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Contents

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1. Traditional Chinese Medicine in the Treatment of Patients Infected with 2019-New Coronavirus (SARS-CoV-2): A Review and Perspective

Yang Yang,[*] Md Sahidul Islam,[*] Jin Wang, et al . *Int J Biol Sci.* 2020; 16(10): 1708–1717. ✉

 Abstract:

Currently, Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2, formerly known as 2019-nCoV, the causative pathogen of Coronavirus Disease 2019 (COVID-19)) has rapidly spread across China and around the world, causing an outbreak of acute infectious pneumonia. No specific anti-virus drugs or vaccines are available for the treatment of this sudden and lethal disease. The supportive care and non-specific treatment to ameliorate the symptoms of the patient are the only options currently. At the top of these conventional therapies, greater than 85% of SARS-CoV-2 infected patients in China are receiving Traditional Chinese Medicine (TCM) treatment. In this article, relevant published literatures are thoroughly reviewed and current applications of TCM in the treatment of COVID-19 patients are analyzed. Due to the homology in epidemiology, genomics, and pathogenesis of the SARS-CoV-2 and SARS-CoV, and the widely use of TCM in the treatment of SARS-CoV, the clinical evidence showing the beneficial effect of TCM in the treatment of patients with SARS coronaviral infections are discussed. Current experiment studies that provide an insight into the mechanism underlying the therapeutic effect of TCM, and those studies identified novel naturally occurring compounds with anti-coronaviral activity are also introduced.

2. Traditional Chinese medicine for treatment of coronavirus disease 2019: a review

Abstract

Since late December in 2019, the coronavirus disease 2019 has received extensive attention for its widespread prevalence. A number of clinical workers and researchers have made great efforts to understand the pathogenesis and clinical characteristics and develop effective drugs for treatment. However, no effective drugs with antiviral effects on severe acute respiratory syndrome coronavirus 2 have been discovered currently. Traditional Chinese medicine (TCM) has gained abundant experience in the treatment of infectious diseases for thousands of years. In this review, the authors summarized the clinical outcome, pathogensis and current application of TCM on coronavirus disease 2019. Further, we discussed the potential mechanisms and the future research directions of TCM against severe acute respiratory syndrome coronavirus 2.

3. Traditional Chinese medicine for novel coronavirus pneumonia treatment: main force or supplement?

Abstract

The nationwide death toll from the coronavirus outbreak in China has risen to 491, with nearly 24,363 individuals infected, according to official figures released on February 5, 2020 . With no proven drugs to treat the infection caused by the deadly coronavirus, China's top health organization has advised hospitals to use various treatments, including traditional Chinese medicine (TCM) and artificial lungs, to tackle it.

4. **Medical workers in traditional medicine who sacrificed their lives in the battle against COVID-19 deserve to be remembered forever**

Key words: Medical workers

Abstract

China held a national day of mourning on April 4, 2020 to commemorate 3,335 victims of the COVID-19 outbreak, including medical workers who sacrificed their lives in the battle against the epidemic. April 4 was also Tomb-sweeping Day in China, known as the Qingming Festival, it is an important occasion for the Chinese to visit cemeteries, clean tombs, and mourn their ancestors.

5. Overview of the plague in the late Ming Dynasty and its prevention and control measures

Key words: Late Ming dynasty   Plague   Infectious diseases   Traditional Chinese medicine   Prevention and control

Abstract

The plague of the late Ming Dynasty (1551-1644 C.E.) was long lasting, affected a wide range of the population, and had serious consequences. The purpose of this study is to review the medical system in place at the time and the measures instituted to prevent and control the plague during the late Ming Dynasty. Information on the history of the Ming Dynasty (1368-1644 C.E.), local chronicles, and related research literature were consulted and analyzed in terms of duration, geographical area, and other dimensions of the epidemic. Because of the abnormal climate, wide range of natural disasters, and the impact of war, the epidemic spread over a wide area during the late Ming Dynasty. The government's epidemic prevention measures were affected by war and other factors, resulting in poor control of the outbreak. However, in terms of the medical system in place during the Ming Dynasty, some of the thinking and methods of prevention and control of the plague were historical and progressive. Some outstanding physicians such as Wu Youke (1582-1652 C.E.) appeared during this period. His theory of plague prevention and control had a profound influence on the formation and development of pestilence deterrence in later generations. In the late Ming Dynasty, rich experiences and measures of prevention

and control were accumulated in the struggle against the plague. These methods and experiences also have a significant, positive guiding influence on the prevention and control of plague in the present day.

6. Network pharmacology studies on the effect of Chai-Ling decoction in coronavirus disease 2019

Abstract

Background: Chai-Ling decoction (CLD), derived from a modification of Xiao-Chai-Hu (XCH) decoction and Wu-Ling-San (WLS) decoction, has been used to treat the early-stage of coronavirus disease 2019 (COVID-19). However, the mechanisms of CLD in COVID-19 remain unknown. In this study, the potential mechanisms of CLD in COVID-19 were preliminarily investigated based on network pharmacology and molecular docking method. **Methods:** Initially, the active components and targets of CLD were screened based on Traditional Chinese Medicine Systems Pharmacology Database and Analysis Platform and PharmMapper database. The targets of COVID-19 were obtained from GeneCards database. The protein-protein interaction network was established using STRING database to analyze the key targets. Gene Oncology (GO) analysis and Kyoto Encyclopedia of Genes and Genomes analysis were also conducted to evaluate the pathways related to the targets of CLD on COVID-19. Moreover, the compound-target-pathway network was established using Cytoscape 3.2.7. Subsequently, the molecular docking method was performed to select the active compounds with high binding affinity on severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and angiotensin-converting enzyme 2 (ACE2), which is the key target of SARS-CoV-2 in entering target cells. The possible binding sites were also visualized by a three-dimensional graph. **Results:** Network pharmacology analysis showed that there were 106 active components and 160 targets of CLD. Additionally, 251 targets related to COVID-19 were identified, and 24 candidates of CLD on COVID-19 were selected. A total of 283 GO terms of CLD on COVID-19 were identified, and 181 pathways were screened based on GO and Kyoto Encyclopedia of Genes and Genomes analyses. CLD might alleviate the inflammatory response and improve lung injury to treat COVID-19 through interleukin 17 signaling, T helper cell 17 differentiation, tumor necrosis factor signaling, and hypoxia inducible factor-1 signaling. Besides, molecular docking indicated that beta-sitosterol, kaempferol, and stigmasterol were the top

three candidates in CLD with the highest affinity to SARS-CoV-2 and ACE2. **Conclusion:** Our study identifies the potential mechanisms of CLD on COVID-19 and beta-sitosterol, kaempferol, and stigmasterol may be the key compounds that exert antiviral effects against SARS-CoV-2.

7. Can Yin-Chai-Xiao-Du decoction be useful of COVID-19? the mechanism research based on network pharmacology

Key words: Coronavirus disease 2019, Bupleuri radix, Scutellariae radix, Artemisiae annuae herba, Cytokine Storm, Tumor necrosis factor, Inteleukin-6

Abstract

Background: In this study, we preliminarily investigated the mechanism of Yin-Chai-Xiao-Du decoction for the treatment of COVID-19 by the method of network pharmacology. **Methods**: The potential targets and pathways of Yin-Chai-Xiao-Du decoction for the treatment of COVID-19 were examined using network pharmacology; the ingredient and active targets of Yin-Chai-Xiao-Du decoction were collected from the Traditional Chinese Medicine Systems Pharmacology Database and Analysis Platform and PharmMapper databases; the COVID-19-related targets were obtained from the online Mendelian inheritance in man, GeneCards, and GeneMANIA databases; the STRING database and Cytoscape were used to build a protein-protein interaction network, and a Network Analyzer tool was used to perform topology analysis to screen for the key ingredients and targets; the ClueGO and KOBAS 3.0 databases were for the enrichment analysis of gene function (Gene Oncology) and gene pathway (Kyoto Encyclopedia of Genes and Genomes); the herb-ingredient-target-pathway network diagram was constructed by Cytoscape. **Results**: The core herbs screened by the network pharmacological analysis were Jinyinhua (Lonicerae japonicae flos), Lianqiao (Forsythia suspensa), Chaihu (Bupleuri radix), Huangqin (Scutellariae radix), Yinchen (Herba Artemisiae Scopariae), Guanghuoxiang (Pogostemonis herba), Roudoukou (Semen myristicae) and Qinghao (Artemisiae annuae herba). A total of 293 active ingredients were screened by Traditional Chinese Medicine Systems Pharmacology Database and Analysis Platform, and the key ingredients were quercetin, kaempferol, isorhamnetin, stigmasterol, beta-sitosterol, and luteolin. Yin-Chai-Xiao-Du decoction has 138 COVID-19-related targets, and the key targets were mitogen-activated protein kinase 3, interleukin-6, tumor necrosis factor, vascular endothelial growth factor A, and CC motif ligand 2. Kyoto Encyclopedia of Genes and Genomes analysis revealed 120 enriched gene pathways, and the key pathways were signaling by interleukins, immune system, cytokine signaling in the immune system, and the signaling pathways of

6

interleukin-17, tumor necrosis factor, and relaxin. **Conclusion**: The core herbs of Yin-Chai-Xiao-Du decoction are Jinyinhua (Lonicerae japonicae flos), Lianqiao (Forsythia suspensa), Chaihu (Bupleuri radix), Huangqin (Scutellariae radix), Yinchen (Herba Artemisiae Scopariae), Guanghuoxiang (Pogostemonis herba), Roudoukou (Semen myristicae) and Qinghao (Artemisiae annuae herba). The key ingredients are quercetin, kaempferol, isorhamnetin, stigmasterol, and beta-sitosterol; the critical targets are luteolin, interleukin-6, mitogen-activated protein kinase 3, tumor necrosis factor, and CC motif ligand 2; and the core signaling pathways are those mediated by interleukin-17, tumor necrosis factor, and relaxin.

8. Treating COVID-19 by traditional Chinese medicine: a charming strategy?

Key words: COVID-19   Traditional Chinese medicine

Zhang, Y. L.; Zhang, W. Y.; Zhao, X. Z.; et al. *Traditional Medicine Research ; 5(4):178-181, 2020.*

Abstract

On April 14, 2020, the State Council of China announced that "three proprietary Chinese medicines and three decoctions" of effective traditional Chinese medicine (TCM) in the treatment of the novel coronavirus pneumonia have passed clinical practice screenings. Some scholars believe that early TCM intervention of mild and moderate cases and recovery period may reduce the ratio of mild cases progressing into severe and critical cases. Some data have also suggested that the combination of TCM and Western medicine may reduce the mortality rate in severe and critical cases.

9. India's indigenous idea of herd immunity: the solution for COVID-19?

Key words: Herd immunity   COVID-19

Ram Shepherd Bheenaveni[1*] (✉)   Bheenaveni RS. India's indigenous idea of herd immunity: the solution for COVID-19?. *Tradit Med Res*. 2020;5(4):182–187.

Abstract

Based on folklore and traditional wisdom, when a shepherd purchases a few new sheep from an unknown seller or from a distant place, he keeps them away from his old flock of sheep for a period of 15 days. This, in other words, is a unique practice of herd quarantine. The new flock is permitted to mingle with the old flock only after the completion of the prescribed quarantine period. In case

someone tries to violate the principle of herd quarantine, the herd council will impose a rigorous punishment.

10. Efficacy of Xuebijing injection for the treatment of coronavirus disease 2019 via network pharmacology

Yu-Liang Zhang[1], Qian Cui[1], Dou Zhang[1], et al. Efficacy of Xuebijing injection for the treatment of coronavirus disease 2019 via network pharmacology. *Tradit Med Res.* 2020;5(4):201–215.

Abstract

Background: To evaluate the mechanism of Chinese patent drug Xuebijing (XBJ) injection in the treatment of a new coronavirus disease 2019 (COVID-19) based on network pharmacology and molecular docking technology. **Methods:** The TCMSP database was employed to collect and screen the active ingredients of the Chinese herb contained in the XBJ injection. The GeneCards database and STRING database were applied to collect and expand the targets of COVID-19 and compare and screen the related targets of COVID-19 by XBJ injection. Cytoscape was employed to build a network connecting Chinese medicine, compounds, targets, disease, and topology analysis was performed via the Network Analyzer to screen the key ingredients and targets. The software of Schrödinger molecular docking was used to verify the binding activity of the key ingredients of XBJ injection and the key targets of COVID-19. Metascape platform and DAVID database were utilized to conduct Gene Ontology analysis and Kyoto Encyclopedia of Genes and Genomes analysis on the key targets of COVID-19 treated by XBJ injection. **Results:** Eight key compounds and 15 key targets were screened and verified by molecular docking; these key compounds included luteolin, quercetin, baicalein, and kaempferol. The key targets included DPP4, AR, ESR1, CALM1, and protein kinase 1. Gene Ontology analysis involved an apoptosis and hypoxia reaction and the changes in blood vessel morphology. Kyoto Encyclopedia of Genes and Genomes analysis involved signaling pathways of hypoxia inducible factor-1, VEGF, and PI3K/AKT/NF-κB. **Conclusion:** The mechanism of XBJ injection when used to treat COVID-19 should be further investigated as the key compounds in XBJ regulated the expression of key targets such as protein kinase 1, VEGF-A, B-cell lymphoma-2, and TNF, which affected the COVID-19 receptors such as angiotensin-converting enzyme 2 and signaling pathways like hypoxia inducible factor-1, PI3K-Akt, and NF-κB, which alleviated the inflammation, respiratory distress, and hypoxia caused by COVID-19 infection.

In the COVID-19 period，all members of ATCM. Please pay an attention to safety ; and please protect yourselves and your families!

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