NETWORK IDENTIFYING PATHOGENIC BIOLOGICAL EVENTS IN KIDNEY STONE

Lu Xiuli, Gao Bing, Yang Baoyu, Mao Jing and **Zhang Weiwen**
Liaoning University, China

A large number of promising genes/proteins have been found to be related to the kidney stone formation. Identifying highly pathogenic biological events in these candidates will advance our understanding of kidney stone formation. We performed protein-protein interaction (PPI) networks analysis by integrating datasets from four genome-wide association studies (GWAS), a microarray study and a urine proteomics study. Highly connected genes/proteins were calculated to construct corresponding direct network, respectively. Permutation tests were performed to evaluate the networks reliability. Backbone networks were extracted to acquire essential genes/proteins for functional enrichment analysis. Overlaps were performed to identify accumulations of abnormal genes, biological processes (BPs) and pathways. We found that the abnormal accumulation were overlapped at three genes, in two pathways and in five BPs. Abnormal changes accumulated in these genes, pathways and BPs may increase risk of stone formation. Our findings provide valuable information for screening potential biomarkers and further clarifying kidney stone formation mechanism.

BIOGRAPHY

Lu Xiuli has completed her PhD at the age of 31 years from Nagoya University, Japan. She is the professor of Liaoning University, China.

Luxiulidr@gmail.com