XU ZHANG, Southwest University, China

Identifying candidate diagnostic markers for tuberculosis: a critical role of co-expression and pathway analysis

We conducted a systematic bioinformatics analysis to explore an important set of gene expression data with 39 samples infected at different time stages with W- Beijing families of Mycobacterium tuberculosis strains. We took a contrast on the samples at different infection time stages to characterize gene expression features of the THP1 cells to identify sensitive and specific molecular markers for diagnosis. We first confirmed, through the multidimensional scaling unsupervised clustering, that samples were clustered well according to different infection times. Building on this classification result and using the linear modelling and empirical Bayes moderation, we found 287 hits as most significant genes associated with tuberculosis. We generated a gene co-expression network map based on the mutual regulation between the differentially expressed genes. We found that 27 genes are regulatory genes associated with tuberculosis. We constructed 4 gene pathway figures to explain the pathogenicity process that involves 24 key genes. This study implicates that contrast on the gene expression of the classifications in different infection stages provides critical information for the detection of tuberculosis, and our method can be utilized to narrow down the shortlist of disease relevant genes and explore tuberculosis pathogenesis.