Computational Systems Biology of Pathogen–Host Interactions and Profiling Interaction between Prion and SOD1

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Introduction

Pathogens use Pathogen–Host Interactions (PHIs) to manipulate host cellular mechanisms in order to take advantage of host cell capabilities, resulting in infections. Because of the critical role of these interspecies molecular interactions in initiating and maintaining infections, a thorough understanding of the corresponding mechanisms is required. Unlike the traditional approach of considering the host or pathogen separately, a systems-level approach that considers the PHI system as a whole is required to elucidate infection mechanisms. PHI data have been produced on a large scale in the last decade as a result of technological advances in the post-genomic era. Because of the availability of omics data, systems biology-based methods for inference and analysis of PHI regulatory, metabolic, and protein–protein networks to shed light on infection mechanisms are becoming increasingly popular. The knowledge gained from PHIs may significantly contribute to the discovery of new and more effective therapeutics to prevent or cure infections [1].

Description

Pathogen-host interactions (PHIs) underpin the infection process. In understanding infection mechanisms, a systems biology view of the entire PHI system outperforms investigating the pathogen or host separately. The properties of the host factors targeted by pathogens are especially important in identifying host-oriented drug targets for next-generation anti-infection therapeutics. We present an overview of computational analysis of PHI networks, with a focus on the properties of pathogen-targeted host proteins. We also provide information about available PHI data and Web-based resources [2].

Every year, infectious diseases are one of the leading causes of death worldwide. Emerging and reemerging diseases, as well as drug-resistant pathogens, have exacerbated the situation for humans. As a result, novel therapeutic strategies are being developed to combat biological threats. These strategic solutions necessitate a systems biological approach that focuses on molecular interactions between pathogenic and host organisms to gain a thorough understanding of the underlying mechanisms of infections [3].

Together with computational methods for heterogeneous data management and integrative analysis via mathematical modelling, systems biology approaches with genome-wide molecular profiling using high-throughput techniques to generate omics data are changing the face of infection biology.

All subsequent molecular analyses and bioinformatics investigations of PHI systems are based on genomic information from the host and pathogen. As a result, genome sequencing is critical. It aids in pathogen typing, virulence and antibiotic resistance detection, and the development of new vaccines and culture media. Single Nucleotide Polymorphism (SNP) typing is important for identifying and characterising pathogen variants (strains, clinical isolates) as well as studying human susceptibility to certain infections. There has been, and will continue to be, an explosion of genome sequence data over the last decade [4].

Proteins play critical roles in PHIs, particularly in pathogen recognition and innate and adaptive immune responses. Pathogen-associated molecular patterns (PAMPs) are molecules or small molecular motifs found in pathogens such as the protein flagellin, lipopeptides, and lipopolysaccharide – LPS that are recognised by proteins known as pattern recognition receptors (PRRs). A description of pathogen proteomes and their interactions within the context of the human host by dedicated bioinformatic pipelines has a significant impact on both diagnostic and clinical treatment of the patient [5].

Future Perspective

On the computational side, PHI systems biology includes

- Modeling of molecular mechanisms of infections;
- Modeling of non-protective and protective immune defences against pathogens in order to generate data for potential immune therapy approaches;
- Modeling PHI dynamics and identifying biomarkers for infection diagnosis and individualised therapy;
- Identifying essential virulence determinants and host factors, and thus predicting potential drug targets
- Understanding of PHIs, particularly the immune system and pathogen immune evasion, as a result of long-term evolutionary adaptation and selection.

References

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