SHORT COMMUNICATION

Preliminary Gene Characterization of α-Amylase from *Bacillus amyloliquefaciens* UMAS 1002

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ABSTRACT

Characterization of α-amylase gene sequence produced by *Bacillus amyloliquefaciens* UMAS 1002, a cellulolytic and amylolytic bacilli isolated from sago pith waste is described here. The *amyE* gene encoding the α-amylase was isolated by polymerase chain reaction. The 1,980 bp of *amyE* gene corresponding to 660 amino acids showed 99% homology to the α-amylase sequence from *Bacillus subtilis* Xq23 (GenBank: BAA31528). The α-amylase sequence of *B. amyloliquefaciens* UMAS 1002 (GenBank: KC800929) differs from that of *B. subtilis* X-23 by 5 amino acids. *In silico* analysis of α-amylase from *B. amyloliquefaciens* UMAS 1002 showed similar characteristics compared to α-amylase from *B. subtilis* X-23.

Keywords: *Bacillus amyloliquefaciens*, starch degrading, amylase, *in silico*, sago waste

Starch is among the most abundant polysaccharides on earth and a very important source of energy for most organisms (van der Maarel et al., 2002). However, for starch to be transformed into usable energy it needs to be hydrolyzed to its monomer, i.e. glucose. Enzymes responsible for this action are the starch-degrading enzymes. Among them is α-amylase (EC 3.2.1.1). This enzyme catalyses random hydrolysis of α-1,4-glycosidic linkages in starch polymers, thus suitable for conversion of starch into glucose, dextrins and limit dextrins. Different amylases have a large number of different substrate specificities in addition to a huge variation in optimal temperature and pH (Pandey et al., 2000). In biotechnological application, this enzyme is of great importance for use in various industries such as food, fermentation, textile and paper production (Pandey et al., 2000). For industrial application, generally these amylases are derived from animal and microbes.

Amylase group of enzymes are commonly found in eubacteria and eukaryotes. Bacterial amylases especially from *Bacillus*, and fungal amylases have a widespread use in industry because of the ease of manipulation for the type of work they are involved in (Svensson & Søgaard, 1992). In general, bacterial α-amylases have been grouped into two; for saccharification and liquefaction of soluble starch (Gangadharan et al., 2009; Matsuzaki et al., 1974; van der Maarel et al., 2002). The α-amylases from *B. amyloliquefaciens*, *B. licheniformis* and *B. stearothermophilus* belong to the liquefaction group of α-amylase. *B. amyloliquefaciens* is one of the most extensively studied among all of the *Bacillus* species due to its ability to secrete amylase at relatively high concentrations (Gangadharan et al., 2009; Priest, 1977). A previous study of *B. amyloliquefaciens* UMAS 1002 showed an interesting capability to degrade starch as well as cellulose (Apun et al., 2000). This unique characteristic of dual enzyme capability has not been described elsewhere before, although it is common to find description of either amylase (Demirkan et al., 2005) or cellulase (Singh et al., 2013) in a single strain. In this study, the nucleotide sequence of α-amylase from *B. amyloliquefaciens* UMAS 1002 is described for the first time.

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