

Nucleotide sequence of crystal protein gene isolated from *B.thuringiensis* subspecies *entomocidus* 60.5 coding for a toxin highly active against *Spodoptera* species

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Submitted May 13, 1988

Accession no.X07518

The isolation of a toxin gene from *B. thuringiensis* subsp. *entomocidus* 60.5, which did not belong to one of three well-described gene families (1), was described (2). Its gene product is highly active against *Spodoptera* species. Here the complete nucleotide sequence of this gene (BTVI) encoding a protein with a calculated weight of 134.740 kDa is presented. Extensive homology with the 4.5 kb-class gene isolated from *B. thuringiensis* subsp. *kurstaki* HD-1 *Dipel* (3), was found downstream from the proteolytic cleavage site.

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5'aacctcagcaactcttggtag ccttaataaaaaaacggggt atcttatcggagaaaaata CAAAATCAATGCATACCTTA CAATTCGTTAAAGTAACTCGT AAGAAGTACTTTTGGATGGA 120
GAACGGATATCAACTGGTAA TTGATCAATTGATATTTCTC TGTCACCTGTTTCAGTTTCTG GTATCTAAGTTTGTACAGG GGGAGGATTTTGTATGGAT TAATAGATTTTGTATGGGA 240
ATAGTTGGCCCTTCTCAATG GGATGCATTTCTAGTACAAA TTGACAAATTAATTAATGAA AGAATAGCTGAATTTGCTAG GAATGCTGCTATTTGCTAAT TAGAAGCATTAGAAAACAAT 360
TTCAATATATATGCGAAGC ATTAAAGAAATGGGAAGAAG ATCTTAATAATCCAGAAACC AGCAGCAGAGTAATTGATGC CTTTGGTACTTGTATGGCC TACTTGAAGGCACTTCTCT 480
TGTGTTGGAATTTCTGGATT TGAGTACCCCTTTTATCGG TTATGCTTCAAGCCGCCAAT CTGCATCTAGCTATATTAA GATTTCTGTAATTTTGGAG AAAGATGGGATGGACAAGC 600
ATAAATCTCAATGAAAATA TAATAGACTAATTAGGCATA TTGATGAATATGCTGATCAC TGTCAAAATACCTATAATCG GGGATTAATAATTTACCGA AATCTACGTATCAAGATTCG 720
ATAACATATAATCGATTACG GAGAGACTTAACATTGACTG TATTAGATATCGCCCLTTC TTCCAAACTATGACAAATAC GAGATATCCAATTCAGCCAG TTGCTCAACTAACAGGGAA 840
GTTTATACGGACCCATTAAT TAATTTAATCCACAGTTAC AGCTGTAGCTCAATTACCT ACTTTTAACTGTTATGGAG CAGCCGAATTAGAAATCTCT ATTTATTGATATATTGAAT 960
AATCTTACAACTTTCACGGA TTGTTTACTGTTGGACCGCA ATTTTATGGGGAGGACAT CGACTAATACTAGCCITAT AGGAGTGGTACATCAATCAT CTCCTATATATGCGAAGCAG 1080
GGCAACCCAGGAGCCTCCAAG ATCCTTTACTTTTAAATGGAC CGGTATTAGGACTTTATCA AATCCTACTTTACGATATT ACAGCAACCTTGGCCAGCCG CACCATTAAATTTACTGGT 1200
GTGGAAGGACTGAATTTTC TAGACCTCAAAATAGCTTTA CGTATCGAGGAAGAGCTACC GTTGATCTTTAACTGAAAT ACCGCCCTCAGGATAATAGT TGCCACCTCCGCAAGATAT 1320
AGTCTCGGTTTATGTCATGC AACTTTTCTGCAAAAGCTCC GAAACACCTTTTAAAGAACT CGTGTAGTATTTTCTTGGAC GATCTGATGGCAACTCTTA CAAATACAATTTGATCGAGAG 1440
AGAATTAATCAAAATACCTTT ACTGAAAGGATTTAGAGTTT GGGGGGACCTCTGTCATT ACAGGACAGGATTTACAGG AGGGGATATCTCTGGAAGA ATACCTTTGCTGATTTGTA 1560
TCTCTACAAGTCAATATTA TTGACCAATTCACCAAGAT ACCCTTTAAGATTTCTGTAC CTTTCCACTAGGGATGACAG GTTTATACTATTAACAGGAG CGGCATCCACAGGATGGCA 1680
GGCCAACTAGTCTAAATAT CCGCTCTCAGAAAATATGG AAATAGGGGAGAACTTAA CA TCTAGAACAATTTAGATATAC CGATTTAGTAATCCTTTTT CATTAGAGCTAATCCAGAT 1800
ATAATGGGATAAGTGAACA ACCTCTAATTTCTGCGAGTT CTATTAGTAGGGCTGAACCT TATATAGATAAAATTTGAAAT TAITTCTACAGATCGCAACT TTGAAGCAGAATCTGATTTA 1920
GAAAGAGCAGAAAAGCCGGT GAATGCCCTGTTACTTCTT CCAATCAAAATCGGGTAAAA ACCGATGTCAGCGATTATCA TATTGATCAAGTATCCAATT TAGTGGATTTTATCAGAT 2040
GAAATTTGCTGAGTGAATA GCGAGAATGCTCCGAGAAA TCAAACATGCGAAGCGACTC AGTATGATGCGGAATTTACT TCAAGATCCAAACTTCAGAG CGATCAATAGACAACACAGAC 2160
COTGGCTGGAGGGAAGTAC AGATATTACATCCAAAGGAC GAGATACGCTATTCAAAGAC AATTACGTCACACTACCGGG TACCCTTGATGAGTGGCTATC CAACGTTATTAATATCAAAA 2280
ATAGATGAGTGGAAAATFAA ACCTTATACCCGTTTATGAAT TAAGAGGATATATCGAAGAT AGTCAAGACTTTAGAAATCTA TTGATCGCTTACAATGCAA AACAGGAAATAGTAAATGTC 2400
CCAGCCAGCCGTTCTTATG CCGCCCTTACCCCAAAGTC CAATCGGAAAAGCTTGGAGAA CCGAATCGATGCGGCCACA CCTGGAATGGAATCCTGATC TAGATTTGCTCTGCGAGACAG 2520
GGGGAAAAATGTGCACATCA TTCCCATATTTCACTTGG ATATTGATGTTGGATGTACA GACTTAAATCAGGACTTACG TGATGGGCTGATATTCAGCA TAAAGAGCGAAAGTGGCCAT 2640
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AATATTGTTTTAAGAGAGCG AAAAGAATCTGTAGATGCTT TATTTGTAACCTTCAATAT GATAGATTACAAGTGGATAC GAACATCCCGATGATTCATG CCGCAGATAAAAGCCGTTTAC 2880
AGAATCCGGAGAGCGTATCT CCGCAGACTGTCTGTGATTC CAGGTGCTCAATCGGCCATT TTCCGAAGAAATAGAGGACCC TATTTTACAGCGGATTTCTC TATATGATGGCAGAAAATGTC 3000
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TCACAAGAGGTTCTGCTGTC TCCAGCTCGTGCTATATGC TTGCTGTACAGCATATAAG GAGGGATATGGAGAGCGGCTC CTAACGATCCATCAGATCG AAGACAATACAGAGCAACTG 3240
AAATTCAGCAACTGCTGTAGA AGAGCAAGTATATCCAACA ACACAGTAACTGCTTAATAAT TATACTGCACTCAAGAACA ATATCAGCGTACCTACACTT CTCGTAATCAAGGATATGAC 3360
GAAAGCCTATGTTAAATACC TCCGCTACCAGCTGATTACG CTTCACTCTATGAAGAAAAA TCGTATACAGATGGAGCAAG AGAGAATCCTGTGGAATCTA ACAGAGGCTATGGGGATTAC 3480
ACACCACCTACCGCTGTTA TGTAAACAAGGATTTAGACT ACTTCCAGAGACCGGATAAG GTATGGATGAGATCGGAGA AACAGAAGAACATTCATCC TCGATAGCCTGGAATTTACT 3600
CTTATCGGGAATAAGatacc gttcaaaatgtaacgctatg cnaataagaatgattactg acctatattancagataaact aaganaaattttatcagcnaat aaaaa 3'

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