PERGAMON

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Erratum

Folylpolyglutamate synthesis in *Neurospora crassa*: primary structure of the folylpolyglutamate synthetase gene and elucidation of the *met-6* mutation [Phytochemistry 49 (1998) 2221–2232][☆]

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The Publisher regrets that Fig. 2 of the above article was shown incorrectly. This figure and its caption are presented overleaf. We apologise for any inconvenience or embarrassment caused.

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PII: S0031-9422(99)00469-0

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GAATTCAAGT   GGAACCTGGC   GCCTTAGACC   GCTCGGCCAC   CTTGCCATCG   ATATTATATT   TTTATCGTGA   AAGTGGCTTT    80
TGAGGACATT   AGGGAAGATG   CTCAGCTTAA   CTAGTAGCCA   CAGCATAGAC   TACCGGTAGT   ACATAGCTGA   GGTGGGGCCA   160
GGTCGTTTTT   GGCGGGGTTC   AAACACAGTT   GAAAAAGCCA   AGATCGGGTA   TGTTACTGAC   GTCGGTGTTC   CAGAGCCGGC   240
GTGTCTAGAA   TAGAGTTCTA   ACCGAATGGG   TAAGCCAAGC   ATCGCGAACG   GAACATCCCG   TCTTCTTTTC   TTTTACCATC   320
GAAGTGACTG   TGAGTGACAA   GGTGGGTTAG   GATTGAATCA   CAGCTGATGG   GATTGGGAGT   TTTGGTATTG   TGAATGCCAC   400
TAACACCAGG   GCAGCTATCA   GACGCCTCGA   GATACTACCC   GATTATCACC   TCTTTGAAAC   CAACGGCCTG                470 (-1)
↓
ATG CAC CAT GTT TTG AGG CCC ATA GCT TTT CGA CTT GCC CTC GTC TCC CCT CTG AGG TCG CTC ACC ATC ACC CAT   545
Met His His Val Leu Arg Pro Ile Ala Phe Arg Leu Ala Leu Val Ser Pro Leu Arg Ser Leu Thr Ile Thr His   (+75)
                                    ∇
CAT CAC CTC TTC TTC ACA AAA CGC ACC ATG GCA TCC AGC GCT AGA ACA TAC AAT gtgagtcaaccaacctttaccgctcc   626
His His Leu Phe Phe Thr Lys Arg Thr Met Ala Ser Ser Ala Arg Thr Tyr Asn                INTRON 1      (+129)

acagaaccccaaacactcactcaccatatcgtag  GAC GCA ATC GAT GCG CTC AAC TCC CTC CAG ACC CCC TTC GCC GTC ATC   708
                                    Asp Ala Ile Asp Ala Leu Asn Ser Leu Gln Thr Pro Phe Ala Val Ile   (+177)
    *
GAA GCC CGG CGC AAA GCG GGT ATC CGT CCC GAT GCG CAC TCG GTA AAG GAA ATG CGT GCC TAC CTC GCC CGC ATC   783
Glu Ala Arg Arg Lys Ala Gly Ile Arg Pro Asp Ala His Ser Val Lys Glu Met Arg Ala Tyr Leu Ala Arg Ile   (+252)

GGC TAC TCC TCC CAA GAT CTC GAT CGC CTC AAC ATC GTC CAC GTA GCC GGT ACC AAG GGC AAG GGC GGC ACC TGT   858
Gly Tyr Ser Ser Gln Asp Leu Asp Arg Leu Asn Ile Val His Val Ala Gly Thr Lys Gly Lys Gly Gly Thr Cys   (+327)
                                                                                                 ⇓
GCC TTT GTC GAC TCC ATC CTC ACG CGT CAT CAG CGG ACT CAC GGT ATC CCT AGG CGC ATC GGT CTC TTC ACC TCC   933
Ala Phe Val Asp Ser Ile Leu Thr Arg His Gln Arg Thr His Gly Ile Pro Arg Arg Ile Gly Leu Phe Thr Ser   (+402)

CCC CAT CTC ATT GCT GTC CGG GAA CGC ATC CGT ATC GAC TCC AAG CCC ATC TCC GAG GAA CTG TTT GCC CGC TAC   1008
Pro His Leu Ile Ala Val Arg Glu Arg Ile Arg Ile Asp Ser Lys Pro Ile Ser Glu Glu Leu Phe Ala Arg Tyr   (+477)

TTC TTC GAG GTC TGG GAT CGT CTC GAG ACA TCT CAG CTG GCT AAG GAT GAG GTG GAA CTG GGA AGC AAG CCC ATT   1083
Phe Phe Glu Val Trp Asp Arg Leu Glu Thr Ser Gln Leu Ala Lys Asp Glu Val Glu Leu Gly Ser Lys Pro Ile   (+552)

TAC GCT CGC TAT CTT ACC TTG ATG AGT TAC CAC GTC TAC CTG TCC GAG GGC GTC GAT GTA GCC ATT TAC GAA ACT   1158
Tyr Thr Arg Tyr Leu Thr Leu Met Ser Tyr His Ala Asn Leu Ser Glu Gly Val Asp Val Ala Ile Tyr Glu Thr   (+627)

GGC ATC GGG GGT GAA TAC GAT GCC ACC AAC GTA GTC  GAC CGT CCC GTG GTC AGC GGT ATC AGC ACC CTT GGT ATC   1233
Gly Ile Gly Gly Glu Tyr Asp Ala Thr Asn Val Val Asp Asn Pro Val Val Ser Gly Ile Ser Thr Leu Gly Ile   (+702)

GAC CAC GTC TTT GTC CTG GGT GAT ACG GTC GAC AAG ATT GCG TGG CAC AAG GCG GGT ATC ATG AAG ACG GGC AGC   1308
Asp His Val Phe Val Leu Gly Asp Thr Val Asp Lys Ile Ala Trp His Lys Ala Gly Ile Met Lys Thr Gly Ser   (+777)

CCT GCG TTC ACG ATT GAG CAG GTT CCC TCC GCA ACT CAG GTG CTC AAG GAT AGG GCG GTG GAA AAG GGC GTG GAT   1383
Pro Ala Phe Thr Ile Glu Gln Val Pro Ser Ala Thr Gln Val Leu Lys Asp Arg Ala Val Glu Lys Gly Val Asp   (+852)

CTC AAG ATC CCT GAT GTT GAT CCC AGG CTC AAC GGC GTC AAG ATC CGT CCC GAT GCA GTC TTC CAG AAG AAG AAC   1458
Leu Lys Ile Pro Asp Val Asp Pro Arg Leu Asn Gly Val Lys Ile Arg Pro Asp Ala Val Phe Gln Lys Lys Asn   (+927)

GCA ACG CTG GCT ATC GCG CTC GCT GAG ACT GCC CTC AAA AAG TTG GAC CCT TCT TTC AAG CCT GGC ACC GAC AGT   1533
Ala Thr Leu Ala Ile Ala Leu Ala Glu Thr Ala Leu Lys Lys Leu Asp Pro Ser Phe Lys Pro Gly Thr Asp Ser   (+1002)

CTA TCA CCC GAG TTT GTC CAA GGC CTC GAA CAG GTT GTC TGG CGT GGC CGA TGC GAG GTC AAG GAG GAG GAT CAG   1608
Leu Ser Pro Glu Phe Val Gln Gly Leu Glu Gln Val Val Trp Arg Gly Arg Cys Glu Val Lys Glu Glu Asp Gln   (+1077)

GCT GTC TGG CAT CTT GAT GGC GCA CAT ACC GTT GAC AGC CTG AAG GTG GCG GGG AGA TGG TTC GTC GAG GAG TGT   1683
Ala Val Trp His Leu Asp Gly Ala His Thr Val Asp Ser Leu Lys Val Ala Gly Arg Trp Phe Val Glu Glu Cys   (+1152)

GTC AAG AAG GCC AAG GGC GGA CCC AAG GTG CTC ATC TTC AAC CAG CAA GGC CGG TCT GAG GCC GTT GAC TTC CTT   1758
Val Lys Lys Ala Lys Gly Gly Pro Lys Val Leu Ile Phe Asn Gln Gln Gly Arg Ser Glu Ala Val Asp Phe Leu   (+1227)

GAT GGG CTT TGC AAC ACT GTC AAG AGT GCT GAT CCG GAG GGA ACT GGC TTT AGC CAT GTG ATT TTT TGC ACC AAT   1833
Asp Gly Leu Cys Asn Thr Val Lys Ser Ala Asp Pro Glu Gly Thr Gly Phe Ser His Val Ile Phe Cys Thr Asn   (+1302)

GTG ACA TAT GCG ACG ACT GGC TAC AAA AAA G gtatgttgtcctgggtctttccatgatttgctcaagctaaccttcaatag AC TTT   1919
Val Thr Tyr Ala Thr Thr Gly Tyr Lys Lys                         INTRON 2                     Asp Phe   (+1338)

GTC AAC CAT CAA TAT AAC CCC AAG GAC ATT GAA AAC ATG ACA CAA CAA CGA GTC TTC GCG GAG AGG TGG TCG ACC   1994
Val Asn His Gln Tyr Asn Pro Lys Asp Ile Glu Asn Met Thr Gln Gln Arg Val Phe Ala Glu Arg Trp Ser Thr   (+1413)

CTC GAC CCC TCT GCG AAT GTC ATG CTT ATC CCC ACT ATT GAG GAG GCC ATC AAC AAG GCC AGG AGC CTG GTA GAC   2069
Leu Asp Pro Ser Ala Asn Val Met Leu Ile Pro Thr Ile Glu Glu Ala Ile Asn Lys Ala Arg Ser Leu Val Asp   (+1488)

ACC CAG AAA ACG GAA GGC GAA GTG CAG GCA CTC ATC ACC GGC AGC CTT CAC CTT GTG GGT GGC GCG CTC GGC ATT   2144
Thr Gln Lys Thr Glu Gly Glu Val Gln Ala Leu Ile Thr Gly Ser Leu His Leu Val Gly Gly Ala Leu Gly Ile   (+1563)

TTG GAA AAA GCA GAT GCT CTC TGA                                                                       2168
Leu Glu Lys Ala Asp Ala Leu STOP                                                                      (+1587)

         A   GGGGACTTGT   GGTTCGGCAG   CAGTTTTCAA   CATTTATATT   TTAGATATCC   GTCCATTTTT   TACATGGTAT   2239
GTACAGGATT   TGGCATTTTG   CTTCGCAGCA   TCTTTTCTTT   GTTACAAAAC   ACAGGGAAAT   ACAGGAAAAG   TACAGGAAAA   2319
TAGAACAAGG   GGGTTAAAGG   AAAACCGGCA   AGCCAGGACT   TAATATTCAA   CATACTCAAC   TGTCTTAGAA   CGGACCCAAG   2399
                                               *
AAGGTGGAAA   GCTTCCCGTT   ACAAGGACAT   TACACGTCTT   GCCGTCCTTC   GCGCGCCTGC   TCAGGATCTT   CTGAACCTGT   2479
TCCATGGCCG   GCTCTACTGC   GTTGTACGAC   GAGGTTCCGT   CTCGCACTAG   CTTCCTGAAT   AATCTTCTGC   CCCTGCAACT   2559
GCACCGCGAG   ATCTCTCTCC   GGCTCACCCT   CTACCGGCGC   CTTTTCCTCG   TTCCTTGTGA   GCACCGCGTA   GGTGAACACC   2639
GGTGTCGTTG   TCCGCTTTGC   TTCTGCGCGG   CCGCAAGAAG   AGCCCTCAAC   AAGACTCCGG   GTCCCTATCC   TGCTGGTTGA   2719
ACACCAAGAC   GTTGACATCG   GCCTCCTTCA   CCTTCCCAGA   AAACCACTGT   CCAACACCCG   CCAGGCTATC   CTCCGTATGC   2799
GCTCCATCAA   CAAACACTCC   GTGCCCTTGG   GGTCTCTAAA   AGACTCGCAC   CTGCCCTTAA   GGCTAGCCTC   CTTCAAACCC   2879
TTCTCAAACT   CAGCCGGATA   TCATCCAATT   TCCAGCCTTC   CTCCCCAAAA   GCCCCCGCGA   ATTTGTGTCC   CACCCTGGTA   2959
AGTGCTCCCT   CGCCCCCCAC   GCCAACGCCA   TGTTAAACTT   TTGAAATGGC   CCTTCCAACT   TGGCCCCCTC   TACGCCCTTC   3039
CACTTCTCAA   CCTGCTCATC   CTCCACTTCT   ACCAGCCTCT   CCACTTCCTT   CTCCTGCGCT   CTATTCCTCA   ACACCTCCAT   3119
CACTCCTTTC   TGAGTTTCCC   ATCCAGCCTC   CTCGTAAACC   CTTTGACCCT   TCCTAAAATC   CGCTCTTATT   CCACGCAAAT   3199
TTTCTCAAGG   GTATTTCCCA   ACATAGCCAC   GTGATCAATT   CCCAGCTCGG   TGACCACGCT   CGCCGTCAGC   ACTGCGGGCT   3279
CAAGAAGTTC   GTCGAGTCGT   ATTCCCCGCC   AATCCCACAC   TCAATCACCG   CTTGCTTGAC   CCCTCGCGAC   AAAGATGTGA   3359
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Fig. 2. Sequence of the 3440 bp plasmid pIA50 (GenBank accession number is AF005040) and subsequent sequence of the putative open reading frame. Translation start site 1 (indicated by the symbol ↓) is postulated to be the hypothetical start to the largest open reading frame of the *met*-6^+ gene (Table 1) at position +1 of the largest open reading frame. Translation start site 2 (indicated by the symbol ∇) is postulated to be a second hypothetical start site, 102 nucleotides smaller than the largest open reading frame of *met*-6^+ gene (Table 1). The single underlined areas refer to the two primers used to amplify the wild-type or mutant PCR products of 2.2 kb from genomic template DNA. At position +400 of the largest open reading frame (indicated by the symbol ⇓ and square box), the triplet codon TCC of plasmid pIA50, 74-OR23-1*A*. Lindegren A and Emerson, giving rise to serine, is a CCC triplet codon in *met*-6 mutant, giving rise to proline. This is the site of *met*-6 mutation. The 5′ end of the three cDNA clones occur at position +182 of the largest open reading frame and is postulated to be truncated and not to be the true 5′ end of the cDNA. The cDNA clone 3′ end occurs at position +1858 of the largest open reading frame and is followed by a 20–25 nucleotide poly(A) tail. Both ends are indicated by asterisk (*).