Ability of T1 lipase to degrade amorphous P(3HB): structural and functional study

ABSTRACT

An enzyme with broad substrate specificity would be an asset for industrial application. T1 lipase apparently has the same active site residues as polyhydroxyalkanoates (PHA) depolymerase. Sequences of both enzymes were studied and compared, and a conserved lipase box pentapeptide region around the nucleophilic serine was detected. The alignment of 3-D structures for both enzymes showed their active site residues were well aligned with an RMSD value of 1.981 Å despite their sequence similarity of only 53.8%. Docking of T1 lipase with P(3HB) gave forth high binding energy of 5.4 kcal/mol, with the distance of 4.05 Å between serine hydroxyl (OH) group of TI lipase to the carbonyl carbon of the substrate, similar to the native PhaZ7 Pl . This suggests the possible ability of T1 lipase to bind P(3HB) in its active site. The ability of T1 lipase in degrading amorphous P(3HB) was investigated on 0.2% (w/v) P(3HB) plate. Halo zone was observed around the colony containing the enzyme which confirms that T1 lipase is indeed able to degrade amorphous P(3HB). Results obtained in this study highlight the fact that T1 lipase is a versatile hydrolase enzyme which does not only record triglyceride degradation activity but amorphous P(3HB) degradation activity as well.

Keyword: Amorphous P(3HB); PhaZ7 Pl; Structure and function; Substrate specificity; T1 lipase