Abstract

Diabetes mellitus is currently the fastest growing chronic disease in the world, its serious complications have caused substantial amount of financial burden in the healthcare sector. *Polygonum cuspidatum* has been commonly used for medical treatment among the Asian population. The stem and root has been known to exhibit anti-cancer property and the ability to attenuate diabetes related complications. Nonetheless, the active compounds of *P. cuspidatum* are still yet to be identified; thus, the objective of this study is to apply the principles of network pharmacology to promptly identify the most promising candidates from *P. cuspidatum* as well as understanding their functions respectively. Network pharmacology is an approach to determine the process of disease development through understanding the system biology and bioworknet of the disease. Furthermore, by understanding the signal transduction pathways and how the compounds modulate the system, this will help to restore the balance in the affected biological processes, improve the efficacy of the compound and reduce its side effects. Using the Traditional Chinese Medicine Integrative Database, 46 compounds were identified in *P. cuspidatum* and bibliometrics was applied to measure the correlation between the compounds and diabetes. Among the 46 compounds, there were six compounds that showed clear correlation with diabetes, namely resveratrol, gallic acid, catechin, quercetin, rhein and apigenin. These compounds will be evaluated in the later stage to fully understand the active compounds from *P. cuspidatum* that could potentially improve the complications of diabetes, and ultimately be used clinically on diabetic patients.

Results

The use of network pharmacology may provide a cost-effective way of identifying herbal medicines that might be highly effective against DM or those containing minimal side effects. On the other hand, utilizing more data sources and statistical software/methods is essential in assisting the identification of active compounds and their predicted functions against targeted diseases. Lastly, inclusion of in vitro and in vivo experiments could also help to verify the effectiveness of the compounds against the target proteins of each disease; hence, achieving the aim of increasing efficiency in drug development.

Conclusion

The use of network pharmacology may provide a cost-effective way of identifying herbal medicines that might be highly effective against DM or those containing minimal side effects. On the other hand, utilizing more data sources and statistical software/methods is essential in assisting the identification of active compounds and their predicted functions against targeted diseases. Lastly, inclusion of in vitro and in vivo experiments could also help to verify the effectiveness of the compounds against the target proteins of each disease; hence, achieving the aim of increasing efficiency in drug development.