Poster Presentation

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Allostery mapping in Enterococcus faecalis Bile Salt Hydrolase (BSH)

Yashpal Yadav[1], Sureshkumar Ramasamy[1]
[1]*Biochemical Sciences, CSIR-NCL, Pune, India*
E-mail: yash07yadav@gmail.com

Bile Salt hydrolase is a member of N terminal nucleophile hydrolase superfamily (Ntn-hydrolase) which consist of conserved αββα fold. Generally, BSH are homotetramer (Dimer of dimer) linked to each other by tetramer loop.Enterococcus faecalis BSH showed high catalytic activity as compared to other existing BSH.Removalof the tetramerization loop changes the oligomerization state from tetramer to dimer and loss in activity. Consurf analysis showed the tetramer loop to be hypervariable, while the core β-sheets are highly conserved and helices in between. The present scenario suggests that difference in BSH activity lies in variability of tetramer loop. Structural analysis showed that Arg207 in tetramer loop is protruding in active site of neighbouring chain which might influence the active site geometry. Molecular Dynamics Simulation was carried out to understand the role of Arg 207 residue on active site geometry.

Hydrogen bonding network of Arg 207 differ in different monomeric chain. The open conformation showed Arg 207 hydrogen bonded to Asp 21 which is a gatekeeper residue. While in closed conformation the hydrogen bonds were absent. This analysis correlates with the change in active site volume of different chains. The combinatorial approach provided detailed insight into the molecular basis of allostery. Using site directed mutagenesis approach we have tried to map theresidue showing significant increase in activity. The contribution of individual residue in allostery may alleviate the need of conventional biochemical characterization and screening of plethora of microbes. In future, this study will complement the gut microbiome project and will be useful for designing the better probiotic drink.

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