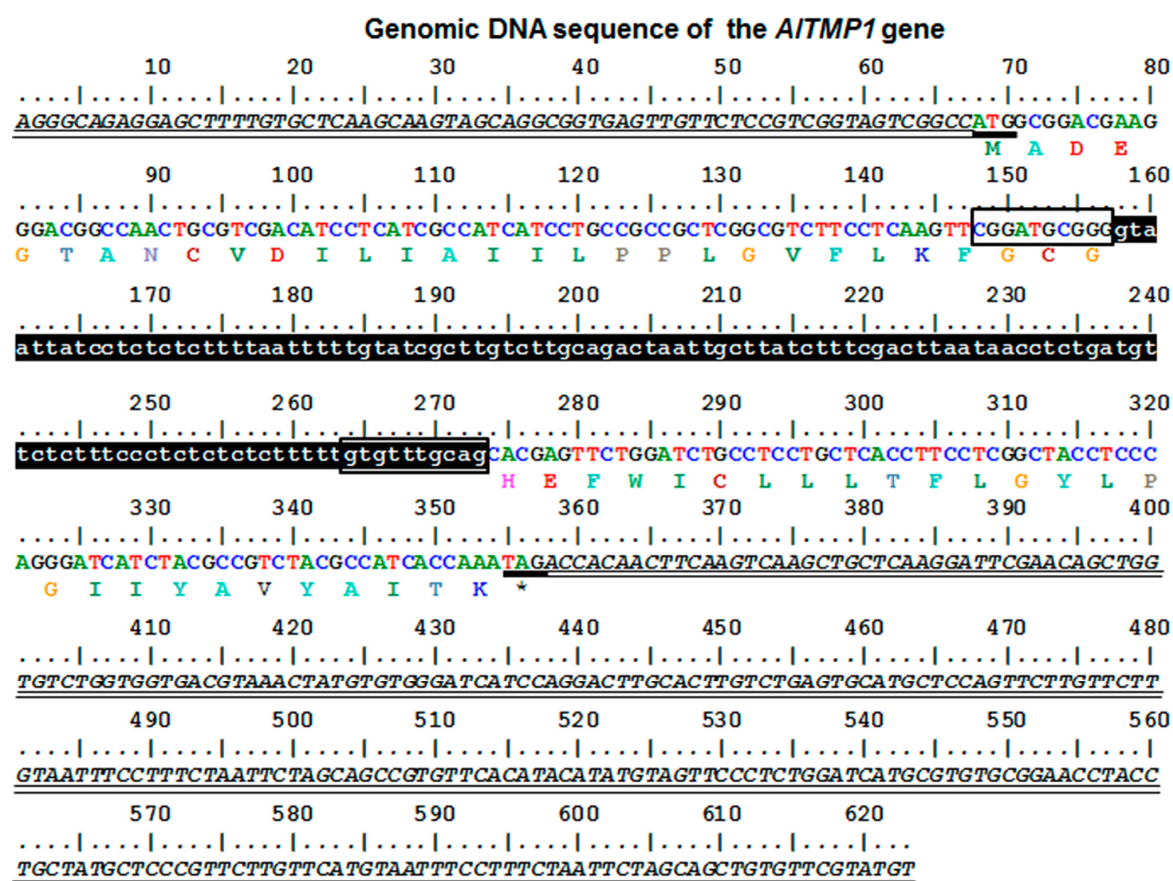
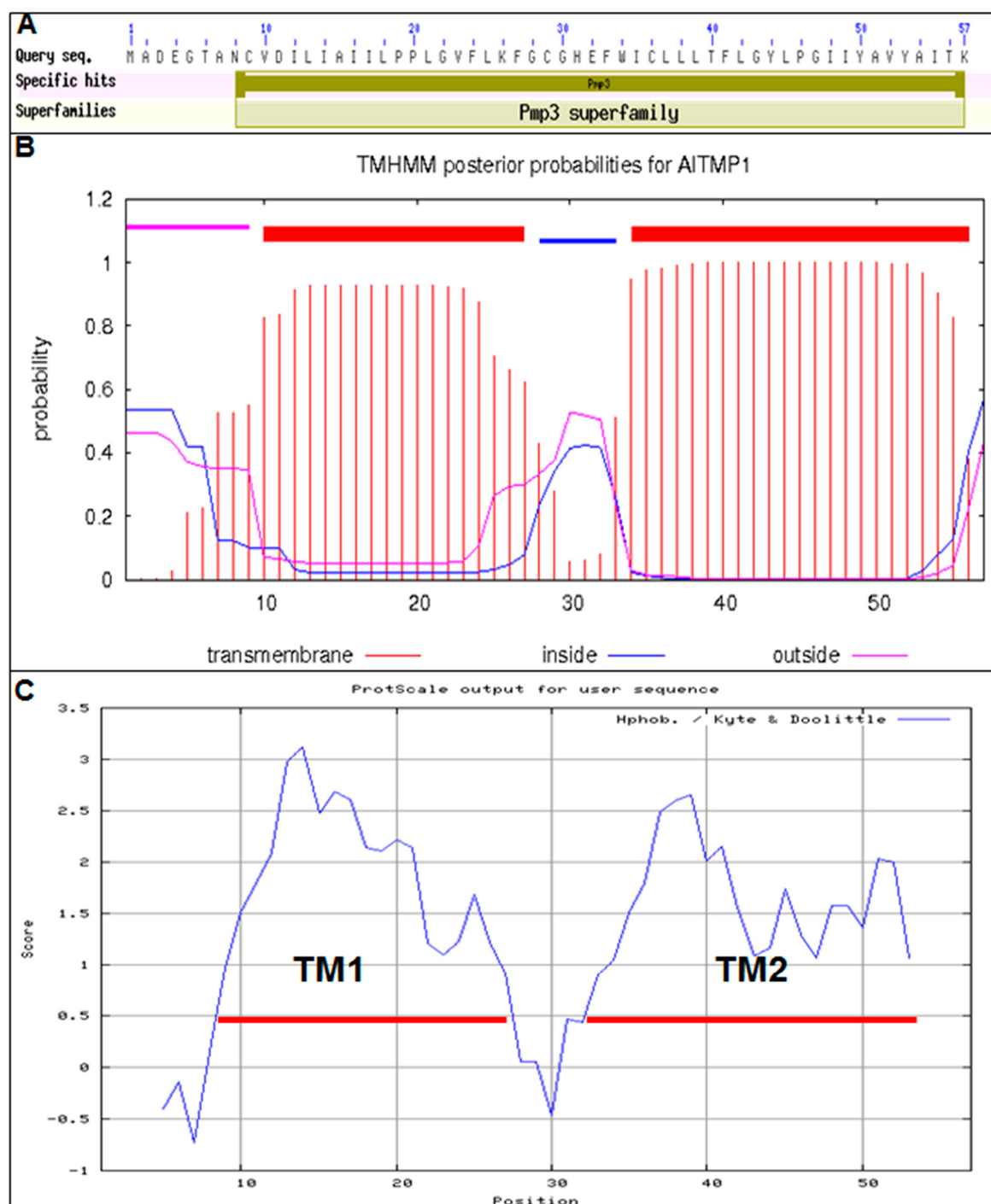


# Supplementary Materials: Ectopic Expression of *Aeluropus littoralis* Plasma Membrane Protein Gene *ALTMP1* Confers Abiotic Stress Tolerance in Transgenic Tobacco by Improving Water Status and Cation Homeostasis

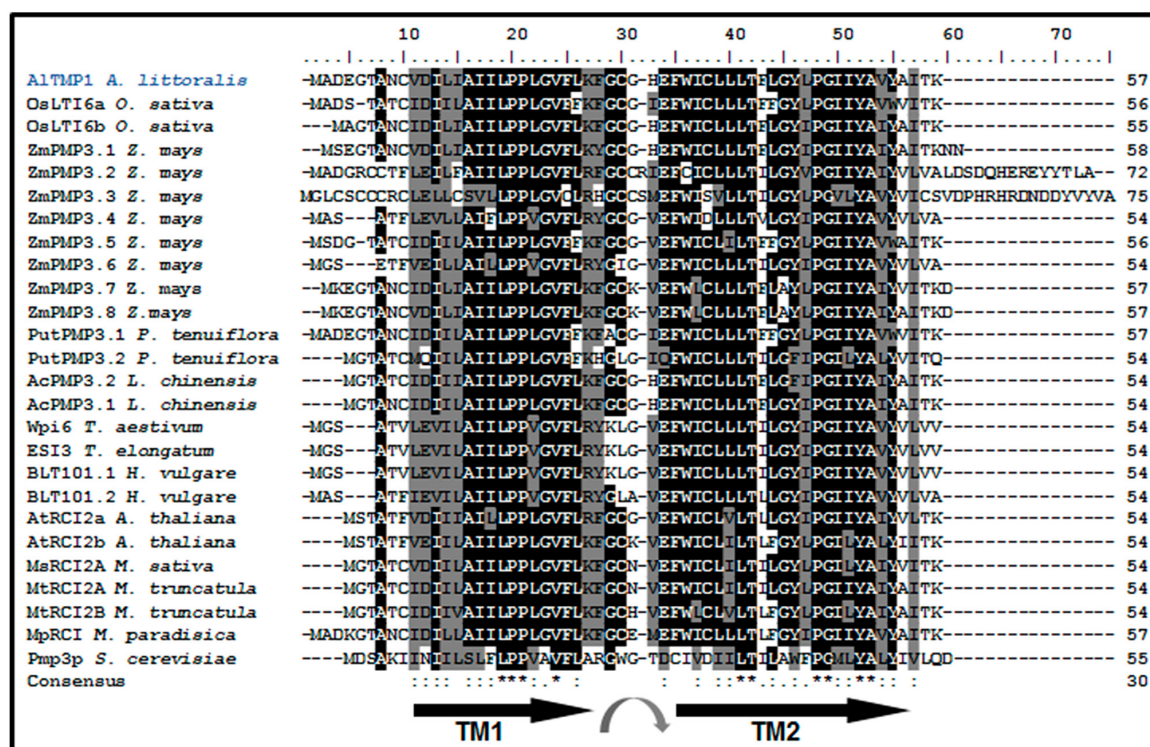
Walid Ben Romdhane, Rania Ben-Saad, Donaldo Meynard, Jean-Luc Verdeil, Jalel Azaza, Nabil Zouari, Lotfi Fki, Emmanuel Guiderdoni, Abdullah Al-Doss <sup>1</sup> and Afif Hassairi



**Figure S1.** Genomic DNA sequence of *ALTMP1*. Translational start codon (ATG) and stop codon (TAG) are underlined. The 5' and 3' non-coding sequences are double underlined. Exon sequences are in uppercase letters, whereas intron sequences are in lowercase letters and shaded in black. The donor splice sites are boxed. The sequence was analyzed with NetGene2 Server.



**Figure S2.** Prediction of conserved transmembrane domains and helices in AITMP1. (A) The putative conserved domain of the AITMP1 protein, Images were generated and taken from the NCBI BLASTp. (B) The transmembrane domains were predicted using the TMHMM Server v. 2.0. (C) Hydropathy Kyte and Doolittle profile for AITMP1 protein.



**Figure S3.** Amino acid sequence alignment analysis of AITMP1 and other PMP3 proteins. The GenBank accession numbers of different PMP3 proteins used in generating the alignment are as follows: ZmPMP3.1 (NP\_001107634), ZmPmp3.2 (ACG31120), ZmPmp3.3 (ACG34525), ZmPmp3.4 (ACG26760), ZmPmp3.5 (ACG47392), ZmPmp3.6 (ACG48459), ZmPmp3.7 (ACG27760), ZmPmp3.8 (NP-001151840); OsLTi6a (AAT37941), OsLTi6b (AAT37942); PutPMP3.1 (BAG54793), PutPMP3.2 (BAG54794); AtRCI2a (NP-187239), AtRCI2b (NP-187240); BLT101.1 (CAA80984.1), BLT101.2 (CAC37082); WPI6 (BAE07207); MpRCI (ACA66247); Pmp3p (EEU06338); ESI3 (P68178); MtRCI2A (AES82350), MtRCI2B (AES82353); MsRCI2A (AFI47457); AcPMP3.1 (BAD34658), AcPMP3.2 (BAD34659). The identical amino acids are shaded in black, while the amino acids with similarity larger than 75% are shaded in dark gray. Black and gray arrows represent the predicted transmembrane domains and the putative loop structure, respectively. Table S1. Sequences of primers used in PCR and qRT-PCR analysis.

**Table S1.** Sequences of primers used in PCR and qRT-PCR analysis.

| Primer Name | Sequence 5'–3'                     |
|-------------|------------------------------------|
| AIT1-F5'    | AGGGCAGAGGAGCTTTTGTG               |
| AIT1-R3'    | AGCAGGTAGGTTCCGCACACG              |
| qAIT1-F     | AGTAAAGCTGCTCAAGGATTTCG            |
| qAIT1-R     | ATGTATGTGAACACGGCTGCTA             |
| AITMP1-B    | AGTCCTGGATCCAGGGCAGAGGAGCTTTTGTG   |
| AITMP1-X    | AGTCCTTCTAGACAGAGGGAACATACATATGTAT |
| 18S-F       | GCAAGTCTGGTGCCAGCAGCC              |
| 18S-R       | CTTCCGTCAATTCTTTTAAG               |
| ACTF        | GTGCCCATTACGAACGATA                |
| ACTR        | GAAGACTCCATGCCGATCAT               |
| M13F        | GTAAAACGACGGCCAGT                  |
| M13R        | AAACAGCTATGACCATGTTCA              |
| qHKT1-F     | CATTGTTTCGGTGCTGTCGAC              |
| qHKT1-R     | AATGCCAAGTTCTGCACCAC               |
| qKT1-F      | GACGGGAGTTCCAGCTGTTT               |
| qKT1-R      | TCCCGGTTTCGGTTTCAACG               |
| qSOS1-F     | TATCAGGTGGAGGCTAGAGC               |
| qSOS1-R     | TCATGCTCCCGTACATGCTC               |
| qNHX1-F     | TTGATGAGAGGCGCAGTGTC               |
| qNHX1-R     | TTGACTGGCTAGAAAGTGGCG              |
| qSOS2-F     | GAGGGCAACAGAAGGAATAC               |
| qSOS2-R     | GAACAGAGGGATCCAAACCA               |
| qDREB1A-F   | ACTGGACGTCCTGAGTGACA               |
| qDREB1A-R   | GGCATCGGAAGCCAGAAAAG               |
| qCAT1-F     | TGCTCCAAAGTGTGCTCATC               |
| qCAT1-R     | GAAGCAAGCTTTTGACCCAG               |
| qAPX1-F     | AACGTTTGGGCTTTTCTCCT               |
| qAPX1-R     | TCAACAGCAACAACCTCCAGC              |