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# Nucleotide sequence analysis of the cyclodextrin glucanotransferase gene from *Paenibacillus* sp. JB-13

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Fourteen CGTase genes derived from various microorganims have been cloned and sequenced. They consisted of approximately 700 amino acid residues with molecular weights of 70-80 kDa. The alignment of the deduced amino acid sequences revealed they are 50-70% identical. The CGTase gene of *Paenibacillus* sp. JB-13 was identified by subcloning and PCR-directed sequence analysis. It has an open reading frame of 2,069 base pairs encoding 687 amino acids with a predicted molecular mass of 75,000 Da. The *Paenibacillus* sp. JB-13 was 96% identical to the alkalophilic *Bacillus* sp. strain 1011 CGTase. It was also 56% similar to the CGTases from other *Bacillus* species.

The $\beta$-type CGTase from alkalophilic *Bacilli* was classified into two groups. Group I enzyme produce mainly $\beta$-CD with small amounts of $\alpha$- and $\gamma$-CDs and group II enzyme produce $\beta$-CD with negligible amounts of $\alpha$-CD. The CGTase from *Paenibacillus* sp. JB-13 exhibited a high similarity of 96% compared to the CGTase from alkolophilic *Bacillus* sp. 38-2 included to group I. Therefore, *Paenibacillus* sp. JB-13 producing $\beta$-CD with small amounts of $\alpha$- and $\gamma$-CDs was classified as group I.