Enhancing thermal stability of the Streptomyces chitinase enzyme using *In Silico* point mutation

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Abstract: Chitin is the second most abundant biopolymer on the earth after cellulose. Chitinase, which hydrolyze chitin, has a broad range of application in agricultural, pharmaceutical and various chemical industries. One of the industrial problems in using enzymes is their relatively low thermal stability at temperatures above 50°C. As we know, the main difference between mesophilic and thermophilic proteins is related to their surface amino acids. Increasing charge and hydrophilic amino acids such as Glu, Arg and Tyr causes thermal stability and amino acids such as Gln, Ser, Ala and Asn cause thermal instability of enzymes [1].

Therefore, in this study, the 3-D model of chitinase was predicted using Modeller 9 & 15 software. Then, the quality of the model was evaluated with PROCHECK and PROSA II servers. Solvent accessibility and hydrophilic areas of the model were studied through Discovry Studio software and Molsoft ICM-Browser softwares, then some of the amino acids of this enzyme were selected for engineering. Using the UCSF Chimera software, site directed mutation was used to replace the stable thermal amino acids in some situations and appropriate mutation selected with PopMusic server [2]. The structural stability of the mutant enzymes were also investigated using Gromacs. Mutant and wild type enzymes will be expressed in *E. coli* and *B. subtilis***.** It should be noted that the Streptomyces chitinase is smaller than relative to similar chitinases, and in this enzyme, the chitin binding site is independent of enzyme active site, which is also an advantage [3].

Keywords: Chitinase; Thermostable; Chitin binding

References

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