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Nucleotide sequence of a cyclodextrin glucosyltransferasse gene, *cgt*A, from *Bacillus licheniformis*

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Cyclodextrin glucosyltransferases (CGTases), EC 2.4.1.19, convert starch into cyclic glucosyl oligosaccharides (cyclodextrins) having a hydrophilic surface and a hydrophobic core (1). Thus, cyclodextrins bind to and solubilize hydrophobic materials. Recently, a potential therapeutic benefit for cyclodextrins was demonstrated (2). Here we report the nucleotide sequence of a unique gene encoding a CGTase cloned from a strain of *Bacillus licheniformis* (3). The *B. licheniformis* gene, called *cgt*A, was cloned using procedures similar to those described (4) except the *B. licheniformis* library was prepared in a pUC19 derivative. *E. coli* transformants expressing a full length *cgt*A gene were initially identified on the basis of starch clearing ability as described (4). The cgtA clones were confirmed by measuring the conversion of 2% maltodextrin solution to cyclodextrin following growth in liquid culture. Cyclodextrins were identified and quantitated by HPLC using a cyclodextrin assay column purchased from Advanced Separation Technologies, Whippany, NJ; α and β cyclodextrins were the principal products obtained. The *cgt*A gene, sequenced as described (5), is contained within a 2516 base pair Sau3A to SphI fragment encoding an open reading frame of 718 amino acids. The translated sequence exhibits 58% and 66% amino acid similarity, respectively, to the *B. macerans* CGTase (4) and either Bacillus sp. 1011 (6) or 38−2 (7). This similarity extends throughout the entire open reading frame except for the amino terminal leader sequences.

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-209  GATCATAACTCGAGGGCCATGCTTTTAAACCCAAGCGGTTTAGGACAACCCCGGTAACTCCCCAGGAGATACCGGGGTTGTTGGCGTGTC
-119  GAAGGAGGGAAGTCTTTAAGCCACAGAATGTCTCCTCGTACAGTTGTAAGCGCTGTTATTCGAGAGCCAGGTTAGTTGTTTTTGTTGAAA
 -29  ACTACTACATTCATGAAGGGTGGATTACC ATGTTTCAAATGGCCAAACGCGTTCTCCTCAGTACCACGCTAACGTTCAGCCTGCTTGCC
  61  GGCAGTGCATTGCCTTTCCTGCCTGCTTCCGCGATTTATGCCGATGCGGATACAGCTGTCACCAACAAGCAGAACTTCAGTACGGATGTC
 151  ATCTATCAAGTTTTTACGGACCGATTTCTGGATGGTAACCCATCCAACAACCCTACCGGGGCTGCCTTTGATGGCACGTGCAGCAACCTG
 241  AAGCTGTACTGCGGTGGGGACTGGCAGGGATTGGTCAACAAAATCAATGACAACTATTTCAGTGACTTGGGTGTCACGGCCCTCTGGATC
 331  TCCCAGCCTGTCGAAAATATTTTCGCTACCATCAACTACAGCGGTGTAACCAATACAGCCTATCACGGCTATTGGGCACGGGATTTCAAG
 421  AAGACCAATCCGTATTTCGGAACCATGACCGATTTTCAGAATCTGGTAACCACCGCCCATGCGAAAGGCATCAAAATCATTATTGATTTC
 511  GCGCCAAACCATACGTCCCCTGCCATGGAAACCGATACCTCCTTCGCCGAGAACGGCAAACTGTACGATAACGGCAACCTGGTTGGCGGG
 601  TACACCAATGATACCAACGGATATTTCCACCACAATGGCGGCTCCGATTTCTCCACTCTTGAGAATGGCATTTACAAAAACCTCTACGAT
 691  CTGGCCGATCTGAATCACAATAACAGCACGATCGATACATATTTCAAAGACGCCATCAAGCTGTGGCTTGATATGGGCGTGGACGGCATT
 781  CGTGTCGATGCGGTCAAGCACATGCCTCAGGGCTGGCAGAAGAACTGGATGTCATCTATCTATGCACACAAGCCGGTATTTACCTTCGGC
 871  GAATGGTTCCTGGGATCTGCTGCACCCGATGCGGATAACACAGATTTTGCCAATGAATCTGGTATGAGTTTGCTTGATTTCCGTTTCAAT
 961  TCGGCTGTCCGCAACGTGTTCCGGGATAACACCTCCAACATGTACGCGCTGGATTCCATGCTGACGGCTACGGCAGCAGATTACAATCAG
1051  GTGAATGACCAAGTCACTTTCATTGACAACCATGATATGGACCGTTTCAAAACCAGTGCTGTGAACAACCGCCGTCTGGAACAGGCTCTG
1141  GCCTTCACGCTGACCTCACGCGGCGTACCTGCCATCTATTATGGTACCGAGCAGTATCTGACTGGGAACGGCGACCCGGATAACCGGGGC
1231  AAAATGCCTTCCTTCTCCAAATCGACTACAGCGTTCAACGTGATCAGCAAGCTGGCACCTCTGCGCAAATCCAACCCGGCGATTGCCTAC
1321  GGTTCCACACAGCAGCGCTGGATCAACAATGATGTATATATCTATGAGCGCAAGTTTGGCAAAAGCGTTGCCGTCGTTGCCGTTAACCGC
1411  AATCTCACGACGCCAACCAGTATCACTAACCTGAATACGTCGCTTCCATCAGGAACCTATACCGATGTGCTCGGCGGCGTGCTGAACGGA
1501  AACAACATCACGTCCAGTGGAGGCAATATTTCTTCCTTCACGCTCGCTGCAGGAGCTACCGCTGTTTGGCAATATACGGCAAGTGAAACG
1591  ACGCCAACCATCGGTCACGTTGGCCCTGTAATGGGTAAACCAGGTAACGTCGTTACCATCGACGGACGCGGGTTCGGTTCCGCCAAAGGT
1681  ACCGTCTACTTCGGTACAACAGCCGTTACGGGCTCAGCCATTACTTCATGGGAAGACACTCAGATCAAAGTCACCATTCCACCAGTAGCA
1771  GGCGGTGACTATGCAGTGAAAGTAGCTGCCAATGGTGTGAACAGCAACGCCTATAACGATTTCACCATCCTTAGCGGCGATCAGGTATCG
1861  GTGCGGTTCGTCATCAATAATGCCACAACTGCGCTGGGCGAGAATATCTACCTGACAGGCAACGTGTCCGAACTCGGTAACTGGACCACA
1951  GGTGCAGCTTCCATTGGACCGGCTTTCAATCAGGTCATCCACGCCTACCCGACTTGGTATTATGACGTAAGTGTTCCGGCCGGGAAACAG
2041  CTGGAATTCAAGTTCTTCAAGAAAAACGGCGCTACCATTACGTGGGAAGGTGGATCCAATCACACCTTTACAACACCGACGAGTGGTACT
2131  GCCACAGTAACGATAAACTGGCAATAACTAGCCATAATCCATTAATGAAGCCCGGAGCAGCGCTTATACAGCGTACACTCCGGGTTTTGA
2221  CGTTTAATCTGTTTCTGGTTTATCGGTAAGTTCGAATGGACTTCAATGTGGTCGCGGCAAGGATTCCGGTTGCGAGCAGCAGCATGC
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