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Anikó Páy

Marvin A. Smith

Ferenc Nagy

László Márton

University of South Carolina - Columbia, martonl@mailbox.sc.edu

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Sequence of the *psbA* gene from wild type and triazin-resistant *Nicotiana plumbaginifolia*Anikó Páy*, Marvin A. Smith[†], Ferenc Nagy and László Márton[‡]Biological Research Center of the Hungarian Academy of Sciences, Institute of Plant Physiology, H-6701 Szeged, PO Box 521, Hungary
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The sequence of the chloroplast-encoded *psbA* gene from the wild type *Nicotiana plumbaginifolia* was compared to that of the TBR2 terbuthrin-resistant mutant isolated from photomixotrophic cell cultures (1). Two nucleotides were found to have been changed in the mutant *psbA* gene. The change at position 791 results in a Ser-Asn amino acid substitution. The change at position 933 does not alter the amino acid sequence. The amino acid substitution described here is at the same position as in all *psbA* genes from triazin resistant mutants so far sequenced in higher plants (2, 3); however this is the first case when Serine is replaced by Asparagine.

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-227                                     -161
CCCCCCCACCCCACTAGCATATCGAAATCTAATCTCTGTAGAGAGTCCGTATTTTTCACATCA
CTTCATTAAAATTTGATAGATTCACATACAGCTGGCTTCCACACGATATATAGTCATGTATTAAGCTCTGAAATACAAAGCCCTTCATTTTCTATTTTATTTTGTAGAAAGTACTGCTGCTTGGAGTCCCTGATGATTAATAAACGAGATTTCAC
-1
+1
ATG ACT GCA ATT TTA GAG AGA CCG GAA AGC GAA AGC CTA TGG GGT GGC TTC TGT AAC TGG ATA ACT AGC ACT GAA AGC GGT CTT TAC ATT GCA TGG TTT GGT GTT TTG ATG ATC GCT ACC 120
M T A I L E R R E S E S L V G R F C K W I I S T E W R L Y I G W F G V L M I P T
TTA TTG AGG GAA ACT TGT GTA TTT ATT ATT GGC TTC ATT GGT GGT GCA GTA CAC ATT GAT GGT ATT GGT GAA GGT GTT TGA GGG TGT CTA CTT TAC GAA AGC AAT ATT ATT TCC GCT 240
L T L A T S V F I L A F I A A P P V D I O G I A I C S T G E P V S G S L L Y C G N H I I S G
GGC ATT ATT CCT ACT TCT GCA GGT ATG GGT TTA CAT TTT TAC CCA ATC TGG GAA GGG GCA TCC GTT GAT GAA TGG TTA TAC AAC GGT GGT GGT GAT GAA CTA ATT GTT CTA CAC TTC TTA 360
A I E P T S A A I G L H F Y P I M E A A S V D E M L Y N G G P Y E L I V L H F L
CTT GGT GAA ACT TGT TAT ATG GGT GAG TGG GAG CTT AGT TTC GGT CTA GCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA 480
L G V A C Y M G R E V E L S F R L G M R P W I A V A Y A P Y A A A T A V F L !
TAC CCA ATC GGT GAA GGA AGT TTT TCT GAT GGT ATG CCA GCA ATC TCT GGT ACT TTC AAT TTC ATG ATT GTA TTT CAG GGT GAG CAC AAC ATC CTT ATG CAC CCA TTT CAC ATG TTA 600
Y P I G C G B F S D G M P L G I S G T F N F M I V F Q A E H N I L M H P F H M L
GGC GTA GCT GGT TTC GGC GGC TCC CTA TTT AGT GGT ATG CAT GGT TTC TGG GTA ACT TGT ACT TGG ATG TGG ATG AGC GAA AGC ACA GAA AAT GAA TGT CTA GAT TAC AGA TTC GGT 720
G V A C G V F G S L F S A M H D S L V T S B L T R E T T E H E S A N E S A N E G Y R G
CAA GAG GAA GAA ACT TAT AAC ATC GTA GGC GGT CAT GGT TAT TTT GGC CCA TTT ATC TTC CAA TAT GCT ACT TTC AAC AAC TGT TGG TTA CAC TTC TCC CTA GGT GGT TGG GGT GTA 840
G E E E T Y M I V A A H G Y F G R L I F D Y A A F W N S R S L H F F L A A W P Y
GTA GGT ATC TGG TTT ACC GGT TTA GGT ATC AGC I S T H A F N A N G GGT TTC AAT TTC AAC CAA TGT GTA GAT GAC ACT CAA GGC GGT GTA ATT AAT TGG GGT GAT GAT ATC 960
V G I M Y G R E V E L S F R L G M R P W I A V A Y A P Y A A A T A V F L !
ATT AAC GGT GGT GAC CTT GGT ATG GAA GTT ATG CAT GAA GGT AAT GGT GGC AGC TTC GGT CTA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA CCA 1086
I N R A W L G H E V H H E R R A N H F P L O L A A I E A P S T H D
TTTTCACACACCCACGATATGATTTTCTGTGATGACAGGCTGCTATT
1141

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Legend: The nucleotide and the deduced amino acid sequence of the *psbA* gene of *N. plumbaginifolia* is shown. The Ser-Asn substitution in the mutant *psbA* gene at codon 264 is boxed. The "silent" nucleotide-change at 933 position is also indicated. The *N. plumbaginifolia psbA* gene spans an *EcoRI*-*PstI* restriction endonuclease fragment of 0.9kb and a *PstI* fragment of 2.3kb.

*To whom correspondence should be addressed

Present addresses: [†] Graduate Section of Biochemistry, Brigham Young University, Provo, UT 84602 and [‡] Institute of Biological Chemistry, Washington State University, Pullman, WA 99164-6340, USA

References:

1. Cséplő, Á., Medgyesy, P., Hideg, É., Demeter, S., Márton, L. and Maliga, P. (1985) *Mol. Gen. Genet.* 200, 508-510
2. Rochaix, J.-D. and Erickson, J. (1988) *TIBS* 13, 56-59
3. Barros, M.D.C. and Dyer, T.A. (1988) *Theor. Appl. Genet.* 75, 610-616