

**S4 Figure. Conserved domains and membrane topology of the NIP isoforms from pearl millet.** Alignment of the NIP 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.

PgNIP1-1	-----MAGGGDNSTNGARD-QRAMEEGRKQ-----EEFAA--DQ-----GC-AALSVPFIQIIAIFGTFFLIFAGCGAVTINASR	68
PgNIP1-2	-----MAG-AEVANGGLHESHTVAMEEGRVG-----DEACR--ERSEQDGAGCRPMFVVPFVQIIAIFGTFFLIFAGCAAVAVNLRT	75
PgNIP1-4	-----MARREDDSYTNGSVFEVSVEDGRKDKSDAHAYADAVQQPAD--EADGDIDAVCGMPASVSFIQOLIAFLATEFFLIFAGCGVITVND-K	86
PgNIP2-1	-----MSTN-----SRSNSRANFNNEIHDISTVQN--STMPPMYYSERSLADFFPPHLLKVVSVVSTELLVFVTCGAAIASASD	74
PgNIP2-2	-----MAASTAPSRNTSRVNSYNEIHDISTVQSGGSAVPTMYYPEKSLADIFFPHLGGKVVISVVVATELLVFVTCGAASIYGAD	79
PgNIP3-1	MEPESTPPNGSAPATPGTPAPLFSNGPRVDSARSMSYDRKSMPCRCLPAVEGEGVATHTCCVVEIPAPDVSLTRGLGAFVGTFFLIFATAAPIVNQKY	100
PgNIP3-2	-----MPFELLSTGGSVS-SHPHNADAAESSDAHAAAHFHR--WNQGLP-----KIKAVPLKKVVAFVLGTFFLIFATVLSIIMNEQH	75
PgNIP3-3	-----MQFELLSAGSVS-SHPHNADAAKSSDAHAAAHYHR--WNQGLP-----KIKAVPLKKVVAFVLGTFFLIFATVLSIIMNEQH	75
PgNIP3-4	-----MIFSKSPSNK-TLPQWVQN-----EAPPPAPFSEKRVALALVKMA--FLGTSLLIPTVLSALIMNEEH	62
PgNIP3-5	-----MDVLVSIPIAAAAPMESMSDDKIAIVPHKSPSNKQILPLGFQEFND--PSPPPPGGFAN-RVALPLIKVAAALLGTFFLIFVLSAATIDEAH	92
PgNIP4-1	-----MAADHVGGNVAAAGSDGDQRSKVNGGQDDLEQQPRRGDQLEPAADHVSSRGLAVAHFVRELMLVGVASEVLLVFS-GVATLMQDM	83
<div> <div></div> <div>*</div> <div>NPA</div> <div>#</div> </div>		
PgNIP1-1	DGQITFPGVAIVWGLAVMMVYAVGISGAFNPFAVTFATCGRFPWRQLPAVVLQMLGATLASCTLLMFGRHEHFF--GTLPTGSDAQSLVITII	166
PgNIP1-2	GGTITFPGICIVWGLAVMMVYVSGISGALNPFAVSIATCGRFPWRQVPAAAAVMGAAAASLTLLFPGNAREHFF--GTVPAGSDVQSLVIELI	173
PgNIP1-4	NGMATFPGVAIVWGMTVMAMIYAVGISGALNPFAVTVGFA-----VPAYMVVQLVAATIASLILMLFDRQHEVAA--VTVPGVSNIQSLVLEFI	175
PgNIP2-1	LNRISQLGQSVAGGLIVTVMYIYAVGISGAMNPFAVTLAFVFRHFPWIQVPFYWAAQFTGAICAFVLAVLHPITVIG--TTTPTGPHWHALVIEVI	171
PgNIP2-2	LKRVSQQLGQSVVGLIVTVMYIATGISGAMNPFAVTLSPACFRHFPWIQVPFYWAAQFTGAMCAAFVLAVLHPITVIG--TTTPTGPHWQALVVEIV	176
PgNIP3-1	GGATSPFGNAACAGLAVTIIILSTGISGALNPSTLIATFAALRHFPWLQVPVSVQVLGSIACAFALGVF--HPFLSGGVTVDPDTISTAQAFTFEII	199
PgNIP3-2	DGVESLLGIATSAGLAVTILVLSLISGCLNPFAVSIAMTFGHLPHGHLLPYITAILGSIASFSVVCIIY-HPVNPFG--IATIPNVGTTEAFFLEFI	172
PgNIP3-3	DGVESLLGIATSAGLAVTILVLSLISGCLNPFAVSIAMTFGHLPHGHLLPYITAILGSIASFSVVCIIY-HPVNPFG--IATIPNVGTTEAFFLEFI	172
PgNIP3-4	GGALGLLGVAAAAGSAVLVIVASLVVSGGLNPFAVSVAMATFGFLPRAHLPLVYAAQFLGSMTASFAAAVYSNPANLGATVATVPTVGGAALVVEFV	162
PgNIP3-5	GGALGLLGVAAAAGSAVLVIVASLVVSGGLNPFAVSVAMATFGFLPRAHLPLVYAAQFLGATAASFAAALYDDPANMAATVATVPTVGGAQAFVFEFA	192
PgNIP4-1	HGTLSPFMVCLVMALTIVGFIICWLG---PAIFNPFAVTFATFAAFGLSWAKLPFYVMVQLAGSVLACLVSNGVMRPREEHFYGTAPMP-GQTRLPFLLILL	179
<div> <div></div> <div>*</div> <div>NPA</div> <div>#</div> <div>#</div> </div>		
PgNIP1-1	TFYFLMFVISGVATINRAIGLAGLAVGATILLNVLIAGPVSGASMNPAITVGPALVSGQYRSIIVVVVGVVGVAGAVAWAYNLIPTNKPLREITKSTS	266
PgNIP1-2	ISPNLMFVVSAVATINRAIGLAGLAVGATVLLNVLFAGPIISGASMNPAITLGPALVAGRTAGIWWYFVGPIILGTVAGAWAYNLIPTDKPLREITQTSS	273
PgNIP1-4	ITFYLMFVIMAVATIDNAVGQAGLAVGGTIMLNALFAGPVSGASMNPAITLGPALVAGRTAGIWWYFVGPIILGTVAGAWAYNLIPTDKTLAEITKSTS	275
PgNIP2-1	VTFNMMEVTVLAVATITAVGELAGLAVGSAVCITSIFAGAVSGGSMNPATLGPALASNLITGLWLYFLGPVGLTSLGAWTYTYIFEEAPSNGKEPQKL	271
PgNIP2-2	VTFNMMEVTVCAVATITAVGELAGLAVGSAVCITSIFAGAVSGGSMNPATLAPAVASNVITGLWLYFLGPVIGTSLGAWTYTYIFEEAPAKDG-PQRL	275
PgNIP3-1	ITPNLLFVVTVAVATITAVGELAGIAGAAVTNLNLVAGPTTGGSMNPVITLGPAAVAGNRQLWYLLATLGLAGAGVYTAVALRDENGETPRAQRS	299
PgNIP3-2	TTFVLLFIITALATDPNAVKELIAGVAGAIMMNALVAGPSTGASMNPAITLGPATIGRYTQIWIYVMVATPLGAVAGTGAYVVAIYLSVGPKNVILEI	272
PgNIP3-3	TTSVLLFIITALATDPNAVKELIAGVAGAIMMNALVAGPSTGASMNPAITLGPATIGRYTQIWIYVMVATPLGAVAGTGAYVVAIYLSVGPKNVILEI	259
PgNIP3-4	TTFVLLFVITATATDPNAVKELIAGVAGAAVMSALASGMSTGASMNPAITLGPATIAAGTYTKIWWYVMVAPPLGAIAGTGAYAAAL-----	248
PgNIP3-5	TTFVLFVVITATATDPNAVKELVAVGAGAAVMSALASGKSTGASMNPAITLGPATIGTYTKIWWYVMVAPPLGAIAGSGAYHAL-----	278
PgNIP4-1	ASAVLMIVIATAARGSSPT--AGGLAIGAAVGTGLGLIGPVSGGSMNPITLGPALVGRYTSVWYVLVAVAGMLLGCALCNRAVSSDAVLAFLCGRGV	277
PgNIP1-1	FLKSTGRNLNSSSSSS-----	281
PgNIP1-2	FLRSARRN-----	281
PgNIP1-4	RTN-----	278
PgNIP2-1	SSFKLRLRQSQSVAADDDLDHIQV----	296
PgNIP2-2	SSFKLRRMQSQSALAAD-EFDTV-----	297
PgNIP3-1	FRR-----	302
PgNIP3-2	LGQIIKEVK-----	281
PgNIP3-3	-----	259
PgNIP3-4	-----	248
PgNIP3-5	-----	278
PgNIP4-1	GAAARKAGGRAPAALTAHAVAVASQQL	306