

Original Article

Usefulness of ginseng in management of dengue: a bioinformatics pathway interrelationship analysis

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Abstract: Objective: The function of traditional herbs in tropical illness therapy is interesting. Many researches are currently being conducted on the effects of traditional herbs on a number of tropical ailments, including dengue fever. Methods: In this short paper, we used network pharmacology to determine a shared biological pathway for the pharmacological impact of ginseng, a traditional Asian herb, and the pathophysiological process of dengue fever, a serious tropical vector-borne disease. Results: Using interrelationship analysis, the authors were able to discover the common pathway via the vimentin node. Conclusion: It's possible that ginseng could help in dengue fever therapy.

Keywords: Dengue, ginseng, effect

Introduction

The role of alternative and complimentary medicine is presently acceptable. There are several traditional medical systems available at this moment. The use of traditional herbs is a frequent practice in traditional medicine. The use of traditional plants in the treatment of tropical illnesses is fascinating. Many plants are regarded to be helpful in the treatment of various illnesses.

Many recent researches on the benefits of traditional herbs on a variety of tropical ailments, including dengue fever [1, 2], have been published. We conducted a network pharmacology study in this short study to determine the shared biological pathway for the pharmacological impact of ginseng, a traditional Asian plant, and the pathophysiological process of dengue fever, an important tropical mosquito-borne disease. Interrelationship analysis allows the authors to demonstrate the common pathway via the vimentin node. It's possible that ginseng could help in dengue fever therapy.

Materials and methods

This work is a clinical informatics study. The biological process network analysis was done. The effect of the classical tradition herb in Asia

evaluated for its connection with the pathophysiological process of dengue, an important tropical vector-borne infection, based on the notion of network pharmacology [3, 4]. The information in biological processes regarding ginseng and dengue was derived from direct database mining using standard international databased, PubMed and SCOPUS. The in silico bioinformatics protocol used in this study is identical to that used in the prior paper [5].

This in silico medical informatics study started from data extraction from international databases. First, published data on the pharmacobiological actions of ginseng and pathophysiological action of dengue were searched from standard databases. International databases such as PubMed (www.pubmed.com) and Scopus (www.scopus.com) were used. The key words "dengue" and "ginseng" were used to recruit publication for further analysis process. All derived publications are extracted for details of pathological/pharmacology processes. The derived pathological/pharmacological processes reported in recruited publications were collected and used for further interrelationship analysis.

For interrelationship analysis, a common pathopharmacological pathway determination was

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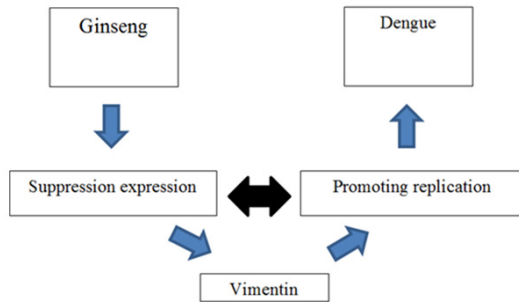


Figure 1. Interrelationship network showing the interrelationship between pharmacological process of ginseng and pathophysiological process of dengue at vimentin.

firstly done. The technique is based on bioinformatics analysis, finding the verbatim word by word matching of described pathological/pharmacology processes in the literature. In terms of the technique, the identified biological processes, both ginseng's pharmacological and dengue's pathophysiological processes, were enumerated and a common pathway was sought using a standard procedure as described in the referencing publication [5]. In brief, the obtained pharmacological actions of ginseng and pathophysiological actions of dengue were reassessed for identifying common biological pathways. A shared node is attributed to both dengue and ginseng's common cross processes. The common node is discovered and used to build the final interrelationship network by adding connection pathways to the discovered common node. The network pathway diagram depicting the association between pathological/pharmacology processes and dengue is derived after the final building of the common pathway with common node connectivity. The conclusion is based on the final network pathway diagram produced from the *in silico* network research discussed above.

Results

According to the findings, vimentin is a common connection between the pharmacological and pathophysiological processes of ginseng and dengue fever. From further interrelationship network analysis, the final interrelationship network is presented in **Figure 1**.

Discussion

Bioinformatics clinical pharmacology network analysis is useful for evaluating the effects of

traditional herbal regimens [6-8]. The method is based on informatics analysis, which entails finding paths, identifying common nodes, rearrangement, and eventually the construction of an interrelationship network. This is the standard clinical informatics analysis used in earlier studies [5, 9, 10]. In this short preliminary study, the authors conduct a preliminary investigation to determine the efficacy of ginseng, a well-known plant, in the treatment of dengue fever, an important tropical blood infection.

Ginseng is a well-known Chinese herb in clinical pharmacology. Its role in antibacterial management is widely studied and confirmed [11, 12]. Some reports suggest ginseng's antiviral potential in relation to the influenza virus [13]. Additional animal investigations have revealed that ginseng may have antiviral properties against circovirus [14], bovine viral diarrhea virus, and classical swine fever virus [15]. There is a scarcity of information regarding arbovirus infection. The current study provides preliminary evidence of ginseng's potential utility in the treatment of dengue fever. According to the findings, there is a common node at vimentin between the pharmacological process of ginseng and the pathophysiological process of dengue. Vimentin is a key target for antiviral medication therapy, and novel drugs targeting vimentin are now being developed [16]. Vimentin expression is known to be reduced by ginseng [17]. Meanwhile, in dengue fever, the utilization of vimentin in the replication process is a critical pathogenic event [18, 19]. It is possible that ginseng has an anti-dengue action, making dengue a valuable traditional herb for dengue management.

The usage of traditional plants is, indeed, an intriguing topic for ethnopharmacology research. Some studies show that ginseng is effective in treating malaria, a common mosquito-borne infection [20, 21]. The current study adds to the growing body of evidence that ginseng may be effective in the treatment of dengue fever. The current medical informatics study can provide basic data for future *in vitro* and *in vitro* research on ginseng's anti-dengue impact. The basic nature of *in silico* bioinformatics research is a significant limitation/deficiency of the current work. This study's findings are all based on *in silico* prediction. It is currently unconfirmed and insufficiently rigorous to draw solid conclusions, but it provides useful information for further research into the

subject. According to the current informatics study, ginseng has an effect on lowering vimentin expression, and dengue has a pathological process that uses vimentin in the replication process. However, without particular scientific data to back it up, ginseng will not be a beneficial traditional herb for the treatment of dengue fever. For the early in silico study to be supported, more in vitro and in vivo studies are required. Conceptually, this study is an in silico study, which is a common bioinformatics technique; consequently, more in vitro and in vivo experiments are required to reach a final result. Updated Chinese medicine guidelines (2018 and 2021 versions) now encourage utilizing ginseng as part of a herbal combination with other Chinese herbs in the treatment of dengue fever, particularly during the recovery period [22, 23].

Conclusion

At vimentin, the pharmacological process of ginseng and the pathological process of dengue have a common node. It can show that ginseng has pharmacological actions that can help to reduce the dengue virus. As a result, ginseng may be an effective traditional treatment for dengue fever. Nevertheless, the results of this research are based on bioinformatics prediction. Due to the limitation resulting from the nature of in silico study, further research support is required for obtaining a reasonable and rigorous conclusion. As a result, more research into the use of ginseng in the treatment of dengue fever is needed.

Disclosure of conflict of interest

None.

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