

Application of Bioactivity Database of Traditional Chinese Medicine on the Therapeutic Prediction, Drug Development, and Safety Evaluation

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Background & Aim :

Traditional Chinese medicine (TCM) has been used for the treatments of various diseases for years. However, it is often difficult to analyze their biological activities and molecule mechanisms because of their complex nature. In this study, we applied DNA microarray to analyze the biological events induced by herbal formulae, herbs, herbal compounds, or acupuncture, and predict the therapeutic potentials of TCM.

Materials & Methods :

Mice were administrated orally with Chinese herb or treated with acupuncture for 7 consecutive days. The gene expression profiles in liver or kidney were further analyzed by transcriptomic tools.

Results :

Our data showed that TCM altered the metabolic pathways, such as glutathione metabolism and oxidative phosphorylation, and regulatory pathways, such as antigen processing and presentation and insulin-like growth factor signaling pathway. By comparing the gene expression signatures of TCM treatment with those of disease states or drugs, we found that mice responsive to TCM treatments might be related to disease states, especially metabolic and cardiovascular diseases, and drugs, which exhibit anti-cancer, anti-inflammatory, and anti-oxidative effects.

Conclusion :

This report applied transcriptomic tools as a novel platform of translational medicine for TCM. This platform can be further used for understanding the therapeutic mechanisms and providing the new theories in drug discovery.

Keywords:

Traditional Chinese medicine, Transcriptomic, Gene expression profile.