Nucleotide sequence of a novel crystal protein gene isolated from *Bacillus thuringiensis* subspecies *kenyae*

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A novel protoxin gene from *Bacillus thuringiensis* subspecies *kenyae*, encoding a 134 kilodalton protein toxic for *Bombyx mori*, has been isolated. The protoxin shares amino acid homology to both cryIA and cryIC protoxin subclasses (80–83%) and to the toxin (amino acids 1–650; 70–72%). However, the C-terminus of the activated toxins (amino acids 300–650) shows more sequence similarity to the cryIC (75%) than the cryIA (61–63%) gene classes. Therefore, until more extensive studies are performed on the pathotype of this protoxin, we tentatively place this gene in the new classification scheme (1) as a cryIC(b) gene.

REFERENCE

1. Höfte,H. and Whiteley,H.R. (1989) *Microbiol. Rev.* **53**, 242–255.

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   1  ATGGAGATAGTGAATAATCAGAATCAATGC GTGCCTTATAATTGTTTAAATAATCCTGAA AATGAGATATTAGATATTGAAAGGTCAAAT   90
  91  AGTACTGTAGCAACAAACATCGCCTTGGAG ATTAGTCGTCTGCTCGCTTCCGCAACTCCA ATAGGGGGGATTTTATTAGGATTGTTTGAT  180
 181  GCAATATGGGGGTCTATAGGCCCTTCACAA TGGGATTTATTTTTAGAGCAAATTGAGCTA TTGATTGACCAAAAAATAGAGGAATTCGCT  270
 271  AGAAACCAGGCAATTTCTAGATTAGAAGGG ATAAGCAGTCTGTACGGAATTTATACAGAA GCTTTTAGAGAGTGGGAAGCAGATCCTACT  360
 361  AATCCAGCATTAAAAGAAGAGATGCGTACT CAATTTAATGACATGAACAGTATTCTTGTA ACAGCTATTCCTCTTTTTTCAGTTCAAAAT  450
 451  TATCAAGTCCCATTTTTATCAGTATATGTT CAAGCTGCAAATTTACATTTATCGGTTTTG AGAGATGTTTCAGTGTTTGGGCAGGCTTGG  540
 541  GGATTTGATATAGCAACAATAAATAGTCGT TATAATGATCTGACTAGACTTATTCCTATA TATACAGATTATGCTGTACGCTGGTACAAT  630
 631  ACGGGATTAGATCGCTTACCACGAACTGGT GGGCTGCGAAACTGGGCAAGATTTAATCAG TTTAGAAGAGAGTTAACAATATCAGTATTA  720
 721  GATATTATTTCTTTTTTCAGAAATTACGAT TCTAGATTATATCCAATTCCAACAAGCTCC CAATTAACGCGGGAAGTATATACAGATCCG  810
 811  GTAATTAATATAACTGACTATAGAGTTGGC CCCAGCTTCGAGAATATTGAGAACTCAGCC ATTAGAAGCCCCCACCTTATGGACTTCTTA  900
 901  AATAATTTGACCATTGATACGGATTTGATT AGAGGTGTTCACTATTGGGCAGGGCATCGT GTAACTTCTCATTTTACAGGTAGTTCTCAA  990
 991  GTGATAACAACCCCTCAATATGGGATAACC GCAAATGCAGACCAAGACGAACTATTGCTC CTAGTACTTTTCCAGGTCTTAACCTATTTT 1080
1081  ATAGAACATTATCAAATCCTTTCTTCCGAA GATCAGAAAAATATTACTCCTACCTTAGGG ATAAATGTAGGTACAGGGATAAATGTAGTA 1170
1171  CAGGGAGTAGGGTTCATTCAACCAAATAAT GCTGAAGTTCTATATAGAAGTAGGGGGACA GTAGATTCTCTTAATGAGTTACCAATTGAT 1260
1261  GGTGAGAATTCATTAGTTGGATATAGTCAT CGATTAAGTCATGTTACACTAACCAGGTCG TTATATAATACTAATATAACTAGCCTGCCA 1350
1351  ACATTTGTTTGGACACATCACAGTGCTACT AATACAAATACAATTAATCCAGATATTATT ACACAAATACCTTTAGTGAAAGGATTTAGA 1440
1441  CTTGGTGGTGGCACCTCTGTCATTACAGGA CCAGGATTTACAGGAGGGGATATCCTTCGA AGAAATACCATTGGTGAGTTTGTGTCTTTA 1530
1531  CAAGTCAATATTAACTCACCAATTACCCAA AGATACCGTTTAAGATTTCGTTATGCTTCC AGTAGGGATGCACGAATTACTGTACCGATA 1620
1621  GGAGGACAAATTAGAGTAGATATGACCCTT GAAAAAACCATGGAAATTGGGGAGAGCTTA ACATCTAGAACATTTAGCTATACCAATTTT 1710
1711  AGTAATCCTTTTTCATTTAGGGTTAATCCA GATATAATTAGAATAGCTGAAGAACTTCCT ATTCGTGGTGGTGAGCTTTATATAGATAAA 1800
1801  ATTGAACTTATTCTAGCAGATGCAACATTT GAAGAAGAATATGATTTGGAAAGAGCACAG AAGGCGGTGAATGGCCTGTTTACTTCTACA 1890
1891  AATCAACTAGGGCTAAAAACAGATGTGACG GATTATCATATTGATCAACTTTCCAATTTA GTTGAGTGTTTATCGGATGAATTTTGTCTG 1980
1981  GATGAAAAGAGAGAATTATCCGAGAAAGTC AAACATGCGAAGCGACTCAGTGATGAACGG AATTTACTTCAAGATCCAAACTTCAGAGGG 2070
2071  ATCAATAGGCAACCAGACCGTTGCTGGAGA GGAAGCACGGATATTACTATCCAAGGTGGA GATGACGTATTCAAAGAGAATTACGTCACA 2160
2161  TTACCGGGTACCTTTGATGAGTGCTATCCA ACGTATTTATATCAAAAAATAGATGAGTCG AAGTTAAAAGCTTATACCCGCTATGAATTA 2250
2251  AGAGGGTATATCGAGGATAGTCAAGACTCA GAAATCTATTTAATTCGCTACAATGCAAAA CACGAGACAGTAAACGTGCCAGGTACGGGT 2340
2341  TCCTTATGGCCGCTTTCAGCCCAAAGTCCA ATCGGAAAGTGTGGAGAACCGAATCGATGC GCGCCACACCTTGAATGGAATCCTAATCTA 2430
2431  GATTGCTCCTGCAGAGACGGGGAAAAATGT GCCCATCATTCCCATCATTTCTCCTTGGAC ATTGATGTTGGATGTACAGACTTAAATGAG 2520
2521  GACTTAGGTGTATGGGTGATATTCAAGATT AAGACACAAGATGGCTATGCAAGACTAGGA AATCTAGAGTTTCTCGAAGAGAAACCACTA 2610
2611  TTAGGGGAAGCACTAGCTCGTGTGAAAAGA GCGGAGAAAAAATGGAGAGACAAATGCGAA AAATTGGAATGGGAAACAAATATTGTTTAT 2700
2701  AAAGAGGCAAAAGAATCTGTAGATGCTTTA TTTGTAAACTCTCAATATGATAGATTACAA GCGGATACGAATATCGCGATGATTCATGCG 2790
2791  GCAGATAAACGCGTTCATAGCATTCGAGAA GCGTATCTGCCAGAGCTGTCTGTGATTCCG GGTGTCAATGCGGCTATTTTTGAAGAATTA 2880
2881  GAAGGGCGTATTTTCACTGCATTCTCCCTA TATGATGCGAGAAATGTCATTAAAAATGGC GATTTCAATAATGGCTTATCATGCTGGAAC 2970
2971  GTGAAAGGGCATGTAGATGTAGAAGAACAG AACAACCATCGTTCGGTCCTTGTTGTTCCA GAATGGGAAGCAGAAGTGTCACAAGAAGTT 3060
3061  CGTGTTTGTCCGGGTCGTGGCTATATCCTT CGTGTTACAGCGTACAAAGAGGGATATGGA GAGGGCTGTGTAACGATTCATGAGATCGAA 3150
3151  GACAATACAGACGAACTGAAATTCAGCAAC TGTGTAGAAGAGGAAGTATATCCAAACAAC ACGGTAACGTGTAATAATTATACTGCGACT 3240
3241  CAAGAAGAACATGAGGGTACGTACACTTCC CGTAATCGAGGATATGACGAAGCCTATGAA AGCAATTCTTCTGTACATGCGTCAGTCTAT 3330
3331  GAAGAAAAATCGTATACAGATAGACGAAGA GAGAATCCTTGTGAATCTAACAGAGGATAT GGGGATTACACACCACTACCAGCTGGCTAT 3420
3421  GTGACAAAAGAATTAGAGTACTTCCCAGAA ACCGATAAGGTATGGATTGAGATCGGAGAA ACGGAAGGAACATTCATCGTGGACAGCGTG 3510
3511  GAATTACTTCTTATGGAGGAATAAtatata tgctttaaatgt 3552
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