On the importance of the small domain in the thermostability of thermoalkalophilic lipases from L1 and T1: insights from molecular dynamics simulation.

ABSTRACT

An all-atom level MD simulation in explicit solvent at high temperature is a powerful technique to increase our knowledge about the structurally important regions modulating thermal stability in thermenzymes. In this respect, two large-sized thermoalkalophilic enzymes from Bacillus stearothermophilus L1 (L1 lipase) and Geobacillus zalihae strain T1 (T1 lipase) are well-established representatives. In this paper, comparative results from temperature-induced MD simulations of both model systems at 300 K, 400 K and 500 K are presented and discussed with respect to identification of highly flexible regions critical to thermostability. From our MD simulation results, specific regions along the L1 lipase and T1 lipase polypeptide chain including the small domain and the main catalytic domain or core domain of both enzymes show a marked increase in fluctuations and dynamics followed by clear structural changes. Overall, the N-terminal moiety of both enzymes and their small domains exhibit hyper-sensitivity to thermal stress. The results appear to propose that these regions are critical in determining of the overall thermal stability of both organisms.

Keyword: Thermostability; Thermoalkalophilic enzyme; T1 Lipase; L1 lipase; Protein dynamics; Flexibility.