CHAPTER 32

MEDICAL SCIENCES
BIOPHYSICS

Doctoral Theses

01. ARSHI KHANAM
To Investigate the Potential Role of TH17 cells and Neutrophils: Protective or Pathogenic in Acute-on-Chronic Liver Failure.
Supervisor : Dr. Shiv Kumar Sarin and Dr. Puja Sakhuja and
Dr. Nirupama Trehanpati
Th 23031

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02. SHIKHA RANI
Analyzing the Chaperon Protein Repertoire in Archaeal Genomes.
SUPERVISOR: DR. Manisha Goel
TH 23080

Abstract
(Verified)

Chaperones are proteins that interact with nascent/unfolded proteins, assisting them in folding correctly to attain their native confirmation. A large number of chaperones are part of the protein folding machinery; however, their composition varies among different organisms. On the basis of earlier comparative genomic studies, it has been proposed that the archaeal protein folding machinery is quite similar to that of eukaryotes. The main aim of this thesis is to address the constitution, working and evolution of protein folding machinery as a whole in various archaeal organisms. A database named CrAgDb (Chaperone repertoire in Archaeal genomes Database) has been developed, annotating a total of 2854 chaperone proteins classified under 11 classes and 18 families from 144 archaeal organisms for which genome sequences were available in public databases. It is hosted at http://www.proteininformatics.org/mkumar/cragdb/. CrAgDb facilitated two main advances, first was an elaborate analysis of all archaeal chaperone protein families. The compilation of all relevant information at a single place has allowed deeper understanding of evolutionary history of many chaperone families, like CsaA. We also compared the modular organization of archaeal chaperone machinery with that of humans, using protein-protein interaction networks. First order networks for chaperone proteins were created for two archaeal organisms, Picrophilus torridus and Sulfolobus solfataricus, which were compared to human chaperone network. Various statistics like degree distribution, betweenness centrality and bottleneck scores were used to predict hubs and essential proteins in these networks. We conclude that participants that are different between archaea and humans seem to play a more important role in controlling the human network rather than the common constituents. These results are expected to help researchers in generating new hypothesis regarding the protein folding machinery in archaea and to evaluate if these organisms can be used as model systems for addressing human protein folding diseases.

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