

Nucleotide sequence of the chitinase B gene of *Serratia marcescens* QMB1466

Mark H.Harpster and Pamela Dunsmuir*

DNA Plant Technology Corporation, 6701 San Pablo Avenue, Oakland, CA 94608, USA

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Previous studies have reported on the cloning (1,2) and sequencing (1) of a gene (*chiA*) from *Serratia marcescens* QMB1466 which encodes a secreted 57-58 kD polypeptide with exochitinolytic activity. Here we present the complete coding sequence and limited flanking regions of a second chitinase gene (*chiB*) from *S. marcescens* whose isolation has been described (1) (Fig.1). The translated region shows no homology with *chiA* and encodes a 55.5 kD apoprotein which we believe is processed at the carboxyl terminus of amino acid 41 to yield a 51-52 kD mature polypeptide. A comparative analysis of *chiA* and *chiB* enzyme activities will be published elsewhere.

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1  TTAATAAAAAATTCATTCTTATGGTATTATTTTCGACTTTTATTCTCGAGGAAATAAACCATTAATGGCGACGGGGAATATTTCCCCATT
91  GAAAAACATCCACTCTGGAGAAATGCCATGCCACACGCGAAAGCCGTTATTGGGTATTATTTTATCCGCAACCAACAAATAATTAC
      M S T R K A V I G Y Y P I P T N Q I N N Y
181  ACCGAGACCGGATACGCTCTGCTGCGGTTCCCGGTTCCCAACATCACGCCGCGCAAGCCAAACAGCTGACGCACATTAACCTTCGTTCT
      T E T D T S V P P P V S N I T P A K A K Q L T H I N F S F
271  CTGGATATCAACGCAACCTGGAATGCGCCTGGGATCCGGCCACCAACGACGCGCAAGCGCGCGATGTGGTCAACCGTTAAACCGCGCTC
      L D I N S N L E C A W D P A T N D A K A R D V V N R L T A L
361  AAAGCGCACAAACCCAGCCTGGCATGTCTCCATCGCGCGGTGGTACTACTCCAACGATCTGGCGGTGTCGCGACCGCAACCTACGTC
      K A H N P S L R I M F S I G G W Y Y S N D L G V S H A N Y V
451  AACCGGTGAAACCCCGCGCGCGCACCAAGTTCGCCCAATCTCGCTGCGCATCAAGGATTACGGCTTCGACGGCGGTGGACATC
      N A V K T P A A R T K F A Q S C V R I M K D Y G D G V D I
541  GACTGGGAGTATCCGACGGCGCGGAGTGGACGGTTTCATCGCCGCGCTGCAGGAGATCCGACCTTGTGCAACCGCAACCCATCCGG
      D W E Y P Q A A E V D G F I A A L Q E I R T L L N Q Q T I A
631  GACGGCGCGCAGCGTTCGCGTATCAGTTGACCATCGCCGCGCGCGCGCGCTTCTTCTGTCGCGCTATTACAGCAAGCTGGCGCAA
      D G R Q A L P Y Q L T I A G A G G A F F L S R Y Y S K L A Q
721  ATCGTCCGCGCATCGATTACATCAACCTGATGACCTACGATCTGGCGGCGCTTCTTCTGCTGTCGCGCTATTACAGCAAGCTGGCGCAA
      I V A P L D Y I N L M T Y D L L A G P W E K I T N H Q Q A A L F
811  GCGCAGCGCGCGCGCAGCTTCAACAGCAGCTGCGCGAAGCAATCTGGGCTGGAGTGGGAAGAGCTGACCCGCGCTTCCCGCAGC
      G D A A G P T F Y N A L R E A N L G W S W E E L T R A F P S
901  CCGTTCAGCTGACGGTTCGACCGCGTGCAGCAGCATGATGATGGAAGGCTGCCGAGCGCAAAATCTGTCATGCGGGCGTCCCTTC
      P F S L T V D A A V Q Q H L M M E G V P S A K I V M G V P F
991  TACGGCGCGCTCAAGGGCTCAGCGCGCGCAACCGCGCGCAGTACAGCAGCCAGCAGCGCGCGGCAAGATCCGTATCCGAACGCC
      Y G R A F G G V S G G N G G Q Y G S H S T P G E D P Y P N A
1081  GATTACTGGCTGGTGGCTCGGACGACTCGCTGCGCGCAGAAGATCCGCGCATCGCCTCTTATCGCCAGCTGGAGCAGATGCTGCAGGGC
      D Y W L V G C D E C V R D K D P R I A S Y R Q L E Q M L Q G
1171  AACTACGGCTATCAGCGGTTGTGGAACGATAAGCAAAACCCCGTATCTGTATATCGCCAGAAGCGGCTGTTGTCCACCTATGACGAT
      N Z G Y Q R L W N D K T K T P Y L Y H A Q N G L F V T Y D D
1261  GCCGAGAGCTCAAATAACAAGCGAATACATCAAGCAGCAGCAGCTGGCGCGTAAATGTTTGGCATTGGGGCAAGCAACCGCAAC
      A E S F K Y K A K A I K Q Q Q L G G V M F W H L G Q D N R N
1351  GCGCATCTGCTGGCGCGCTGGATCGCTATTCAACGCGCAGACTACGACGACGACGCTGGATGGGACCGCGGCTGCGATATACC
      G D L L A A L D R Y F N A A D Y D D S Q L D M G T G L R Y T
1441  GCGCTCGCGCGCAACCTGCGGATCATGACCGCGCGGCTATGTGCGCGCACCACTTACGCCAGGGCGCTGGTGTCTTACCAAA
      G V G P G N L P I M T A P A Y V P G T T Y A Q G A L V S Y Q
1531  GGCTACGCTGGCAGCAAGTGGGTTATATCACTCGCGCGCGCTCAGACGCGCGCTGAAAGTGGGCGCGCTGGCGCTAAGCC
      G Y V W Q T K W G Y I T S A P G S D S A W L K V G R L A
1621  GTAAAAAACCCTGACCGAATGCTCGCGGGTTTTCATTGAGTTAACCGTTTGTATTTTCGCGCTTCCTGCTTATT
    
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Figure 1. Nucleotide sequence of *chiB*. Hexameric consensus sequences characteristic of bacterial promoters are underlined (3), as is a near-perfect repeat in the 3' flanking region which is characteristic of rho-dependent transcription termination (4). The transcription start site is indicated by an asterisk and was determined by the method of primer extension (5).

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* To whom correspondence should be addressed.

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