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Molecular cloning, expression and sequence analysis of a phenylalanine ammonia-lyase gene from *Poncirus trifoliata* under iron deficiency

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1 61 AAGAACAACAATTACAGTTCTGGGGATGCGTTGAACTGGGGAGTGATGGCGGAGACGTTG 21 NYSSGDALN W G V M AAGGGGAGCCATTTGGAGGAAGTGAAGCGAATGGTGGCGGAGTACAGGAAGCCGGTGGTC 121 41 \mathbf{E} E R Mr E. K AATCTCGGTGGTGAGACATTGACTGTAGCACAAGTGGCTGCCATTGCGACAGCTGGCGAC
N L G G E T L T V A Q V A A I A T A G D
GTCAACGCCCAAGTCAAAGTGGAGCTCTCAGAATCCGCCAGGGAAGGTGTCAAGGCCAGC 181 61 241 V K V E L 81 SESAREG AGTGATTGGGTGATGGAGAGCATGAATAAGGGCACCGACAGTTACGGCGTTACCACTGGC 301 S D W V M E S M N K G T D S Y G V T T G TTTGGTGCCACTTCTCATCGGAGAACCAAGAACGGCGGTGCTCTTCAGAAAGAGCTCATT 101 361 F G A T S H R R T K N G G A L Q K E L I AGATTTTTGAACGCTGGAATCTTTGGAAACGGAACAGAGTCATCTCACATGCTGCCTCAC 121 421 R F L N A G I F G N G T E S S H M L P H TCAGCAACAAGGGCAGCCATGCTTGTGAGGGTCAACACTCTTCTTCAGGGCTACTCTGGC 141 481 161 M L R N ATCCGATTTGAAATCCTGGAAGCGATTACAAAGCTGCTCAATCACAGCATCACTCCATGC 541 I R F E I L E A I T K L L N H S I T P C CTGCCTCTTCGCGGCACAATCACTGCTTCAGGGGATCTGGTTCCTCTGTCCTACATTGCC 181 601 201 Α G GGACTGCTCACCGGCCGGCCCAATTCTAAGGCCACCGGGCCTAATGGAGAGATCATTGAT 661 221 G R P N S K A Т G N GCTCAGGAAGCCTCTAAACAAGCGGGTTTCGGGTTCTTTGAGTTGCAGCCTAAGGAGGGT 721 241 Q G G Ε A CTCGCTCTTGTCAATGGCACTGCTGTTGGTTCTGGCCTGGCTTCTATGGTTCTGTTCGAC 781 261 N A G G A L GCTAACAACCTTGCTCTGTTATCAGAAATTTTGTCAGCTATTTTTGCTGAAGTCATGCAA 841 281 E S Ħ N S Ε Α L. A T Ι T Ι GGAAAACCTGAATTCACTGACCACTTGACACACAAACTGAAGCATCATCCTGGCCAAATT 901 E 301 F. Τ D H Т H K L K H H L GAGGCTGCTGCTATAATGGAACATATTCTCGACGGCAGCTCTTATGTCAAGGCGGCTAAG 961 321 M F. Н D G S A Т Т Ι. К AAGTTGCATGAGATTGATCCTCTGCAGAAGCCGAAACAGGATCGTTATGCTCTGAGAACT 1021 D P H E Q K P 341 L. K Q D R TCTCCACAATGGCTCGGCCCTCAGATCGAAGTGATTCGGTTTGCAACCAAGTCTATTGAA 1081 Ρ V 361 W Ι. G ລ Т F. R F A Т К CĞĞĞAĞAŤCAÄCTČĞĞTĞAATĞĂCAĀTCČCCTĞATCĞACĞTTTCAAĞĞAACAAĞĞCCTTA R E I N S V N D N P L I D V S R N K A L 1141 381 CATGGTGGCAATTTCCAGGGGACTCCAATTGGTGTCTCAATGGACAATACCCGTTTGGCT 1201 Q G T P I G V S M D N T R L A 401 GGNF 1261 ATTGCGGCAATAGGAAAGCTCATGTTTGCCCAATTTTCCGAACTTGTCAACGATTTTTAC 421 G K I M E A Q F F. AACAATGGATTGCCGTCAAATCTTTCCGGTGGCAGGAATCCTAGCCTGGATTATGGTTTC 1321 LPSNLSGGRNP 441 S I D AAGGGCGCTGAAATTGCTATGGCTTCCTATTGTTCCGAGCTCCAATTTCTTGCCAATCCT 1381 461 M S E GTTACTAACCACGTCCAAAGTGCTGAACAGCACAACCAAGATGTAAACTCCTTGGGACTG 1441 481 NHVQSAEQHNQDVN S ATCTCTTCCAGGAAGACTGCTGAAGCTGTCGACATCCTGAAGCTCATGTCTTCCACATTC 1501 501 R K Т A E A V D Т К M TTGGTAGCGCTTTGCCAGGCTATTGATTTGAGGCATTTGGAGGAGAATTTGAAGCATACA 1561 521 V A L C Q A I D L R H L E E N GTCAAGAÂTACTGTGAĞCCÂAGTAGCGAĀGAÂAGTCTTGACTGTCGGTGCTAĞTGĞAGAG 1621 541 V SQVA K CTTCATCCATCAAGATTCTGCGAGAAGGATCTGCTCAAAGCGGCTGATCGCGAACACGTC 1681 L H P S R F C E K D L L K A A D R E H V TTTGCATACATTGATGACCCCTGCAGCGCTACCTATCCATTGATGCAAAAGCTAAGGCAA 561 1741 FAYIDDPCSATYPLMQKLRQGTACTTGTTGATCATTGAACAACGGAGAACGAGAAGAATGCCAACTCTTCAATC 581 1801 V L V D H A L N N G E N E K N A N S S I TTCCAGAAGATTGCAGCCTTTGAGGAGGAATTGAAAACCGTTTTGCCCAAAGAAGTTGAG 601 1861 Ε 1921 AATGCCAGGCAGACTGTTGAGAATGGAAGTCCAACAATTCCCAACAGGATCAAAGAATGC N A R Q T V E N G S P T I P N R I K E C AGGTCTTACCCTTTGTACAGGTTAGTGAGGGAGGAGCTCGGGACTAATTTTCTGACTGGG 641 1981 661 R GAAAAAGTTACATCGCCCGGCGAGGAATTTGACAAAGTGTTTACAGCAATGTGCCAGGGC 2041 681 G F. Ε D Κ AAGATCATTGATCCAATGCTGGAATGTCTCAGGGAATGGAACGGTGCCCCTCTTCCAATA 2101 701 D P M L E C L R E W N G A P 2161 TGCTAG

Fig. S1. The full-length cDNA sequence and translated amino acid sequence of Pt-PAL1 in Poncirus

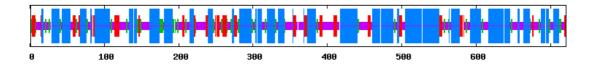


Fig. S2. The secondary structure of the deduced *Pt-PAL1* protein of *Poncirus trifoliata*. Alpha helix, extended strand, beta turn, random coil are denoted by the blue, red, green and yellow bars respectively.

Table S1. Amino acid of composition of Pt-PAL1 of Poncirus trifoliata

Name	Number	Percentage	Name	Number	Percentage
Ala(A)	66	9.2	Arg(R)	30	4.2
Asn(N)	46	6.4	Asp(D)	27	3.7
Cys(C)	11	1.5	Gln(Q)	27	3.7
Glu(E)	54	7.5	Gly(G)	58	8.0
His(H)	20	2.8	Ile(I)	38	5.3
Leu(L)	76	10.5	Lys(K)	42	5.8
Mer(M)	17	2.4	Phe(F)	25	3.5
Thr(T)	39	5.4	Ser(S)	51	7.1
Tyr(Y)	14	1.9	Trp(W)	4	0.6
Pro(P)	30	4.2	Val(V)	46	6.4