

## Short Review

### A Short Review Based on the Article Entitled “Network Pharmacology-Based and Molecular Docking-Based Analysis of *Cornus Officinalis* for the Treatment of Spinal Cord Injury”

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In this study, we utilized network pharmacology and molecular docking techniques to investigate the active ingredients and potential targets of *Cornus Officinalis*, a traditional Chinese herbal medicine, for the treatment of spinal cord injury. Eighteen active compounds, including tetrahydroalstonine and ethyl linoleate, were obtained from public databases and selected for further analysis. A total of 390 potential targets associated with the active ingredients of *Cornus Officinalis* were collected and predicted, among which 50 targets were found to be related to spinal cord injury, including AKT1, MAPK1, TNF, PTGS2, EGFR, and MMP9. The active compounds of *Cornus Officinalis* primarily exert their therapeutic effects on spinal cord injury through the MAPK pathway, HIF-1 pathway, calcium signaling pathway, and PI3K-Akt pathway. These active components of *Cornus Officinalis* demonstrate a strong affinity with the core targets involved in spinal cord injury. In conclusion, our findings indicate that *Cornus Officinalis* shows promising potential as a multi-target and multi-pathway treatment for spinal cord injury, highlighting its significant research value and prospects in this field.

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### Overview of Research Background and Purpose

Spinal Cord Injury (SCI) refers to the impairment of sensory and motor functions in the corresponding segments of the spinal cord due to trauma or endogenous factors [1]. SCI is characterized by a high incidence rate, high treatment costs, high disability rate, and low age of onset, resulting in significant physiological, psychological, and economic burdens on patients and their families. SCI can be divided into two stages based on the type of injury: primary SCI and secondary SCI. Primary SCI is mainly caused by mechanical damage resulting from traumatic violence, including vascular trauma rupture and immediate tissue swelling. Secondary SCI involves degeneration in blood supply, biochemical processes, and inflammatory cascade reactions, leading to neural dysfunction, such as disruption of the blood-spinal cord barrier, neuroinflammation, oxidative stress, and glutamate neurotoxicity [2,3]. Network pharmacology is a discipline that interprets the occurrence and development of diseases from the perspective of system biology and the balance of biological networks. It aims to understand the interaction between drugs and organisms and guide new drug discovery by improving or restoring the overall balance of biological networks [4]. By constructing networks based on the “multi-components-multi-targets-multi-pathways” concept, network pharmacology provides a more intuitive and clear understanding of the action mechanism and various physiological and pathological processes, making it advantageous for identifying the main active components and potential mechanisms of traditional Chinese medicine treatments [5,6]. Network pharmacology has been rapidly applied in various research fields, demonstrating its important theoretical and practical value. *Cornus Officinalis* is a traditional Chinese herbal medicine that has been found to possess anti-inflammatory, neuroprotective, and cognitive-enhancing effects in the treatment of neurological disorders [7,8]. In this study, we employed network pharmacology and molecular docking techniques to collect the active ingredients and potential targets of *Fructus Corni* and analyze its potential targets and mechanisms in the treatment of SCI.

### Research Summary and Outlook

The active constituents of *Cornus officinalis* and their corresponding target proteins were retrieved from the Traditional Chinese Medicine Systems Pharmacology Database and Analysis Platform (TCMSP). The target genes associated with the active constituents of *Cornus officinalis* were obtained from the UniProt Knowledgebase. Subsequently, the target proteins corresponding to the active constituents of *Cornus officinalis* were identified through the UniProt database, and their mapping with SCI genes was performed using the GeneCards and DrugBank databases. The Venny 2.1 tool was employed to analyze the intersection and target proteins involved in the treatment of spinal cord injury by the active constituents of *Cornus officinalis*. Additionally, a network depicting the interactions between the active constituents and their target proteins in *Cornus officinalis* was constructed using CytoScape 3.7.2 software. Furthermore, protein-protein interaction (PPI) networks illustrating the interactions between the target proteins and other proteins were established using the STRING platform and CytoScape 3.7.2 software.

The targets associated with the treatment of spinal cord injury by *Cornus officinalis* were analyzed utilizing the Metascape analysis platform, as well as GO analysis and KEGG pathway enrichment analysis. Ten key targets were identified among the 50 targets related to spinal cord injury, namely AKT1, MAPK1, TNF, PTGS2, EGFR, MMP9, APP, MTOR, ERBB2, and MPO. These targets are implicated in four major signaling pathways, including the MAPK pathway, HIF-1 pathway, calcium pathway, and PI3K-Akt pathway. The active constituents of *Cornus officinalis* exhibited strong affinity towards the core targets of spinal cord injury.

To conclude, our study provides a comprehensive overview of the active constituents of *Cornus officinalis* and their mechanisms of action in the treatment of spinal cord injury. This research offers valuable insights and directions for the development of these active constituents in the context of spinal cord injury treatment. Moreover, our findings serve as a theoretical foundation and reference for future investigations focused on the further development of the active constituents in *Cornus officinalis*.

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