Nucleotide sequence of a cyclodextrin glucosyltransferase gene, cgtA, from Bacillus licheniformis

David E. Hill*, Robert Aldape§ and J. David Rozzell**
Genetics Institute, 87 CambridgePark Drive, Cambridge, MA 02140, USA

Submitted November 16, 1989
EMBL accession no. X15752

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 cgtA, 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 cgtA 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 cgtA gene, sequenced as described (5), is contained within a 2516 base pair Sau3A to Sphl 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.

REFERENCES


* To whom correspondence should be addressed