10.1071/FP12242_AC

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Supplementary Material: *Functional Plant Biology*, 2013, 40(4), 329–341.

Supplementary Material

ACCACTTCACCACCATCGTCATCGCCGGCATGGGCTTCTTCACCGATGCCTACGACCTGTTCTCG
GCCTCCCTCATCGCCGACCTCCTGGGCCACATCTACTACCACTCGGCGGACGGCAAGCTCCCCGG
TCACGTCGCCGGCGCCGTCAGCGGCGTGGCGCTCTGCGGCACAGTCCTGGGGCAGCTCTTCTTCG
GCTGGCTCGGCGACAGGATGGGGCGGAAGCGGATCTACGGCGTCACGCTCAAGCTCATGGTGGTG
TGCTCGCTCGCGTCCGGCCTCTCCTTCCACAACAAGCCCAAGTGCGTCGTGGCCACGTTGTGCTT
CTTCCGCTTCTGGCTCGGCTTCGGCATCGGCGGCGACTACCCGCTCTCGGCGACTATCATGTCTG
AGTATGCCAACAAGAGGACTCGCGGCGCCTTCATCGCAGCGGTCTTTGCTATGCAGGGTCTTGGG
AACCTGGCTGCTGGGGCTGTTGTTCTGGTGCTCTCTGCGAGCTTCAAGAACACGGCCGCGT

Fig. S1. Expressed sequence tag (EST) sequence identified in a root subtractive suppression cDNA library upregulated by low-Pi stress.

GACCAATTCTGTTTGACAGAAGAGGAAGTCGGAGCATGAGGACGTTGTGACACTCTATAGTGTCCCCAATTGGGATTTTGGTG +3878
GTGCCAGTGACCTTCCTCCCTTGCCAATTTTCCTCGTATGTGCGTTGGTGAGATCTTCGTCGTTCCGAGCCTTCGGTGGCCAT +3795
CAATACTTGCTGCGGCTTGACTGTATGCTCGTGCGGGTATGGTCTTCACTGGCGTGGCATCTCACGTCAAGACTATGCAATAC +3712
ACGTAGCTGTTGGGATCATGGAAAATGGTGATGACAACATGATGACTTTGATTTGGTGGTGCTTCTCGAGTATTCGGCCTCGA +3629
GCTCGAGTGAAAACCCAAGGTTTGAACCTAATTGGTTATACCTAGCAATGGCGGGATTTTACGTGGTTACATTGTTGAAAGCA +3546
CTACTCGGATTTGCTCGACCTTATCTTCAGGGTGAAAACCCATGATTTCATCTTTCGTGCTCAGATCCAGAGACATCAGCGCT +3463
TGACTGGCTTCCTGATCTCTCCATAACATGGTGTCCCCGGTTTGGCCGTCGTCGTCCCATGTTGCTACTTTTCCGATCTTTTC +3380
CGATCTGGCAGCTATATGGTGATTCAGGCTCCAATCTGGATGATCTCCATGGCCTGGAGTGTAATCAGGGGAAATACACGGGG +3297
CTGGTGCATGGAGGCATATGCATACACATGCGTGGACATGCATGCACATGATCGTTGGCCTCCCAGGCTGCCGGCTAGCTACA +3214
ACCCATGGTGCTGGCTGTTGGCGTCCACCTAGGTCTTGGTGGCCAATGGCATGGCCGGGTGGCACGGCTAGGCGGTGCTTTTG +3131
ACCACGTCATGGGAAATTGGATCTGGGACGGCGGCGGCCTGGCCATGGATTATGGTCTCCATCAAAAGATTGTGTGAGAGTTT +3048
CATCTCTGCAAATGTGATGATTGACTTCGGCGGCGAAATGCAAACTGTGGATGATGTCTTGATGCGGAGGGATTGTTGTGCGG +2965
TGGCGGCAGACATATTGCCTGTAGCTACTGGGACCGTGAAAAAAATGGCGGCGACAACACATGAATGACCTCGATGGTGGTGC +2882
TACTTGAGCACCTAGTCTAGAGCTCCGGGGTGAAAGCCTTGATCTCGCCCGTGTTGAGTATACCTAACAATGGCGATGTTTTT +2799
ACATCGTTACCTTGTTAAAGGCATTGTTCGGAATGCTCGGACTGATTCTTCAGGGTGAAAACCTAGAATATAGCCTTGGATGG +2716
CTGGATCCGGTGACAGTGATACTTGAGTGTCGCTCCCTTCCTTAAGGCGTTGCTGTTGAAGAACGTCATCATCCGCGTGGTGT +2633
CATGAGATTGTTGGTGTAAATATGATCATTGTTATAGTTTGCCGATCATGATCTGATCGCTTTGGGGCTTTTTTTGATTTTTT +2550
CTCGCCTACGCATAGCTTTGGTCTAGTATGACTTTGCTATTTGTCGGCGTGTTTTTGTGTGTGTGCGTTGGTGTTGACTGTGT +2467
GCATCTTAACTATGCAGAGGTCGGGTGTGTACTCATTTGTTTGTATCCTCTTGATGCTTCACTTTGAGTCAATAAAATCCATC +2384
CTTTAGCGAAAAAAGGTAAGAGTTTCGGTCTTGTATGACTTAGCTCTTTGCTGACGCAATACTTTGTGTGTGTACGCGCGCGT +2301
CCATTAGTGTTGGTTGTGTGCATCTTATTTATGCAAAGACCGGGTCTCTCATTGTGTTTGTATCCTTGAGAATGAAAACAACC +2218
TTTATCAAGAATGACTAATCAGATACCCTGATCTTGTTGTTTCCGTCCTTTTGTCTCGATACGGAACAACTGTAGTCGTCGTC +2135
TTCAACAAACGTAGGGCTAAGCGAGTTCGTCAGCAAAGTTGTCAATTTTGTGTGTTCTTCGGAGAATGTAAGGTGGATGTGAT +2052
GCGGTTGGGGGCGCTGTCGTAATCATATTCCACGGGACATTCGTCCAGCTGTATACAGGGCAAAATCACTACGTTCTATATAT +1969
GGCAAACATGAAGCACTTGGTTTTCCAAGGGAATTTTTTTCGCAGAGACTACCACGCACAATGTTCACGACCTGGCCTGCGAG +1886
GAGGCACGCGTGCAGCTCCCTCTTCTGCCACCTCCATGGCGCCGGGAGCGCCATGCTGTACCGCGTGCTGGACGCGGTGACAT +1803
CGGTGAAATGCGAGACCCGTCGGGCGCGCAAGCAGATCAAGGTGCTGGAGGCCCTGGACGTCGCCGGGACGCAGCTGTACCAC +1720
TTCACCACCATCGTCATCGCCGGCATGGGCTTCTTCACCGATGCCTACGACCTGTTCTCGGCCTCCCTCATCGCCGACCTCCT +1637
GGGCCACATCTACTACCACTCGGCGGACGGCAAGCTCCCCGGTCACGTCGCCGGCGCCGTCAGCGGCGTGGCGCTCTGCGGCA +1554
CAGTCCTGGGGCAGCTCTTCTTCGGCTGGCTCGGCGACAGGATGGGGCGGAAGCGGATCTACGGCGTCACGCTCAAGCTCATG +1471
GTGGTGTGCTCGCTCGCGTCCGGCCTCTCCTTCCACAACAAGCCCAAGTGCGTCGTGGCCACGTTGTGCTTCTTCCGCTTCTG +1388
GCTCGGCTTCGGCATCGGCGGCGACTACCCGCTCTCGGCGACTATCATGTCTGAGTATGCCAACAAGAGGACTCGCGGCGCCT +1305
TCATCGCAGCGGTCTTTGCTATGCAGGTGTGTAAGTAAAACCATCACAATATTTTTTGGAGCCTGTGCTGCATCTCATTCTTA +1222
ATCTACAACCTGCATTTCTTTTTTCTCGTCTAACTCAGTCGTCAAAGATAATATTCTAATCCTTATCTTATTATGCTTGCCCT +1139
GCATAAAG**GGTCTTGGGAACCTGGCTGCTGGGGCTGTTGTTCTGGTGCTCTCTGCGAGCTTCAAGAACACGGCCGCGTACGAT** +1056
ACTGACCATCTCGGGCAAGCAGACTACGTATGGCGCATAGTACTCATGCTCGGCGCCGTTCCTGCCCTGCTCACCTACTACTG +973
GCGCATGAAGATGCCCGAGACGGCGCGCTACACCGCGCTCATCGCCAAGAACCTCAAGCTAGCGGCGTCTGACATGGCCGCAG +890
TCCTCGACATCGACTTCGTGTCCGACATGGACGCAGAGGCCGTTGTTAAGCAGGACGAGTTTGGCCTCTTCTCCATGGAGTTC +807
CTTCACAAGCATGGCCGCCAGCTCCTCGGAACCACTGTGTGCTGGTTCGTCCTCGACGTCGTCTTCTACTCCCTCAACCTCTT +724
CATGAAGGACATCTTCAACGGCATCGGCTGGTTTGGAGACGCGGCCGAGATGAGCCCTCTCGAGCAGACCTACAAGATAGCCC +641
GCACGCAGGCCATCATTGTGGTCGGCGGTTCCCTACCAGGGTACTTCCTCACTGTCCTCTTCGTTGACCGCATCGGCCGCATC +558
AAGATCCAGCTCATGGGGTTCACCATGATGACCATCTTCATGATCGGGCTCGCCGCGCCCTACAAGTTCTGGTCCAAACCCAG +475
CATGCACGCAGGCTTCGCCATCATGTATGCATTGATCCTCTTCTTCGCAAACTTCGGCCCCAACTCCACCACCTTCATCCTGC +392
CCACCGAGATATTCCCGACGCGGCTGCGGTCGACGTGCAACGGCATATCGGCTGCCGGGGGTAAGTGTGGTGCCATCATCGGT +309
GTTCTCTGGTTCCAGTATTCTCATACGAGCATCCGGAGCTCTCTCCTTCTTCTGGCAGGGTGTAACCTCGTTGGAGTCATGTT +226
CACTCTTGCCTTGCCGGAATCCAAAGGGATGTCACTCGAGGATATCACCGGGGAAATGGAGGAAGAAAGCGAACCATCTCAAG +143
AATCTACGGTTGCTGAAGTTGAGTTCATCCACAGCGTGGAAATTTTGTAACCAGTACCACCCGGTTGCTGATTTTAGTGTCTT +60
CTCAAAATTACTCAAACATTGGAAACTTGTATCTTTGAGATGTTTGGATTATATATAGT +1

Fig. S2. *TaPht1;4* sequence at the genomic level. The translation start codon ATG and the terminator codon TAA are boxed. Exon1 and exon2 are shown in bold font. The primers for the PCR amplification of the promoter region are underlined. The PIBS *cis*-regulatory element (ATATGCA) involved in gene regulation under low-Pi stress, highlighted by a gray background.

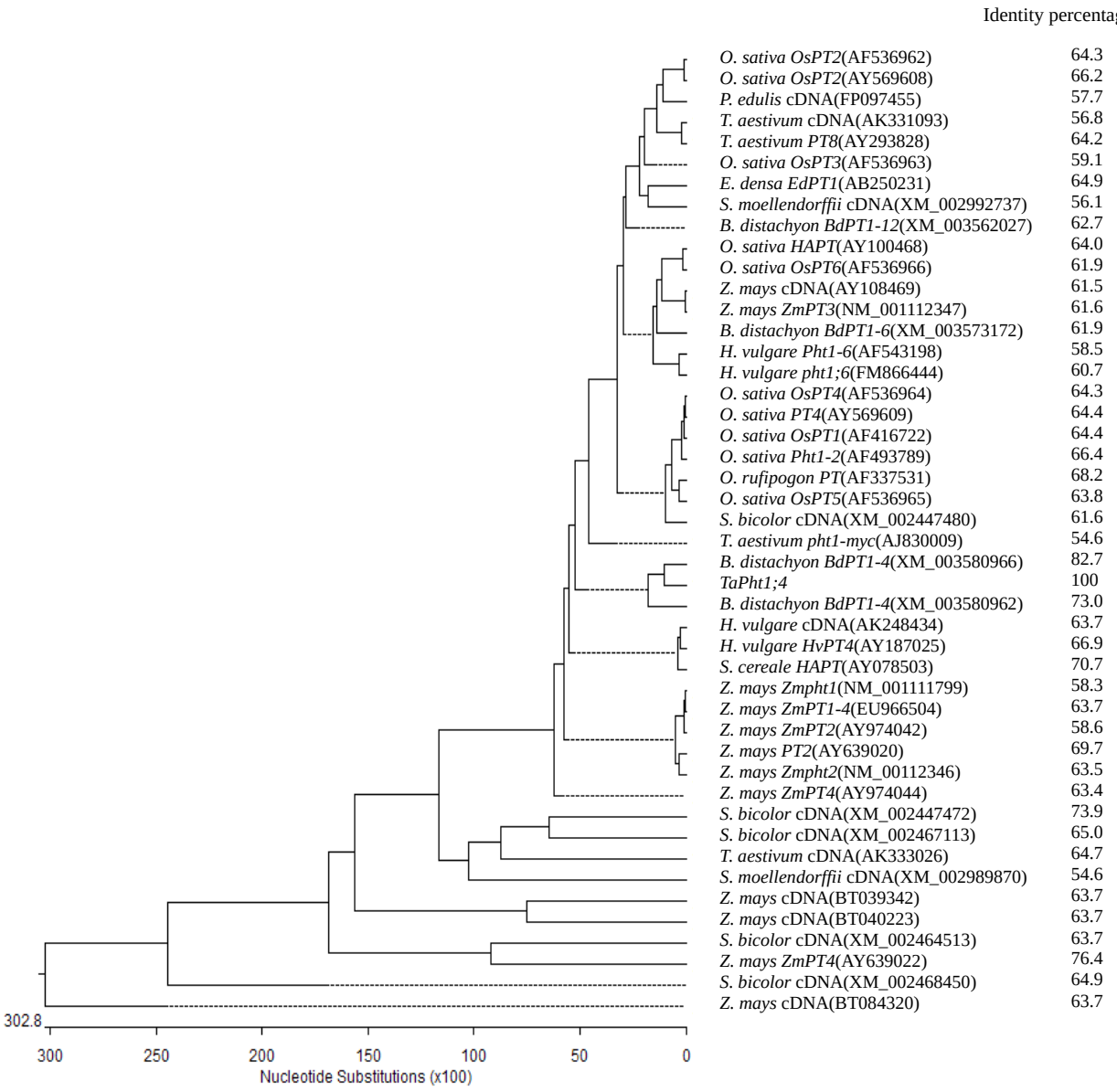

Fig. S3. Phylogenetic analysis of *TaPht1;4* and its homologous counterparts in diverse plant species.