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Sequence of the *Bacillus thuringiensis* phosphatidylinositol specific phospholipase C

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A number of eukaryotic proteins have been shown to be anchored to membranes by covalent linkage to a phosphatidylinositol molecule(1). Bacterial phospholipases have been instrumental in the identification of proteins which are anchored by this mechanism. To increase the availability of this enzyme, and to possibly understand its mechanism of action, we have isolated the gene for the phosphatidylinositol specific phospholipase C of *B. thuringiensis*. Oligonucleotide probes based on the amino acid sequence (2) of the purified enzyme were used to isolate clones in pBR322. The sequence was determined by the dideoxy sequencing method(3). The amino acids corresponding to the determined amino acid sequence are underlined. When either *E. coli* or *B. subtilis* was transformed with this gene on a plasmid, enzymatic activity could be detected in amounts at least 500-fold higher than nontransformed cultures. No obvious sequence similarities were found in the Dayhoff protein sequence data base, nor were there similarities to the recently reported sequence of a mammalian phosphoinositide-specific phospholipase C (4).

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   1 AAGTTCCTTTAAATTTTTCTAATTTAGTATATGTGAATGATTTTTTAACTTTACTTCTATGCAATATTTCATATTGATGAAATGTTATTTATTTTTTATG

 101 AACTAGCTTATATTATATTCAATAAGTTTGATGTAAAAACAGAAAAAGTGAGGGATAATAATGAGCAATAAGAAGTTAATTTTGAAATTATTCATATGTA
   1                                                                   M  S  N  K  K  L  I  L  K  L  F  I  C  S

 201 GTACAATATTTATCACATTTGTATTTGCTTTACATGATAAGAGAGTAGTTGCAGCTAGCTCTGTTAATGAGCTTGAAAATTGGTCAAAATGGATGCAACC
  15  T  I  F  I  T  F  V  F  A  L  H  D  K  R  V  V  A  A  S  S  V  N  E  L  E  N  W  S  K  W  M  Q  P

 301 TATACCTGATAATATCCCGTTAGCACGAATTTCAATTCCAGGAACACACGATAGTGGGACGTTCAAGTTGCAAAATCCGATTAAGCAAGTGTGGGGAATG
  48  I  P  D  N  I  P  L  A  R  I  S  I  P  G  T  H  D  S  G  T  F  K  L  Q  N  P  I  K  Q  V  W  G  M

 401 ACGCAAGAATATGATTTTCGCTATCAAATGGACCATGGAGCTCGCATTTTTGATATAAGAGGACGTTTAACAGATGATAATACGATAGTTCTTCATCATG
  81  T  Q  E  Y  D  F  R  Y  Q  M  D  H  G  A  R  I  F  D  I  R  G  R  L  T  D  D  N  T  I  V  L  H  H  G

 501 GGCCATTATATCTTTACGTAACACTGCATGAATTCATAAATGAAGCGAAACAATTTTTAAAAGATAACCCGAGTGAAACAATTATTATGTCTTTAAAAAA
 115   P  L  Y  L  Y  V  T  L  H  E  F  I  N  E  A  K  Q  F  L  K  D  N  P  S  E  T  I  I  M  S  L  K  K

 601 AGAGTATGAGGATATGAAAGGGGCAGAAGGTTCATTTAGTAGTACGTTTGAAAAAAATTATTTTGTTGATCCTATCTTTTTAAAAACAGAAGGAAATATA
 148  E  Y  E  D  M  K  G  A  E  G  S  F  S  S  T  F  E  K  N  Y  F  V  D  P  I  F  L  K  T  E  G  N  I

 701 AAACTTGGAGATGCTCGTGGGAAAATTGTACTACTAAAAAGATATAGTGGTAGTAATGAATCTGGAGGATATAATAATTTTTATTGGCCAGATAATGAGA
 181 K  L  G  D  A  R  G  K  I  V  L  L  K  R  Y  S  G  S  N  E  S  G  G  Y  N  N  F  Y  W  P  D  N  E  T

 801 CGTTTACCACAACTGTAAACCAAAATGTAAATGTAACAGTACAAGATAAATATAAAGTGAATTATGATGAGAAAGTAAAATCTATTAAAGATACGATGGA
 215   F  T  T  T  V  N  Q  N  V  N  V  T  V  Q  D  K  Y  K  V  N  Y  D  E  K  V  K  S  I  K  D  T  M  D

 901 TGAAACGATGAACAATAGCGAGGATTTAAATCATCTATATATTAATTTTACAAGCTTGTCTTCTGGTGGTACAGCATGGAATAGTCCATATTACTACGCT
 248  E  T  M  N  N  S  E  D  L  N  H  L  Y  I  N  F  T  S  L  S  S  G  G  T  A  W  N  S  P  Y  Y  Y  A

1001 TCTTATATAAATCCTGAAATTGCAAACGATATAAAACAAAAGAATCCTACAAGAGTAGGCTGGGTAATTCAAGACTACATAAATGAAAAGTGGTCACCAT
 281 S  Y  I  N  P  E  I  A  N  D  I  K  Q  K  N  P  T  R  V  G  W  V  I  Q  D  Y  I  N  E  K  W  S  P  L

1101 TATTGTATCAAGAAGTTATAAGAGCGAATAAGTCATTAATAAAAGAATAAAGATGATGAGAGTAAGAAGCGATAAAATATATCGCTTCTTTTTCTTTTCC
 315   L  Y  Q  E  V  I  R  A  N  K  S  L  I  K  E  O

1201 AATAACCAACAATAGAAATTGTACTTTTATAATAGAAAAA
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