Atomic Docking demonstrated that Five Dynamic Fixings could Restrain IL-6 amp by Means of Dually Restricting to IL-6 and STAT3

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Introduction

COVID disease 2019 (COVID-19) keeps spreading globally. Chinese medicine (cm) exerts a critical role for the prevention or therapy of covid-19 in an integrative and holistic way. In any case, mining and development of early, efficient, multisite binding CMS that inhibit the cytokine storm are imminent [1]. The formulae were extracted retrospectively from clinical records in Hunan province. Clinical data mining analysis and association rule analysis were employed for mining the high-frequency herbal pairs and groups from formulae. Network pharmacology methods were applied to initially explore the most critical pair's hub targets, active ingredients, and potential mechanisms [2].

Description

The binding power of active ingredients to the hub targets was verified by molecular docking. COVID disease 2019 (covid-19), a pandemic caused by the severe acute respiratory syndrome coronavirus 2 (sars-cov-2), has spread rapidly worldwide. The ongoing pandemic has already placed a heavy burden on the global public health system, global economy, and social stability. Most covid-19 patients are moderate. Albeit some drugs and vaccinations have been recommended for use, new effective strategies are still being developed due to side effects, toxicity and allergic reactions [3].

Conventional Chinese medicine (TCM) is considered as an indispensable component in Chinese traditional medicine. In the early stage of covid-19 outbreak, TCM schemes have been recommended in the guidelines for covid-19. TCM mainly exerts the effect of anti-viral infection indirectly by regulating and restoring the equilibrium of the body's immune system. Utilizing of Chinese medicine was confirmed to be associated with regional cure rate in china. A series of clinical trials, case reports and observational studies confirmed the broad prospects of chinses medicines in preventing or treating covid-19 in different periods [4]. Integrative traditional Chinese and western medicine has been confirmed to significantly reduce recovery time and decrease the transfer rate from the mild to severe covid-19. Numerous herbal prescriptions showed excellent efficacy, for example, Lianhua Qingwen capsule, Qingfei Paidu decoction, Xuebijing injection and maxing Shigan decoction. These formulae play multiple roles through multi-targets and multi-pathways, including mostly antivirus, anti-inflammation and immunoregulation. In any case, the valuable Chinese medicines (CMS) pairs beneficial to COVID-19 and their pharmacological mechanisms remain to be thoroughly investigated [5].

Network pharmacology dedicated to connection of drugs, ingredients, targets and diseases, thereby describing the complex relationship between organisms, potential drugs and specific diseases. Without a doubt, it is a powerful tool for mining drug combinations, especially prescriptions of TCM. The mechanisms of CMS groups or prescriptions for the potential treatment of COVID-19 have been gradually uncovered by network pharmacology. ACE2 is a well-recognized therapeutic target for COVID-19. Sadly, ACE2 may no longer be an optimal target because of the potent chronic inflammation in the latter stage. During the inflammatory outbreak, the interleukin-6 (IL-6) family can activate the nf-κb pathway via signal transducer and activator of transcription 3 (STAT3), which further leads to the activation of IL-6 amplifier (IL-6 amp), forming a cascade of amplification loops, inducing a series of inflammatory and autoimmune disorders. A retrospective study reported that 15.3% (41/227) cases with moderate COVID-19 showed increased serum il-6. Amazingly, the proportion with above normal serum IL-6 increased as the diseases progress (severe: 49.25%; critical: 83.33%). The IL-6 elevation is observed very early after viral infection. In this way, drugs synergistically binding the il-6 and stat3 are crucial to block progress for moderate COVID-19

Conflict of Interest

The authors declare that there is no conflict of interest associated with this manuscript.

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