

S3 Figure. Conserved domains and membrane topology of the TIP isoforms from pearl millet.

Alignment of the TIP isoforms were obtained using ClustalW in Mega7. Sequence identities and similarities (80%) are highlighted in colors. The transmembrane domains are represented by orange bars and the N-terminal and C-terminal ends of the protein are located in the cytosol. NPA: Asparagine-Proline-Alanine motifs; *: Aromatic/Arginine selectivity filters; #: Froger's residues.

PgTIP1-1	-----MPISRIAVGSHQE-VYHPGALAAFAFISTLIFVFAGQSGMAFSLSPGGS-----SPAGLISAAIAHAFALFVAVSVGANISGG	81
PgTIP2-1	-----MVKLAFGSGID-SFSAASLAAVVAFFIATLLVFAGVGSIAIAYSQLTKGGAL-----DPAGLVIAIAHAFALFVGVSMANISGG	80
PgTIP2-2	-----MTGNIAFGSFGD-SFSAASLAAVVAFFISSLVVFAGVGSIAIAYRKLSDGAPL-----DATGLVAVVCHGFALFVAVAIKANISGG	81
PgTIP2-3	-----MVKLAFGSGVD-SFSATSLAAVVAFFIATLLVFAGVGSIAIAYGQLSHGGAL-----DASGLVAIAIAHAFALFVGVSTAAISGG	80
PgTIP3-1	MSTGARPGRRFTVGRSED-ATHPDTIAAISEFLATAIFVFAAEGSVLSLGRMYHDS-----TAGGLVAVALAHALASVAVAVAVNISGG	86
PgTIP4-1	-----MQKFVDSYDDAGQDAGCVAAVLAFVLTFLFVFTVVSAAMGAGEATP-----MATLAAVALANALAAAGVLVTAGFHVISGG	76
PgTIP4-2	-----MAKLTGRRGE-SSEPDPFFKGVLGELVLTFLFVVFQVGAAMAIHVG-----GNLAAVALGQALVVCVIATAGFHISGG	72
PgTIP4-3	-----MAKFALGHHRE-VADAGCISVIAFFILTFLFIFAGVGSAMATSKLGDGAD-----TVVGLTAVSLAHTLVVAGMVSAGLHVSAG	79
PgTIP5-1	-----MASNLLTKLKR-CVSPPSLSYFAFFISTFLFVFAAVGSAISARMVTTAPDVGTAASHCGTASDAASLVATAVAQAFGLFAAVLIAADVSGG	92
<div> <div>NPA</div> <div>#</div> <div>*</div> </div>		
PgTIP1-1	AVNPAVTFGAFVGGNITLFRGILYWAQLLGSTVACFLLRFTGGLPTGT-FGLT-GISVWEALVLIIVMTFGLVYTVYAT----AVDPK---GSLG-T	171
PgTIP2-1	VLNPAVTFGLAVGGHITILTGLFYWVAQLLGASAACLLRFVTHGQAIPT-HGVS-GISEVEGVVMEIVITFALVYTVYAT----AADPK---GSLG-T	170
PgTIP2-2	AVNPAVTFGLVGGQITMLTGLFYWIAQLVGAIVGAVLVQFST-GVATPT-HGLS-GIGTLEGVVMIIIVTFGLVYTVYAT----AADPK---GSLG-T	170
PgTIP2-3	VLNPAVTFGLAVGGHITILTGLFYWVAQLLGASVACLLKFTVTHGKAIPT-HGVA-GISELEGVVFIIITFALVYTVYAT----AADPK---GSLG-T	170
PgTIP3-1	AVNPAITFGALIGGRVSLVRAVFYWAAQLLGAVAASLLRLATGGARPPG-FALATGVGDWHAVLLAAMTFGLMYAYYAT----VIDPK---GSVG-T	177
PgTIP4-1	VLNPSVSVAMMVRGHLKSLRTVLVTAQLLASSLACVLLRLYLTGGMVTPV-HALGAGIRPMQGVVMEVILTFSLLEFVYAM----ILDP---SQVR-T	166
PgTIP4-2	AVNPAVTLSLAVGQITLFRSALYVVAQVAGSSAACLLLRWLKGLATPV-HALAAGVGPAQGVVAHAVFTFSLLEFVIYAT----ILDPSP---KVLP-G	164
PgTIP4-3	VINPAVTLGLAATGRVTLTLLSAAFVAAQLLASASACVLLRYLTGGAPIVRHSLAAGVGPLQGVLMFAVLTFSLLFTVYAT----IVDP---RTVG-G	170
PgTIP5-1	AVNPAVTFFAIGGHIGVPSAIFYWASQMLGSTFACLAVPTTRIAVAMTG-----FGAIIIVAVITFMLVYSAHVAGDLRAAGSGGKQGLAATA	182
<div> <div>*</div> <div>NPA</div> <div>#</div> <div>*</div> <div>#</div> <div>#</div> </div>		
PgTIP1-1	IAPIAIGFIVGANILVGGAFDGAASMPAVSFGPALVSWSGYQWVYVWVGLIGGGLAGIIVVLFISHT-----HEQLPTTDY-	249
PgTIP2-1	IAPMAIGFIVGANILAAGPFGSGSMTPASFGPAVAAGNFAGNWWVWVGLIGGGLAGLVYGDVFIAS-----YQPVG-QEYP	247
PgTIP2-2	IAPIAIGFIVGANILVAGPFGSGSMNPASFGPAVASGDFTNIIYVWVGLVGGGLAGIVRYIYMGCD-----HAPVASSDF-	248
PgTIP2-3	IAPIAIGFIVGANILAAGPFGSGSMNPASFGPAVAAGNFAGNWWVWVGLIGGGLAGLVYGDVFIGGN-----YQVADQDYA	249
PgTIP3-1	IGPLAVGFLGANVLAGGPFDDGAGMNPANVFGPALVGRWRHWHVYVWVGLIFLAGIAGIVVEYLVIIPAADAAAAHAHPHQPLAPEDY-	266
PgTIP4-1	IGPLLTGLIVGANSLAGGNFTGASMNPAISFGPALATGDTTHHWVYVWVGLLGGPLAAVVEVSVFIN-----KTHEPLNNSDC-	245
PgTIP4-2	AGPLLTGLLVGANSVAGAVLSGASMNPAISFGPAVATGVVTHHWVYVWVGLAGGPLAVVVEWLFMTAAA-----AHHQHLLTGEEA	247
PgTIP4-3	TRPLLVALLVVGANIAGGPFSGASMNPAISFGPALAAGVDDHWVYVWVGLVGGALAGMVVDGLFMAQAG-----EHEQLPKG---	248
PgTIP5-1	LGALAVGLVAGALVLSAGPLTGASMNPAISFGPAVVSQDKNQAVVWVGMIGAATAAALAHQILAGPSDAATAG-LSSSRHGSYETVVV-	270