Nucleotide sequence of the barley chloroplast *psbE*, *psbF* genes and flanking regions

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The sequence presented is part of 13.5 kbp Pst I - Pst I barley chloroplast DNA fragment (P4). It contains genes of *psbE* and *psbF* coding correspondingly for 9.4kDa and 4.4kDa polypeptides of cytohrome b-559 in photosystem II complex. Sequences showed close similarity to *psbE,F* genes from other plant species - e.g. tabac, and especially wheat. The deduced amino acid sequence is presented.

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                      psbE ---->
                      M_S_G_S_T_G_E_R_S_F_A_D_I_I_T_C_I_R_Y_W_V_I_R_S_I_T_
AATCAATTCCTTTTTGAATGTACAAAAATTTTGGGAGTTCAGCATGTCTGGAAGCACGGGAGAACGTTCTTTTGCTGATATTATTACCTGTATTCGATACTGGGTTATTCGTAGCATTAC  120


_I_P_S_L_F_I_A_G_W_L_F_V_S_T_G_L_A_Y_D_V_F_G_S_P_R_P_N_E_Y_F_T_E_S_R_Q_G_I_P_L_I_
TATACCTTCCCTATTCATTGCGGGTTGGTTATTTGTCAGTACGGGTTTAGCTTATGACGTGTTTGGAAGTCCTAGGCCAAACGAATATTTCACGGAAAGCCGACAAGGAATTCCGTTAAT  240
                                                              psbF ---->
_T_D_R_F_D_S_L_E_Q_L_D_E_F_S_R_S_F_ter       M_T_I_D_R_T_Y_P_I_F_T_V_R_W_L_A_I_H_G
AACCGACCGTTTTGATTCTTTAGAACAACTCGATGAATTTAGTAGATCCTTTTAGGAGGCCCTCAATGACCATAGATCGAACCTATCCTATTTTTACAGTGCGGATGGCTGGCTATTCACG  360
                                                              ORF 38 ---->
_L_A_V_P_T_V_F_F_L_G_S_I_S_A_M_Q_F_I_Q_R_ter         M_T_Q_S_N_P_N_E_Q_N_V_
GACTAGCTGTACCTACTGTTTTTTTCTTGGGATCAATATCAGCAATGCAGTTCATCCAACGATAAACCAAATTCCAACTATAGAACTATGACACAATCAAACCCGAATGAACAAAATGTT  480


E_L_N_R_T_S_L_Y_W_G_L_L_L_I_F_V_L_A_V_L_F_S_N_Y_F_F_N_ter
GAATTGAATCGTACCAGTTTATACTGGGGTTTATTACTCATTTTTGTACTTGCTGTTTTATTTTCCAATTACTTCTTCAATTGAGAGAAAGAAAGAGACTAATAAGAATTCTCTTATCCC  600
                                                              ORF 40 ---->
                                                              M_A_D_T_T_G_R_I_P_L_W
ATTTGGAAAGATACCATCCTTATAAACTACCCATGACTGTTTTTGTCTCTAGCATGACCAATTGATAAAATGTGGAGGAAAGTAGGGGAAATGGCCGATACTACTGGAAGAATTCCTCTTT  720


_L_I_G_T_V_A_G_I_P_V_I_G_L_V_G_V_F_F_Y_G_S_Y_S_G_L_G_S_S_L_ter
GGCTGATAGGTACTGTAGCTGGTATTCCTGTGATTGGTTTAGTAGGTGTTTTCTTTTATGGTTCATATTCTGGATTGGGTTCATCTCTATAG  812
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