Poster Presentation

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Structural characterization of a UbiA superfamily member of archaeal origin

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One of the unique characteristic features of the domain archaea, are the lipids that form the hydrophobic core of their cell membrane. These membrane lipids are characterized by unique isoprenoid biochemistry and the building blocks are two core lipid structures, sn-2,3-diphytanyl glycerol diether (archaeol)and sn-2,3-dibiphytanyl diglycerol tetraether (caldarchaeol). Archaeol has two phytanyl chains (C20) in a bilayer structure connected to the glycerol moiety by an ether bond. The enzyme involved in this bilayer formation is Di-O-geranylgeranyl glyceryl phosphate synthase (DGGGPS), which is a member of a very versatile superfamily of enzymes known as UbiA superfamily. Enzymes of this prenyl-transferase family are known to catalyze the transfer of a prenyl group to various acceptors with hydrophobic ring structures in the biosynthesis of respiratory quinones, hemes, chlorophylls, vitamin E, and shikonin.

In this study, we attempt to delve into more details on the structural aspect of this enzyme DGGGPS and thereby gain crucial insight into its active site morphology and try to understand why the core structure of this family of enzymes are conserved over such a wide range of organisms in spite of being involved in key steps of many different biosynthetic pathways. Multiple sequence analysis of the typical members of the UbiA superfamily indicate that a few major conserved residues around the central cavity is also centrally implicated in several human diseases, on basis of the major mutations reported against these diseases in the earlier studies. The flexibility in the binding and active site of these enzymes for different substrates (ranging from aromatic to linear compounds), also gives a unique opportunity to possibly engineer the pocket residues to synthesize lipids of biomedical applications.

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