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Integrating Omics Technologies for Prospective Antimicrobial Drug Development

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Infectious diseases remain a serious global public health threat. Increasing frequencies of deadly infections caused by microbial pathogens and their rapid resistance development to existing antibiotics in market makes the treatment procedure less effective, which underscore the need for vigilance in continuing war against the microbial pathogens[1]. The drug discovery effort needs high throughput and novel technologies to keep up with the emerging problem of antimicrobial drug resistance. Several tools have been implemented in drug discovery and development process. However, controversies concerning with high throughput drug screening, difficulties in characterizing drug actions, cost effectiveness of antimicrobial drug research have hindered the drug discovery processes[2]. During recent years, omics technologies have revolutionized the field of cellular and molecular biology, which fostered great hopes in antimicrobial research[3]. Omic technologies have broad range of applications that primarily involved mining of genes (genomics), mRNA (transcriptomics), proteins (proteomics) and metabolites (metabolomics). The routine implementation of high throughput omic tools have made significant achievements in antibiotic research, which led to development of tremendous genetic and molecular approaches that help us to gain deeper understanding of diverse range of microbial species, microbial physiology, metabolic functions and number of cellular events such as DNA synthesis, transcription, translation, secretion, cell division, etc[4].

Genomic and transcriptomic research has progressed due to advances in Next-generation sequencing (NGS) and microarray technologies that led to development of numerous databases which contains both genomic sequence and functionality information's readily accessible by researchers. The availability of those information's for all microbial species including pathogens in databases allows the use of comparative genomics and genome mining tools to enlist gene candidates that represent potential targets for broad- (or) narrow- spectrum antibiotics[5,6]. Thus, genome mining and comparative genomics offers an attractive platform to explore the unrevealed biosynthetic potential in sequenced microbial genomes and getting insight into novel antimicrobial drug targets. Furthermore, analyzing changes in the expression pattern of genes in response to antimicrobial drug at the level of transcriptome may precisely define the antimicrobial action of the drug. Moreover, identifying unique signatures of differential gene expression in response to antimicrobial drugs led to deeper understanding of resistomes that influences antimicrobial resistance mechanisms in microbial pathogens. And also, the list of genes in microbial genomes identified by genomic or transcriptomic approaches as relevant potential antibiotic targets can be further validated by gene knockout studies to find their real utility as potential targets for antibiotic development[7,8].

Metabolomics and proteomic research has progressed with advances in mass spectrometry and 2 dimensional gel electrophoresis that offers an attractive and promising tools to uncover novel drug targets, identify new source of bioactive proteins or compounds, characterize drug actions and discover new biomarkers in monitoring the health status of patients[6,9]. Metabolomics

approaches uses synthetic biology technologies allowing the identification of DNA sequences that encode secondary metabolites of natural origin. Metabolomic approaches offer powerful tools for drug discovery processes and are helpful in measuring the metabolic effect of bioactive molecules with diverse mechanism of actions. This approach has also been proven to be useful in classification of different antimicrobial substances, prediction of drug interactions and design of new approaches for antimicrobial therapy[10]. Proteome are dynamic entities that changes rapidly in responding to environmental conditions. Analyzing changes in the expression pattern of protein in response to antimicrobial drug at the level of proteome may define the physiological functions targeted by respective antibiotics. Moreover, the collection of diverse expression profiles of proteome aids in identification and characterization of drug-responsive regulatory networks, which helps in prioritizing antimicrobial drugs with respect to their selectivity and specificity during the drug discovery process[11].

During recent years, omics technologies have become more powerful tools in fostering our knowledge towards prospective antimicrobial drug development. Therefore, integrating omics technologies including genomics, transcriptomics, proteomics and metabolomics would provide new direction that influences the field of antimicrobial research and facilitates the discovery of novel drug candidates in near future to combat emerging infectious diseases.

Conflict of Interest: The author declare no conflict of interest

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