

Editorial

Metabolomics Usefulness in Mosquito Borne Infectious Disease

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EDITORIAL

Metabolism is an important biological process in any living things. The normal physiology links to normal metabolism whereas the disease and pathology is usually related to abnormal metabolism. Hence, understanding metabolism is a basic step for understanding any disease. To study metabolism, the classical way is based on the classical physiological and biochemical approach. That approach requires times and attempt in *in vitro* and *in vivo* studies. Due to the influx of new biomedical technology, *in silico* approach becomes the new approach in medicine. The bioinformatics is the approach based on computational approach and is the direct way for the *in silico* study. There are many new bioinformatics techniques such as genomics and proteomics. Of several new bioinformatics, the metabolomics is the new omics science focusing on metabolism via computational analysis of metabolome. Metabolomics is an important new bioinformatics technology that can be applied in medicine. The tracking on metabolism is the main approach of metabolomics that can be useful for diagnostic and therapeutic purpose. The application in tropical medicine is possible. The usefulness of metabolomics in mosquito borne infectious disease should be mentioned. Birungi et al., mentioned for the “application of metabolomics to improve understanding of the effect of dengue infection on endothelial cells’ metabolome [1].” With use of metabolomics, “expressive predominancy of amino acids, organic acids, carbohydrates, nucleosides, lipids, fatty acids, and derivatives” can be studied [2].

The good example is the use of metabolomics in dengue. The identifications of metabolome by metabolomics technique can help better understand the pathophysiology of dengue [3] as well as difference of clinical feature among different groups of patients [4]. The approach can be useful for finding new diagnostic and therapeutic tools. For example, Voge et al., recently purposed the finding of biomarker from using metabolomics approach [5]. In another study, Shrinet et al., performed a serum metabolomics analysis of patients with chikungunya and dengue mono/co-infections and could finding distinct metabolite signatures in the three disease conditions [6]. The use of metabolomics is also the basic approach for finding new vaccine [7]. Similar to dengue, there are also many new interesting reports on metabolomics study for malaria. The use of metabolomics in study of

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pathophysiology and finding new diagnostic and therapeutic approach of malaria can be seen in the many publications [8,9]. The clarification of pathogenesis of malaria as well as host response to the infection by metabolomics approach is possible [10]. The good example is the report on using metabolomics for clarification of the drug resistance phenomenon in malaria [11]. It is no doubt that metabolomics approach is useful in study on mosquito borne infectious disease. In the present day, due to the improved computational technology, the new online tool is already available for metabolomics analysis and can be approach for the case of mosquito borne infectious disease. The good example is the new online tool namely “Met Tailor [12].” The example of using this new tool on dengue was recently reported in the publication by Chen et al. [12].

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