Centre for Biosystems Science and Engineering
Seminar

HLA polymorphism and disease susceptibility to H1N1 Influenza : A multi-scale modelling study

by

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Pathogenic viruses are often engaged in an arms-race with their hosts. They evolve rapidly, often under negative selection, leading to large pools of closely related viral strains, yet diverse enough to be differently virulent. Besides pathogen diversity, host genetic heterogeneity leads to different disease outcomes, affecting different human populations differently. Host responses are highly complex in nature and inadequately studied. Despite extensive work on influenza, a number of questions remain open pertaining to why individuals are differently susceptible to the disease. In this talk, the speaker will discuss how some of these questions could be answered through a multi-scale modelling approach.

HLA molecules and peptides present a complex molecular recognition pattern, as many peptides bind to a given allele and a given peptide can be recognised by many alleles. The talk will entail a discussion on a newly developed grouping scheme based on comparison of binding-site structures, which provides an insightful classification, rationalises the physicochemical basis of recognition specificity and how this has also led to the development of a sensitive predictor of HLA epitopes from genome sequences.

Finally, the speaker will discuss how large populations can be classified into a small number of groups called ‘response-types’, where each response-type theoretically sees a pathogen in the same way. Grouping is seen to be pathogen-specific and strain-specific, explaining why some strains are more virulent than the others. Overall, epidemic strains are predicted to have poor T-cell response in populations and an increase in genetic heterogeneity leads to lowering disease susceptibility.

About the speaker

Dr. Nagasuma Chandra obtained her PhD from the University of Bristol, UK for her work in the area of structural biology of enzymes and subsequently moved to the Indian Institute of Science, Bangalore to work structural biology of lectins, initially as a postdoctoral fellow, and subsequently starting her own research group in 1999. She is currently an Associate Professor at the Department of Biochemistry, Indian Institute of Science and additionally affiliated with BSSE and Mathematical biology initiatives at the institute. Her group applies systems biology approaches to study infectious diseases by using different types of molecular interaction networks at different levels ranging from the systems to protein structures.