1. Record Nr. UNINA9910220037403321

Autore	German Bou
Titolo	Proteomics of Microbial Human Pathogens
Pubbl/distr/stampa	Frontiers Media SA, 2017
Descrizione fisica	1 electronic resource (152 p.)
Collana	Frontiers Research Topics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia

Sommario/riassunto

According to the World Health Organization (WHO), in 2012 infectious diseases and related conditions account for more than 70% of premature deaths across 22 African countries and estimated 450 000 people worldwide developed multi-drug resistant tuberculosis. This alarming situation, of great public health concern, calls for the urgent development of novel and efficient responding strategies. The employment of important research platforms, such as genomics and proteomics, has contributed significant insight into the mechanisms underlying microbial infection and microbe-host interaction. In this Frontiers Research Topic, we aim to produce a timely and pertinent discussion regarding the current status of “Proteomics of microbial Human pathogens” and the role of proteomics in combating the challenges posed by microbial infection and indeed acquired anti-microbial resistance. As the field of proteomics progressed from 2-DE gel based approaches to modern LC-MS/MS based workflows, remarkable advances have been reported in terms of data quantity and quality. Given the immediate and enormous advantages that high resolution and accurate mass spectrometers have brought to the field, proteomics has now evolved into a robust platform capable of generating large amounts of comprehensive data comparable to that reported previously in genomics studies. For example, detection of the complete yeast proteome has been reported and other small proteomes, such as those of bacteria, are within reach. Mass

spectrometry-based proteomics has become an essential tool for biologists and biochemists, and is now considered by many as an essential component of modern structural biology. Additionally, the introduction of high-resolution mass spectrometers has driven the development of various different strategies aimed at accurate quantification of absolute and relative amount of protein(s) of interest. Emerging targeted mass spectrometry methodologies such as; Selected Reaction Monitoring (SRM), Parallel Reaction Monitoring (PRM) and SWATH, are perhaps the latest breakthrough within the proteomics community. Indeed, through a label free approach, targeted mass spectrometry offers an unequalled capability to characterize and quantify a specific set of proteins reproducibility, in any biological sample. Usefully, Aebersold and colleagues have recently generated and validated a number of assays to quantify 97% of the 4,012 annotated Mycobacterium tuberculosis (Mtb) proteins by SRM. As such, the Mtb Proteome library represents a valuable experimental resource that will undoubtedly bring new insight to the complex life cycle of Mtb. Finally, as reviewed recently in Frontiers Research Topic, mass spectrometry-based proteomics has had a tremendous impact on our current understanding of post translational modification (PTM) in bacteria including the key role of PTMs during interaction of pathogenic bacteria and host interactions. We believe that our understanding of microbial Human pathogens has benefited enormously from both 2-DE gel and modern LC-MS/MS based proteomics. It is our wish to produce an integrated discussion surrounding this topic to highlight the existing synergy between these research fields. We envisage this Research Topic as a window to expert opinions and perspectives on the realistic practicalities of proteomics as an important tool to address healthcare problems caused by microbial pathogens.