Networks in M. tuberculosis: Deriving optimal strategies for drug discovery

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Tuberculosis continues to be a largest killer among infectious diseases, indicating an urgent need for newer and more effective drugs and newer approaches to discover them. Availability of the whole genome sequence and the resulting annotations as well as different types of '*omics*' scale experimental data have made it feasible to employ a systems approach so as to obtain a global view of the causative organism *Mycobacterium tuberculosis*. Systems biology has the potential to address several important issues that arise in drug discovery such as choice of the drug target, interaction between the drug, the target and the system as a whole, possible side effects and even more complex issues such as emergence of drug resistance.

In this talk, our recent work on constructing genome scale networks capturing metabolism and protein-protein influences in the organism will be presented. Analysis of these networks to identify strategies for efficient disruption of metabolism in the pathogen, as well as understanding metabolic adjustments upon drug exposure, will be discussed. The analysis of protein-protein influence networks for understanding possible routes of information flow for the emergence of drug resistance will be discussed. Finally, insights obtained from these studies for use in drug discovery will also be presented.