFADVNRHYE-EGDVV	234		
MeTPS4	176	YNGYCNVNLWPLFHYLGLPQEDRLATTRSFQSQFAAYKKANQMFADVNRHYE-EGDVV	234		
MeTPS5	148	FYLGFCQQLWPLFHYMLPMCPD--HGDRFDRNLWQAYVSANKIFADKVMETISPEEDYV	205		
MeTPS6	145	FYLGFCQQLWPLFHYMLPMCPD--HGDRFERVWQAYVSANKMFADKVMETISPEEDYV	202		
MeTPS7	145	FYHGFCQQLWPLFHYMLPMFPD--HGERFDKLLWQAYVSANKVFADKVMETINPEEDYV	202		
MeTPS8	145	FYHGFCQQLWPLFHYMLPMCPD--HSNRFDKLLWQAYVSANKIFADKVMETINPEEDHV	202		
MeTPS9	147	FYHGFCQQLWPLFHYMLPFSAS--HGGRFDRSLWEAYVAANKIFSQRVVEVLNPEEDYV	204		
MeTPS10	146	FYHGFCQQLWPLFHYMLPLSPD--LGGRFDRSLWQAYVSANKIFADKVMETISPDDEYV	203		
MeTPS11	148	FYHGFCQQLWPLFHYMLPLSPE--LGGRFDRSLWQAYVSANKIFADKVMETINPEEDFV	205		
MeTPS12	148	FYHGFCQQLWPLFHYMLPLSPD--LGGRFDRSLWQAYVSANKIFADKVMETINPEEDFV	205		
		GG3	GP3	UG1	GG4
MeTPS1	235	WCHDYHLMFLPKCLKEYNSKMKVWFLHTFPFSSSEIHRMLPSRSELLRSVLAADLIGFHT	294		
MeTPS2	224	WCHDYHLMFLPKCLKEYNSKMKVWFLHTFPFSSSEIHRMLPSRSELLRSVLAADLVGFHT	283		
MeTPS3	235	WCHDYHLMFLPKCLKEYNSKMKVWFLHTFPFSSSEIHRMLPSRSELLRSVLAADLVGFHT	294		
MeTPS4	235	WCHDYHLMFLPKCLKEYNSKMKVWFLHTFPFSSSEIHRMLPSRSELLRSVLAADLVGFHT	294		
MeTPS5	206	WIHDYHLMMLLPTFLRKGYNRVKLGFFLHSPFSSSEIYRTLPRDEILRGLLNCDLIGFQT	265		
MeTPS6	203	WVHDYHLMMLLPTFLRKGYNRVKLGFFLHSPFSSSEIYRTLPRDEILRGLLNCDLIGFHT	262		
MeTPS7	203	WVHDYHLMMLLPTFLRKGYNRVKLGFFLHSPFSSSEIYRTLPRDEILRGLLNCDLIGFHT	262		
MeTPS8	203	WVHDYHLMMLLPTFLRKGYNRVKLGFFLHSPFSSSEIYRTLPRDEILRGLLNCDLIGFHT	262		
MeTPS9	205	WIHDYHLMMLLPTFLRRFRNLRMGFFLHSPFSSSEIYRTLPRDEILRGLLNCDLIGFHT	264		
MeTPS10	204	WVHDYHLMMLLPTFLRKGYNRVKLGFFLHSPFSSSEIYRTLPRDEILRGLLNCDLIGFHT	263		
MeTPS11	206	WVHDYHLMMLLPTFLRKGYNRVKLGFFLHSPFSSSEIYRTLPRDEILRGLLNCDLIGFHT	265		
MeTPS12	206	WVHDYHLMMLLPTFLRKGYNRVKLGFFLHSPFSSSEIYRTLPRDEILRGLLNCDLIGFHT	265		
MeTPS1	295	YDYARHFVSACTRILGLEGTP----EGVEDQGKLTRVAAPFIDSDRIFIRALELPQVQD	350		
MeTPS2	284	YDYARHFVSACTRILGLEGTP----EGVEDQGKLTRVAAPFIDSDRIFIRALELPQVQD	339		
MeTPS3	295	YDYARHFVSACTRILGLEGTP----EGVEDQGKLTRVAAPFIDSDRIFIRALELPQVQD	350		
MeTPS4	295	YDYARHFVSACTRILGLEGTP----EGVEDQGKLTRVAAPFIDSDRIFIRALELPQVQD	350		
MeTPS5	266	FDYARHFLSCCSRMLGLDYESKRGHIGLDYFGRTVYIKILPVGIHVCRLSVMLNLPYTS	325		
MeTPS6	263	FDYARHFLSCCSRMLGLDYESKRGHIGLDYFGRTVYIKILPVGIHVCRLSVMLNLPYTS	322		
MeTPS7	263	FDYARHFLSCCSRMLGLDYESKRGHIGLDYFGRTVYIKILPVGIHVCRLSVMLNLPYTS	322		
MeTPS8	263	FDYARHFLSCCSRMLGLDYESKRGHIGLDYFGRTVYIKILPVGIHVCRLSVMLNLPYTS	322		
MeTPS9	265	FDYARHFLSCCSRMLGLDYESKRGHIGLDYFGRTVYIKILPVGIHVCRLSVMLNLPYTS	324		
MeTPS10	264	FDYARHFLSCCSRMLGLDYESKRGHIGLDYFGRTVYIKILPVGIHVCRLSVMLNLPYTS	323		
MeTPS11	266	FDYARHFLSCCSRMLGLDYESKRGHIGLDYFGRTVYIKILPVGIHVCRLSVMLNLPYTS	325		
MeTPS12	266	FDYARHFLSCCSRMLGLDYESKRGHIGLDYFGRTVYIKILPVGIHVCRLSVMLNLPYTS	325		
		UP1	UP2		GP4
MeTPS1	351	HIKELKDKFS--GRKVMLGVDRLDMIKGIPQKILAFEFLEENPEWRDKVLLQIAVPSR	408		
MeTPS2	340	HIKELKERFA--GRKVMLGVDRLDMIKGIPQKILAFEFLEENPEWRDKVLLQIAVPT	397		
MeTPS3	351	HIKDLKERFA--GRKVMLGVDRLDMIKGIPQKILAFEFLEENSHWRDKVLLQIAVPT	408		
MeTPS4	351	HIKELKERFS--GRKVMLGVDRLDMIKGIPQKILAFEFLEENSHWRDKVLLQIAVPT	408		
MeTPS5	326	KVKEIQEQFS--GKKVILGIDDMDFKGISLKLAMEQLLQHPDLQGVVLLVQIVNPAR	383		
MeTPS6	323	KVKEIQEQLG--GKKVILGIDDMDFKGISLKLAMEQLLQHPDLQGVVLLVQIVNPAR	380		

Figure S1. Cont.

MeTPS7	323	KVKEIKKQFE--GKRIIVGADDMDIFKGISLKLAMEHLLQQNPGLRGKVVVMQIVNPAR	380
MeTPS8	323	KVKEIQTQFE--GKKIIVGVDDMDIFKGISLKLAMEQLLQQNPGLRGKVVVMQILNPAR	380
MeTPS9	325	RVGELKQQFE--GKTVLLGVDDMDIFKGVNLKLAMEQMLKQHPKWQGRAVLVQIANPAR	382
MeTPS10	324	KVAELHDQFR--GQTVILGVDDMDIFKGISLKLAMEQLLLQHPDKRGEVVLVQIANPAR	381
MeTPS11	326	KVMKLIKQFGDRGRIMLLGVDDMDIFKGISLKLAMEQLLVQHPWGRGKVVVLVQIANPAR	385
MeTPS12	326	KVVELIKQFNDQGRIMLLGVDDMDIFKGISLKLAMEQLLVQHPWGRGKVVVLVQIANPAR	385
UU			
MeTPS1	409	THVPEHQKLTSSQVHKIVTRINGRFGTLTAVPIHHLDRSLDFHALCALYAVTDVALVTSR	468
MeTPS2	398	TDVPEYQKLTSSQVHEIVGRINGRFGTLTAVPIHHLDRSLDFHALCALYAVTDVALVTSR	457
MeTPS3	409	TDVPEYQKLTSSQVHEIVGRINGRFGTLTAVPIHHLDRSLDFHALCALYAVTDVALVTSR	468
MeTPS4	409	TDVPEYQKLTSSQVHEIVGRINGRFGTLTAVPIHHLDRSLDFHALCALYAVTDVALVTSR	468
MeTPS5	384	GSGKDVQEAARETYLIAKRINDVYGSHEYEPVILIDRPVPRYEKTAYYAVAECCEIVNAVR	443
MeTPS6	381	GSGKDVQEAARETYLTAKRINEVYGSPEYEPVILIDRPVPRYEKTAYYALAECCEIVSAVR	440
MeTPS7	381	SSGKDVQEAARETYLITKRINRIFGFGPYEPVILIDRHVPFYEKTAYYALAECCEIVNAVR	440
MeTPS8	381	SSGKDVQEAARETYLTTRKINSIFGFGPYDPVILIDRHVPFYEKTAYYSLAECCEIVNAVR	440
MeTPS9	383	GKGKDLLEIIQAEIQASCKRINETFGQPGYEPVVFIDRPVSLSERAAYYTVAECVVAAVR	442
MeTPS10	382	GRGRDVQEVQSETKATVRRINEIFGRPGYAPVVLIDTPLQFYERIAYYVIAECCLVTAVR	441
MeTPS11	386	GRGKDVKEVQAETYSTVKRINEMFGKPGYDPVVLIDAPLKFEKVAYYVVAECCLVTAVR	445
MeTPS12	386	GKGKDVKEVQAETYSTVKRINETFGKPGYDPIILIDAPLKFEKVAYYVVAECCLVTAVR	445
UG4-5			
UG3 UP3-5 UR2			
MeTPS1	469	DGMNLVSFEFVACQ-----TSKKGVLILSEFAGAAQSLGAGAILVNPWNI	513
MeTPS2	458	DGMNLVSFEFVACQ-----ASKKGVLILSEFAGAAQSLGAGAILVNPWNI	502
MeTPS3	469	DGMNLVSFEFVACQ-----DAKKGVLILSEFAGAAQSLGAGAILVNPWNI	513
MeTPS4	469	DGMNLVSFEFVACQ-----DSKKGVLILSEFAGAAQSLGAGAILVNPWNI	513
MeTPS5	444	DGMNLVPIKYIVCRQGTPLYMDKAMGITS DSPRTSMLVVSEFVGCSPSLSG-AIRVNPWDI	502
MeTPS6	441	DGMNLVPIKYIVCRQGTPLYMDKAMGTASDSPRKSMLVVSEFVGCSPSLSG-AIRVNPWDI	499
MeTPS7	441	DGMNLPIKYIVCRQGTPLYMDKAMGTASDSPRKSMLVVSEFVGCSPSLSG-AIRVNPWDI	499
MeTPS8	441	DGMNLPIKYIVCRQGTPLYMDKAMGTASDSPRKSMLVVSEFVGCSPSLSG-AIRVNPWDI	499
MeTPS9	443	DGMNLPIKYIVCRQGTPLYMDKAMGTASDSPRKSMLVVSEFVGCSPSLSG-AIRVNPWNI	499
MeTPS10	442	DGMNLPIKYIVCRQGTPLYMDKAMGTASDSPRKSMLVVSEFVGCSPSLSG-AIRVNPWNI	500
MeTPS11	446	DGMNLPIKYIISRQGNELDKVLRLEACTPKKSMLVSEFVGCSPSLSG-AIRVNPWNI	504
MeTPS12	446	DGMNLPIKYIISRQGNELDKVLRLEACTPKKSMLVSEFVGCSPSLSG-AIRVNPWNI	504
MeTPS1	514	TEVASSISYALNMPADERENRHHNFRHVTHTSQEWAATFVSELNDTIVEAQLR-----	568
MeTPS2	503	SEVASSIGYALNMPADEREKRHHNFRHVTHTSQEWAATFVSELNDTIVEAQLR-----	557
MeTPS3	514	TEVADSIRQALTMSCEREKRHHNFRHVTHTSQEWAATFVSELNDTIVEAQLR-----	568
MeTPS4	514	TEVADSIRQALTMSCEREKRHHNFRHVTHTSQEWAATFVSELNDTIVEAQLR-----	568
MeTPS5	503	DAVADALNLAITMRESEKQLRHEKHYRYVSTHVDVAYWARSFMDLERACQDHYNKRWCWI	562
MeTPS6	500	DAVADALNLAITMPESEKQLRHEKHYRYVSTHVDVAYWARSFMDLERACQDHYNKRWCWI	559
MeTPS7	500	EAVADALNLALTMPDLEKQLRHEKHYRYISSHDVAYWARSFMDLERACKDHYNKRWCWI	559
MeTPS8	500	EAVADALNLALTMPDLEKQLRHEKHYRYISSHDVAYWARSFMDLERACKDHYNKRWCWI	559
MeTPS9	500	EATAEAMNEAISMSSEKQLRHEKHYRYVSTHVDVAYWARSFMDLERACKDHYNKRWCWI	559
MeTPS10	501	DAVAEAMDSALVPEPEKQMRHEKHYRYVSTHVDVAYWARSFMDLERACKDHYNKRWCWI	560
MeTPS11	505	DAVADAMDYALEMAEPEKQLRHDKHYRYVSTHVDVGYWARSFMDLERACKDHYNKRWCWI	564
MeTPS12	505	DAVADAMDCALEMAEPEKQLRHDKHYRYVSTHVDVGYWARSFMDLERACKDHYNKRWCWI	564

Figure S1. Cont.

		Motif I	
MeTPS1	569	-----TRQVLPLLPIDHAVERYLQSNRRLLILGFNATLTPVDSLGRSSGQIREM	618
MeTPS2	558	-----TRQVLPLLPVNDIVERYTQSSNRLLILGFNATLTPVHTLGRSSGQIREM	607
MeTPS3	569	-----TRQVPPILPEEDAIAKRYLQSNRRLLILGFNATLTPVDTPGRRVDQIKEM	618
MeTPS4	569	-----TRQVPPILPEEDAIAERYLQSNRRLLILGFNATLTPVDTPGRRVDQIKEM	618
MeTPS5	563	GFGLGFRVVSLSPSFRKLCIEHIVSAYKRTNRRRAIFLDYDGTVPQTSIVKSPS-----	616
MeTPS6	560	GFGLGFRVVSLSPSFRRLGVEHIVSAYKRTNRRRAIFLDYDGTVPQTSIVKSPS-----	613
MeTPS7	560	GFGLNFRILSLSPSFRKLSNEHIVSAYKRTYRRVIFLDYDGTVPQTSIVKTPS-----	613
MeTPS8	560	GFGLNFRILSLSPNFRKLSSEHIVSAYKRTYRRVIFLDYDGTVPQTSIVKTPS-----	613
MeTPS9	560	GFSGFRVVALDPNFRKLSTDAIVSAYLRSKNRAILLDYDGTVPQTSINKTPS-----	613
MeTPS10	561	GFGLGFRVIALDPNFRKLSVEHIVSAYKRTKHRAILLDYDGTMLSGSISTAPS-----	614
MeTPS11	565	GFGLSFRVVALDPNFRKLSMEHIVSAYKRTTTRAILLDYDGTLMQASIDKSPS-----	618
MeTPS12	565	GFGLSFRVVALDPNFRKLSMEHIVSAYKRTTTRAILLDYDGTLMQASIDKSPS-----	618
		Motif II	
MeTPS1	619	EPRLHPGLKEPLKKLCDDQMTTIVVLSGSDRTILDENFGGYN-MWLAAENGMSLRITTG-	676
MeTPS2	608	EPRLHPQLKEPLKKLCDDQMTTIVVLSGSDRTILDENFGGYN-MWLAAENGMSLRITTG-	665
MeTPS3	619	ELKLHPGLKEPLKKLCDDQMTTIVVLSGSDSNVLDKNFGEFD-MWLAAEHGMFLRFTKG-	676
MeTPS4	619	ELKLHPGLKEPLKKLCDDQMTTIVVLSGSENVLDENFGGYN-MWLAAEHGMFLRLTKA-	676
MeTPS5	617	-----AEVISVLKTLCDNQNTVFIVSGRGKNSLSEWLDPCERLGLIAAEHGYFMRYNKTS	671
MeTPS6	614	-----PEVMSVLTTLCDNQNTVFIVSGRARNLSLSEWLDPCERLGLIAAEHGYFMRWDKTC	668
MeTPS7	614	-----SEVISVLNLCSDPKNTVFIVSGRGKNSLSEWLDPCERLGLIAAEHGYLMRWKTS	668
MeTPS8	614	-----PEVISVLSNLCTDPKNTVFIVSGRAKDTLSWFTQCENLGLIAAEHGYFMRWSRMS	668
MeTPS9	614	-----QEVISIINALCGDVKNVFIVSGRGRESLGKWFSPCKKLGLIAAEHGYFIRWSVDE	668
MeTPS10	615	-----TEAVGILNLCRDPKNVFVVSFGKDKETLAEWFSSEKLGIAAEHGYFVRPNHDV	669
MeTPS11	619	-----PKSIDILNLCRDKNMVFVLSARSRKTLTEWFSQCEKLGIAAEHGYFRLRTRDA	673
MeTPS12	619	-----SKSIDILNLCRDKNMVFVLSARSRKTLTEWFSQCEKLGIAAEHGYFLRLTRDA	673
MeTPS1	677	EWMTTMPENLNMDWVDSVKHVFYFTERTPRAYYELRETSLVWNYKYADVEFGRLQARM	736
MeTPS2	666	KWMTTMPENLNMDWVDSVKHVFYFTERTPRSHFELRETSLLWNYKYADVEFGRLQARM	725
MeTPS3	677	EWMTTMPEHLNMEWVDSVKHVFYFTERTPRSHFELRETSLVWNYKYADVEFGRLQARM	736
MeTPS4	677	EWMTTMPDHLNMEWVDSVKHVFYFTERTPRSHFELRETSLVWNYKYADVEFGRLQARM	736
MeTPS5	672	DWETNPVTDNDLDWKNIVEPIMRSYTEATDGSSIEVKESALVWHHQDADPDFGSCQAKEL	731
MeTPS6	669	EWETKSVAD-DLDWKNIVEPIMGLYTETTDGSSNIELKESALVWHHQDADPDFGSCQAKEL	727
MeTPS7	669	SWETSSLVA-DFDWKRIAPVVIKLYTEATDGSSYIETKESALVWHHQYADPDFGSCQAKEL	727
MeTPS8	669	NWETSNLVA-DFDWKRIAPVVMKLYTEATDGSSYIETKESALVWHHQYADPDFGSCQAKEL	727
MeTPS9	669	QWETCGQNS-DFGWIHIAEPVMKLYTESTDGSSYIETKESALVWHHRDADPDFGSCQAKEM	727
MeTPS10	670	DWETCVSVP-DFDWKQIAEPVMKLYTETTDGSAIETKESALVWNYQYADPDFGSCQAKEL	728
MeTPS11	674	EWETCVPVT-DTAWKQIAEPVMHLYTETTDGSTIEDKETAVVWCYEDADPDFGSCQAKEL	732
MeTPS12	674	EWETCVPVT-DIAWKQIAEPVMQLYTETTDGSTIEDKETALVWCYEDADPDFGSCQAKEL	732
		Motif III	
MeTPS1	737	LQHLWTGPISNAADVQGGRSVEVRAVGITKGAAIDRILQIVHNQGMRTPIDYVLCVG	796
MeTPS2	726	LQHLWTGPISNAADVQGGRSVEVRAVGVTKGAAIDRILGEIVHNQGMKAPIDYVLCVG	785
MeTPS3	737	LQHLWTGPISNASVDVQGGRSVEVRAVGVTKGAAIDRILGEIVHKSMTTPIDYVLCIG	796
MeTPS4	737	LQHLWTGPISNASVDVIQGGRSVEVRPVGVTKGAAIDRILGEIVHKSMTTPIDFVLCVG	796

Figure S1. Cont.

MeTPS5	732	LDHLEN-VLANEPVAVKRGQHIVEVKPQG IS K SSVAEKVLLDMVNHG---KPPDFVLCIG	787
MeTPS6	728	LDHLEN-VLANEPVAVKRGQHIVEVKPQG IS K GFVAEKVLLNMVNRG---KPPDFVLCIG	783
MeTPS7	728	LDHLEN-VLANEPVVVKRGQHIVEVKPQGV T K GLVAERVLSAMINNG---KSPDFVMCIG	783
MeTPS8	728	LDHLET-VLANEPVVVKRGQHIVEVKPQGV T K GLVAEKVLYAMVTSG---KSPDFVMCIG	783
MeTPS9	728	LDHLES-VLANEPVAVKSGQFIVEVKPQG IS K SFVAERIFTSMVERG---KQADFVLCIG	783
MeTPS10	729	LDHLES-VLTNEPVSVKSGQHIVEVKPQGV N K GLVAQCCLLETMQKKG---MLPDFVLCIG	784
MeTPS11	733	LDHLES-VLANEPVTVKSGQNTVEVKPQGV S K GLVAKRLLSTMQEKG---MSPDFVLCIG	788
MeTPS12	733	LDHLES-VLANEPVTVKSGQNIVEVKPQGV S K GLVAKRLLSTMQERG---MSPDFVLCIG	788
MeTPS1	797	HFLAK DE DIYTFEPEHPSES PG IVRTKS-----VPKVPYGG SRAQYHRQ KQ-	843
MeTPS2	786	HFLV KDE DIYTFEPELPIETPPIVRCRLPE-----PVGLPV KIP CGRSR SKTHL KQ-	839
MeTPS3	797	HFLG KDE DVYTFEPEVLPSDGIGIARAKQTDGLKSPGER PSLKL PASKSG SQ SGKTQ	856
MeTPS4	797	HFLG KDE DVYTFEPEVLPSDGVGIARTKQTDGLKSPGE KRP PKLPA-KSGSG SQ SGKS-	854
MeTPS5	788	DDK-S DE DMFGSILSTVSDPTLPVA-----	811
MeTPS6	784	DDK-S DE DMFESILSTVSGPTLTVA-----	807
MeTPS7	784	DDR-S DE DMFESISRTASSLSFCSA-----	807
MeTPS8	784	DDR-S DE DMFESISRKGS SW FSNSA-----	807
MeTPS9	784	DDR-S DE DMFEIIGNATANGVLSSS-----	807
MeTPS10	785	DDR-S DE DMFEVIMSARAGPSLSFV-----	808
MeTPS11	789	DDR-S DE DMFEVITSSMAGPSIAPR-----	812
MeTPS12	789	DDR-S DE DMFEVITSSMAGPSIAPR-----	812
MeTPS1	844	RSLSTLEG--NTAGSAGWRPIVSDRVSEHEGSS ILD LKRENYFSCAVSRKQSIARYLLGT	901
MeTPS2	840	RSLSTLEG--NYLGSGGWRPMVDDRISVHEGSS VLD LKGENYFSCAVSRKRSNARYLLGT	897
MeTPS3	857	RSPSPNDK KLNNH SCSGRRQ SPE KISWN----VLDLKGDN YF SCSVGRTRTNARYLLHS	912
MeTPS4	855	RSPSPNDK KMTNN SCASGRRQ SPE KISWN----VLDLKGDN YF SCAVGRTRTNARYLLQS	910
MeTPS5	812	-----PEIFACTVGQKPSKAKYYLDD	832
MeTPS6	808	-----PEIFACTVGRKPSKAKYYLDD	828
MeTPS7	808	-----PEIFACTVGQKPSKARYYLLD	828
MeTPS8	808	-----PEIFACTVGQKPSKARYYLLD	828
MeTPS9	808	-----TSVFACTVGQKPSKAKYYLDD	828
MeTPS10	809	-----AEVFACTVGQKPSKAKYYLED	829
MeTPS11	813	-----AEVFACTVGRKPSKAKYYLDD	833
MeTPS12	813	-----AEVFACTVGRKPSKAKYYLDD	833
MeTPS1	902	SDDVVALLKQ MADSS SLT	919
MeTPS2	898	TDDVVTLKQ LAD CLH	913
MeTPS3	913	SDDVVSFLK KLAR ASS	928
MeTPS4	911	SDDVVSFLK KLAN ASP	926
MeTPS5	833	AVDVVKLLQGLATASCPKPKHTEQVLVSFESAI	865
MeTPS6	829	TVDVVKLLQGLSAASCPKPKCIENILVSFESAI	861
MeTPS7	829	TVDVLALLQGLANASSSKLRVSTEVQVSFDNLV	861
MeTPS8	829	TVDVLALLQGLAAASSSKPRGSEEVQVSFDNVI	861
MeTPS9	829	TTEVINMLEALAEASDSSPSPGNSP	853
MeTPS10	830	TSEILRMLEGLANASELAARSSPPIGAKTDH	860
MeTPS11	834	TAEIVRLMQGLASVSEQTVNNVS	856
MeTPS12	834	TTEIVRLMQGLASVSEQTVAV	854

Figure S1. Predicted enzymatic domains and activity sites in cassava TPS proteins. Predicted TPS domains are highlighted in red; Predicted TPP domains are highlighted in green; Conserved motifs are highlighted in bold. GG1-4: Binding sites 1-4 to Glucose moiety in Glucose-6-Phosphate (G6P); GP1-4: binding, sites 1-4 to Phosphate moiety in G6P; UU: binding sites to Uracil moiety in UDPG; UR1-2: binding sites 1-2 to Ribose moiety in UDPG; UP1-5: binding sites 1-5 to phosphate moiety in UDPG; UG1-5: binding sites 1-5 to glucose moiety in UDPG.

MeTPP1	1	MDMKSNNKSSPVLTDPAPINKSRLGIHNSLLPYPQSGASFSSGKHINIPRKKPGKL----	D	56	
MeTPP2	1	MDINSNNSSPVLTDPAPIN-----LLPYPQSGASFSS----	NIPRKKPEKL----	D	43
MeTPP3	1	MDLKSNNHTAPVLTDPAPISKSRGLGVHSSLLPYSP-GTAFSSNLFLTIPWKKTGVL----	D	55	
MeTPP4	1	MDLKSNNHTAPVLTDPAPISKSRMGVHSSLLPYTP-GAAFSSNLFLTIPRKKTGVL----	D	55	
MeTPP5	1	MTN-QNVVVSDDPKSTINLAITVHVSDDSIPTAAQKPPAAPGGYISISRKKLLKNLEING		59	
MeTPP6	1	MTN-QNVVVSDDPKTTINLATTVHVSDDSIPTAAQKPPAAPGGYISISRKKLLNHLEINE		59	
MeTPP7	1	MTN-QNVVASDAKSGIDIRIRVILP-KSLFSSAEPKPLPAPR-----LAKKIETG---TA		50	
MeTPP8	1	MTN-QNVVASDEKSAVDIRIRFLLP-KSLFSPDGPKPLPAPR-----LAKKIETGGVATA		53	
MeTPP9	1	MFT-RN--IAKFNQAMGFQRS-----STNKPQTQPGSGRSIR-----		34	
MeTPP10	1	MF-KRS--IAKLNQAMGFQRS-----STNKPQMPPGNDRSTS-----		34	
MeTPP1	57	DVRNNGWLDAMKSSSPRKKLIKDFNFEVAADET--DIAYFSWMLKYPSALNSFEQITNF		114	
MeTPP2	44	EVHYNGWLDAMKSSSPRKKLIKDLNFEDAADEIEIEIAYFSWMLKYPSALNSFGQITKF		103	
MeTPP3	56	DVRSSSWLDAMKSSSPTHKRITKEN----ASADN--DVAYATWTLKYPSAIASFEQIANF		109	
MeTPP4	56	DFRSSWVDTMKSSSPPHKKMTKDLNLSFADT--DVAYRTWTLKYPSALTSFEQIANF		113	
MeTPP5	60	GARINAWVDSMRASSPHTLKSTPSITD-----DQGSWILHHPSSALDMFEQIIEA		108	
MeTPP6	60	VARINAWVDSMRASSPHTIKSTPSITD-----DQGSWILRQPSALDMFEQIIDA		108	
MeTPP7	51	AAKTNAWVDSMRDSSPTRVKSTASLSET-----EEKNSWIMNHPSSALSMFEQIVNA		101	
MeTPP8	54	AAKTNAWVNSMRDSSPTRVKSTCSLSES-----EEKNSWIMNHPSSALSMFEQIVNA		104	
MeTPP9	35	-MGASNLCHH-IAGGPISIED-----ASYISWVVEHPSALRSFDQMMKA		76	
MeTPP10	35	-MRTTNIKSHPIITSGPISIND-----ASYDTWVVEHPSALGSFDQMMKA		77	
		Motif I	Motif II		
MeTPP1	115	AKTKKIAIFLDYDGTLSPIVDDPDQATMSDEMRSVVRNVAKYFPTAIISGRSRDKVYELV		174	
MeTPP2	104	AKNKKIAIFLDYDGTLSPIVDDPDQALMSDDMRSAVRNVAKYFPTAIITGRNRDKVFELV		163	
MeTPP3	110	AKGKRIALFLDYDGTLSPIVDNPDRAFMSSDAMRSAREKVKCFPTAIISGRSRDKVHEFV		169	
MeTPP4	114	AKGKRIALFLDYDGTLSPIVDNPDCAFMSNAMRSARVKKVAKCFPTAIISGRSRDKVYEFV		173	
MeTPP5	109	SKGKQIVMFLDYDGTLSPIVDDPDRAFMSSKKMRATVRKLAKCFPTAIVSGRCRDKVYNFV		168	
MeTPP6	109	SKGKQIVMFLDYDGTLSPIVDDPDRAFMSSKKMRATVRKLARCCPTAIVSGRCRDKVYNFV		168	
MeTPP7	102	SKGKQIVMFLDYDGTLSPIVEDPDRAFMNTNEMREAVRDVARYFPTAIVTGRCDRKIYSFV		161	
MeTPP8	105	SKGKQIVMFLDYDGTLSPIVEDPDRAFMNTNEMREAVRDVARYFPTAIVTGRCDRKVYSFV		164	
MeTPP9	77	AKGKKIALFLDYDGTLSPIVDNPDLAFMSSDEMRAAREVAKYFPTAIISGRSRDKVKEFV		136	
MeTPP10	78	AKGKKIAVFLDYDGTLSPIVDNPDLAFMSSDEMRSAREVAKYFPTFIITGRSRDKVKEFV		137	
MeTPP1	175	GLTELYYAGSHGMDIMGPINKAVSNNQPNCKSIDQKGKVNLFQPARFIPMIDEVFRT		234	
MeTPP2	164	GLTELYYAGSHGMDIMGPVNEAVSSNHPDCIKSTDQKGKVNLLQPARDFIPMIDEVFRT		223	
MeTPP3	170	GLKELYAGSHGMDIMGPVRQYISDDQPNQSVRSTDEQKGKVNLFQPARFIPMIDEVYSS		229	
MeTPP4	174	GLTELYYAGSHGMDIMGPVRQSVSDDQPNQSVRSTDEQKGKVNLFQPARFIPMIDEVYSS		233	
MeTPP5	169	RLAELYAGSHGMDIKGPA-----KGSYKKGSEALIFQPARFIPMIDEVYKE		217	
MeTPP6	169	RLAELYAGSHGMDIKGPA-----KGSYKKGSEALIFQPARFIPMIDEVYKE		217	
MeTPP7	162	KLGLYAGSHGMDIKGPS-----KSRKYKKGHQAALLFQPARFIPMIDEVYKV		210	
MeTPP8	165	KLGLYAGSHGMDIKGPS-----KSRKYKKGHQAALLFQPARFIPMIDEVYKV		213	
MeTPP9	137	QLSNVYAGSHGMDIMAPPRPVKTCDGKYPTVALDKKNEV-LFQPAKKFLPAIQKIQT		195	
MeTPP10	138	QLSNVYAGSHGMDILAPPRPVKSCDGKYQSIALDKKNEV-LFQPAKKFLPAIQKIQT		196	

Figure S2. Cont.

MeTPP1	235	LVENTKEIKGAKVENNHKFCASVHYRNVDEKNWHTIAQCVHDILTQYPRRLRTHGRKVLEI	294
MeTPP2	224	LVENTKDIKGARVENNHKFCASVHYRNVDEKNWPIIAQRVHVDVLKLYPRRLRLAHGRKVLEV	283
MeTPP3	230	LVENTKYIKGVKVENNKFCVSVHYRNVDDKSWKSVAQCVDVIKNYPRLRLTHGRMVLEV	289
MeTPP4	234	LVDSTKDIKGAKVENNKFCVSVHYRNVDEKSWKSVAQCVDVIKNYPRLRLTHGRKVLEV	293
MeTPP5	218	LIEKTKSTPGAKVENNKFCVSVHFRCVDEKKWSELAQVVRSVLKDYPKLRLTQGRKVLEI	277
MeTPP6	218	LVEKTKSTPGAKVENNKFCVSVHFRCVDEKKWSELGQVVRSVLKDYPKLRLTQGRKVLEI	277
MeTPP7	211	LIEKTKSISGAKVENNKFCVSVHFRCVVEEKMWAALAEQVRSVLNDYPKLRLTQGRKVLEI	270
MeTPP8	214	LVEKTKSIPGAKVENNKFCVSVHFRCVVEEKMWAALAEQVRSALNDYPQLRLTQGRKVLEI	273
MeTPP9	196	LKEKVVEIQGAMVEDNSFCVSVHFRQVREKDYGILEKQVKSVEHYPEFHLSWGKKVMEI	255
MeTPP10	197	LEEKVVKIQQGARIEDNRFCSVHFRQVREEDYETLEKDVKSVEHYPEFHLSWGKKVMEI	256

Motif III

MeTPP1	295	RPVIDWN K GRAVEFLLESGLSKRDDVLPYI GDDRT DEDAFKVLRERNQGYGILVSCVP	354
MeTPP2	284	RPEIDWN K GKAVEFLLESGLGNSDDVLPYI GDDRS DEDAFKVLRERNRGYGILVSSAP	343
MeTPP3	290	RPVINWN K GKAVTFLESGLSNCDDVLPYI VGDRT DEDAFKVLRERNCGLGILVSPVP	349
MeTPP4	294	RPVINWD K GKAVTFLESGLSNCDDVLPYI VGDRT DEDAFKVLRERNCGYGVLTSPVP	353
MeTPP5	278	RPTIKWD K GKALEFLLESGLFANCTDVFPVYI GDDRT DEDAFKVLRERGGGFGILVSKFP	337
MeTPP6	278	RPTIKWD K GKALEFLLEYLGFTNCTDVFPVYI GDDQT DEDAFKVLRERGGGFGILVSGIP	337
MeTPP7	271	RPTIKWD K GKALEFLLESGLYANSNDVLPVYI GDDRT DEDAFKVLRNRGGGLGILVSKFP	330
MeTPP8	274	RPTIKWD K GKALEFLLESGLYANSNDVLPVYI GDDRT DEDAFKVLRNRGGGLGILVSKFP	333
MeTPP9	256	RPSIEWD K GHALEYLLDTLGLSNSNDVLPYI GDDRT DEDAFKVIQRRGGGYPIIVSSSP	315
MeTPP10	257	RPSIQWD K GDALEYLLDTLGLSNSNDVIPVYI GDDRT DEDAFKVIQRRGGGYPIIVSSSP	316
MeTPP1	355	KETNAFYSLRDP IEVLQFLSSLVRWKKLGEER -RSMNNRRSI	395
MeTPP2	344	KETNAFYSLRDPSEVMKFLCWLVRWKKLGE GV -SSVNKRWSI	384
MeTPP3	350	KETNAFYSLRDPSEVMEFLEYLVMWKK	376
MeTPP4	354	KESNAFYSLRDPSEVMEFLKSLVMWKKSSAL	384
MeTPP5	338	KDTNASYSLQ EP TQVMDFLQRLVEWKQVSLRG-QPRL	373
MeTPP6	338	KDTNASYSLQ EP TQ	351
MeTPP7	331	KETNASYSLQ EP TEVKDFLRLVEWKRF SIG	361
MeTPP8	334	KETNASYSLQ EP AEVKDFLRLVEWK RISFAR -ACRV	369
MeTPP9	316	KDTKASFS LHDP SEVLTFLSRLARWRKSSSSS-RSLAQIWGVGD	358
MeTPP10	317	KDTKASFS LHDP SEVLTFLRLARWRKSSSSSSRSLAQIWGVSN	360

Figure S2. Predicted enzymatic domains and active motifs in cassava TPP proteins. Predicted TPP domains are highlighted in green; Conserved motifs are highlighted in bold.

Table S1. Accession numbers of genes used in this study.

Cassava		Maize	
Gene Name	Accession Number	Gene Name	Accession Number
<i>MeTPS1</i>	cassava4.1_001215m.g	<i>ZmTPSI.1.1</i>	GRMZM2G068943_T01
<i>MeTPS2</i>	cassava4.1_001223m.g	<i>ZmTPSI.1.2</i>	GRMZM2G001304_T01
<i>MeTPS3</i>	cassava4.1_021281m.g	<i>ZmTPSII.2.1</i>	GRMZM2G019183_T02
<i>MeTPS4</i>	cassava4.1_023440m.g	<i>ZmTPSII.2.2</i>	GRMZM2G099860_T01
<i>MeTPS5</i>	cassava4.1_001517m.g	<i>ZmTPSII.3.1</i>	GRMZM2G304274_T01
<i>MeTPS6</i>	cassava4.1_001537m.g	<i>ZmTPSII.3.2</i>	GRMZM2G123277_T01
<i>MeTPS7</i>	cassava4.1_001541m.g	<i>ZmTPSII.3.3</i>	GRMZM2G118462_T01
<i>MeTPS8</i>	cassava4.1_029065m.g	<i>ZmTPSII.4.1</i>	GRMZM2G527891_T01
<i>MeTPS9</i>	cassava4.1_001591m.g	<i>ZmTPSII.4.2</i>	GRMZM2G008226_T01
<i>MeTPS10</i>	cassava4.1_001558m.g	<i>ZmTPSII.4.3</i>	GRMZM2G366659_T01
<i>MeTPS11</i>	cassava4.1_001575m.g	<i>ZmTPSII.5.1</i>	GRMZM2G007736_T02
<i>MeTPS12</i>	cassava4.1_001584m.g	<i>ZmTPSII.5.2</i>	GRMZM2G079928_T01
<i>MeTPP1</i>	cassava4.1_009204m.g	<i>ZmTPSII.5.3</i>	GRMZM2G312521_T01
<i>MeTPP2</i>	cassava4.1_031249m.g	<i>ZmTPSII.5.4</i>	GRMZM2G122231_T01
<i>MeTPP3</i>	cassava4.1_009837m.g	<i>ZmTPPA.1</i>	GRMZM2G178546_T01
<i>MeTPP4</i>	cassava4.1_031945m.g	<i>ZmTPPA.3</i>	GRMZM2G112830_T01
<i>MeTPP5</i>	cassava4.1_009931m.g	<i>ZmTPPB.1.1</i>	GRMZM2G347280_T01
<i>MeTPP6</i>	cassava4.1_026633m.g	<i>ZmTPPB.1.2</i>	GRMZM2G140078_T01
<i>MeTPP7</i>	cassava4.1_028041m.g	<i>ZmTPPB.1.3</i>	GRMZM2G174396_T01
<i>MeTPP8</i>	cassava4.1_010043m.g	<i>ZmTPPB.1.4</i>	GRMZM2G055150_T01
<i>MeTPP9</i>	cassava4.1_022149m.g	<i>ZmTPPB.1.5</i>	GRMZM2G151044_T01
<i>MeTPP10</i>	cassava4.1_032922m.g	<i>ZmTPPB.1.6</i>	GRMZM2G080354_T01
<i>MeTRE1</i>	cassava4.1_004491m.g	<i>ZmTPPB.2.1</i>	GRMZM2G014729_T01
<i>MeTRE2</i>	cassava4.1_015916m.g	<i>ZmTPPB.2.2</i>	GRMZM2G117564_T01
	cassava4.1_023202m.g	<i>ZmTPPB.2.3</i>	GRMZM5G840145_T01
Rice		Arabidopsis	
Gene Name	Accession Number	Gene Name	Accession Number
<i>OsTPS1</i>	OS05G44210	<i>AtTPS1</i>	AT1G78580
<i>OsTPS2</i>	OS01G54560	<i>AtTPS2</i>	AT1G16980
<i>OsTPS3</i>	OS01G53000	<i>AtTPS3</i>	AT1G17000
<i>OsTPS4</i>	OS03G12360	<i>AtTPS4</i>	AT4G27550
<i>OsTPS5</i>	OS02G54820	<i>AtTPS5</i>	AT4G17770
<i>OsTPS6</i>	OS05G44100	<i>AtTPS6</i>	AT1G68020
<i>OsTPS7</i>	OS08G31980	<i>AtTPS7</i>	AT1G06410
<i>OsTPS8</i>	OS08G34580	<i>AtTPS8</i>	AT1G70290
<i>OsTPS9</i>	OS09G25890	<i>AtTPS9</i>	AT1G23870
<i>OsTPS10</i>	OS09G23350	<i>AtTPS10</i>	AT1G60140
<i>OsTPS11</i>	OS09G20990	<i>AtTPS11</i>	AT2G18700
<i>OsTPP1</i>	OS02G44230	<i>AtTPPA</i>	AT5G51460
<i>OsTPP2</i>	OS10G40550	<i>AtTPPB</i>	AT1G78090
<i>OsTPP3</i>	OS07G43160	<i>AtTPPC</i>	AT1G22210
<i>OsTPP4</i>	OS02G51680	<i>AtTPPD</i>	AT1G35910
<i>OsTPP5</i>	OS04G46760	<i>AtTPPE</i>	AT2G22190
<i>OsTPP6</i>	OS08G31630	<i>AtTPPF</i>	AT4G12430
<i>OsTPP7</i>	OS09G20390	<i>AtTPPG</i>	AT4G22590
<i>OsTPP8</i>	OS06G11840	<i>AtTPPH</i>	AT4G39770
<i>OsTPP9</i>	OS03G26910	<i>AtTPPI</i>	AT5G10100
<i>OsTPP10</i>	OS07G30160	<i>AtTPPJ</i>	AT5G65140
<i>OsTPP11</i>	OS02G44235	-	-
<i>OsTPP12</i>	OsI_34594	-	-
<i>OsTPP13</i>	OS12G09060	-	-