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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* X-23 (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 amyliquefaciens*, 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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