Editorial

Network Pharmacology Analysis: A Promising Approach for the Research of Traditional Chinese Medicine

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Network pharmacology is a new strategy to explore the molecular mechanisms underlying the action of traditional Chinese medicine (TCM) formula by analyzing the biological network of multi-biological processes and signaling pathways, and identifying the key components of druggable targets.[1,2] Network pharmacology approaches have been applied in elucidation of the potential therapeutic effects and action of TCM in several chronic diseases, such as chronic kidney disease, diabetes, rheumatoid arthritis and cancer.[1,3] Using network pharmacology analysis, Peng[4] predicted that Xia Sang Ju (XSJ) granule, a traditional TCM, might exert its anti-hypertensive effects by targeting 11 genes, among which *ESR2* and *SLC6A2* were the uppermost hypertension-related targets. The author further revealed that XSJ might affect multi-biological processes and multi-pathways to prompt their anti-hypertensive effects, which coincided with the TCM formula's therapy concept of multiple compounds, targets, and pathways.[4]

The findings open new avenues for the application of network pharmacology in the study of TCM formula. With the concept of integrity, comprehensiveness and systematic approach, network pharmacology provides new strategies and approaches for the study of TCM formula, because it may change TCM from experience-based medicine to evidence-based medicine.[2] However, we have to understand that current network pharmacology has limitations. First, the results of network pharmacology analysis are affected by the accuracy and integrity of the related databases. In addition, the efficacy of a TCM formula is dependent on the levels of absorbed constituents *in vivo*.[5,6] Thus, it would be more credible and complete if the compounds of XSJ selected in the study were screened from the serum samples for pharmacological experiments. Second, the data from network pharmacology analysis are predictive and static.[2] Although the study validated by a virtual strategy, the results still need further experimental validation *in vivo* or *in vitro* to exclude potential false positives and observe the dynamic process of XSJ for anti-hypertensive actions. Third, the research on TCM formula employed network pharmacology and mainly provided qualitative analysis results, and there was little reported on the quantity of these constituents.[2] In the future, how to achieve a quantitative analysis will be a new challenge for the development of network pharmacology.

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Conflict of interest

The authors declare that they have no competing interests.

Author contributions

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Abbreviations: TCM, traditional Chinese medicine; XSJ, Xia Sang Ju.

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