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# Exploring the Mechanism of Tripterygium Wilfordii Treating Epilepsy based on Network Pharmacology

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*Methods:* TCMSP database was used to screen the active components and genes of Tripterygium wilfordii. On-line text mining server (GeneCards) was used to query epilepsy genes, and the genes of epilepsy and tripterygium wilfordii were standardized and intersected. The mapped genes were imported into Cytoscape software, and the relationship network of "drugs-ingredients-diseases-targets" was obtained. Based on David database, gene ontology (G0) function enrichment analysis and (KEGG) pathway enrichment analysis were performed on the target. And construct KEGG path relation network. On-line database String constructs protein-protein interaction PPI network, and imports relational network layout into Cytoscape software to obtain core sub-network. AutoDockTools and AutoDockVina software are used for molecular docking, and Pymol is used for docking visualization.

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Keywords: tripterygium wilfordii, epilepsy, network pharmacology.

GJMR-A Classification: DDC Code: 616.853 LCC Code: RC372

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*Results:* There are 21 kinds of active ingredients of Tripterygium wilfordii, including kaempferol,  $\beta$ -sitosterol, triptolide and other active ingredients. 72 cross genes were obtained. Through pathway construction and enrichment analysis, it was found that the potential mechanism may be related to cell proliferation, differentiation, apoptosis, GABA-mediated pathway and so on. The docking results showed that the binding energies of the core targets were all small-5 kcal mol-1, which indicated that there was a good affinity between genes and components.

*Conclusion:* Tripterygium wilfordii has the characteristics of multi-components, multi-targets and multi-pathways in treating epilepsy. It provides theoretical basis and basis for new drug development and experimental research.

Keywords: tripterygium wilfordii, epilepsy, network pharmacology.

# I. INTRODUCTION

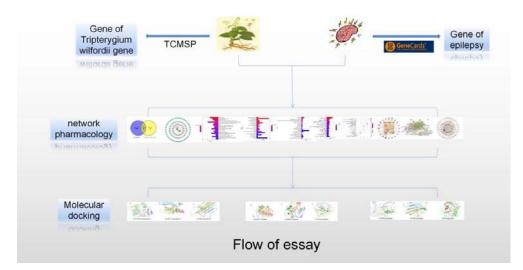
pilepsy is one of the most common chronic brain diseases affecting more than 70 million people all over the world. It greatly affects the quality of life of patients and poses a serious threat to their health [1-2]. At present, antiepileptic drug therapy is the most important clinical treatment scheme. Although it can alleviate the symptoms of patients, it can't inhibit the development of epileptic process, and long-term use will also cause various adverse reactions, which will also reduce the drug sensitivity [3]. For short-term clinical seizures of epilepsy,  $60\% \sim 70\%$  of patients can achieve seizure-free symptoms [4], but there is no satisfactory treatment plan for long-term treatment of epilepsy [5]. Therefore, it is of great clinical significance to develop drugs with high curative effect, good safety and little side effects and new treatment methods.

Traditional Chinese medicine (TCM) is effective in treating epilepsy, with few side effects and wide clinical application. Therefore, this study aims to explore the mechanism of TCM tripterygium wilfordii in treating epilepsy and provide new drug ideas for the treatment of epilepsy. It is a woody vine of Tripterygium wilfordii belonging to Celastraceae. It is cold in nature, bitter in taste and poisonous, and belongs to the four meridians of heart, liver, stomach and kidney. It has the effects of promoting blood circulation, removing blood stasis, clearing away heat and toxic materials, and is distributed in the middle and lower reaches of the Yangtze River [6]. It was first published in Shennong's Materia Medica, and is named Mangcao, which is mainly used for treating scalp wind, carbuncle, breast swelling and hernia [7]; There are detailed records in the Compendium of Materia Medica, which can treat swelling, edema, swelling, jaundice, chronic malaria, poison in the mouth of fish, etc [8]. Studies have shown that triptolide has protective effect on neurons of KAinduced epileptic rats [9]. Moreover, Tripterygium wilfordii polyglycoside can effectively improve the learning and memory ability of epileptic rats induced by PTZ, which is closely related to the up-regulation of Ng and PKC expression levels in hippocampus of rats [10]. Looking at the existing literatures about the effective components of Tripterygium wilfordii, it can be found that there is still a lack of overall and systematic understanding of the anti-epileptic mechanism of Tripterygium wilfordii. In this study, the target of Tripterygium wilfordii was found out through its active ingredients and fused with the epileptic target, and the potential target of Tripterygium wilfordii in treating epilepsy was obtained. The signal pathway or metabolic pathway related to Tripterygium wilfordii in treating

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epilepsy was obtained through function and pathway enrichment analysis, which provided a new idea and direction for comprehensively and systematically expounding the action mechanism of Tripterygium wilfordii in treating epilepsy.



# II. MATERIALS AND METHODS

#### a) Prediction of Active Components and Targets of Tripterygium wilfordii

The effective components and targets of Tripterygium wilfordii were searched in TCMSP database with keywords "tripterygium wilfordii", "leigongteng" and "thunder god vine". Taking oralbioavail-ability (OB)  $\geq$  30% and drug-likeness property (DL) $\geq$ 0.18[11] as screening criteria, the active ingredients of Tripterygium wilfordii were obtained. According to the active components of Tripterygium wilfordii, the corresponding target protein was predicted in TCMSP platform, and then the protein was imported into UniProt database (https://www.Uniprot.org/) for gene standardization.

#### b) Prediction of epileptic targets

Through the online text mining server Genecards (https://www.genecards.org/), the target of epilepsy is predicted, and the data is arranged and duplicated to get the target related to epilepsy.

# c) Prediction of Tripterygium wilfordii's effect on epileptic targets

The online software Venny2.1 (https://bioinfogp.cnb.csic.es/tools/venny/) was used to intersect the active components of Tripterygium wilfordii with epilepsy-related targets, and the potential targets of the interaction between Tripterygium wilfordii and epilepsy were obtained.

#### d) Build a "drug-ingredient-disease-target" relationship network

After arranging the active ingredients and potential targets of Tripterygium wilfordii, the network of "Tripterygium wilfordii-active ingredients-epilepsypotential targets" was initially obtained by guiding people to Cytoscape 3.9.0 software for visualization.

#### e) Gene Enrichment Analysis

David database was used to analyze the potential targets by GO and KEGG, and to explore the possible biological function and main signal pathway of Tripterygium wilfordii in treating epilepsy. In this study, the first 20 GO biological functions and KEGG enrichment pathways of enrichment results were selected by using P from small to large as screening conditions.

#### f) Construction of "Target -KEGG" Pathway Relationship Network

Import the KEGG path relationship file into Cytoscape 3.9.0 software, calculate the Degree value, and adjust the size of nodes according to the Degree value, and further obtain the "target -KEGG path" relationship network diagram.

#### g) Construction of Protein-Protein Interaction Network (Ppl Network)

In order to understand the interaction among proteins, the potential targets of Tripterygium wilfordii for epilepsy treatment were input into online database String(https://string\_db.org/) to construct a network, and the interaction network between potential target proteins was obtained. The tsv file of PPI network relationship was obtained, and the file was imported into Cytoscape 3.9.0 software for PPI protein interaction analysis. Use plug-in Cyto hubba to screen core targets. Build a core network diagram.

#### h) Component-Target Molecule Docking

Molecular docking of the screened core target and its corresponding active components was carried out to verify the binding activity between components and targets. Firstly, the protein crystal structure of the core target was downloaded from RCSB PDB database (http://www1.rcsb.org/), and the original ligand and water molecule were removed by PyMol. In addition, the components were introduced into ChemBio3D Ultra for energy minimization. Then, AutoDockTools is used for file conversion before docking, and then AutoDockVina is used for molecular docking. Finally, the sample with the lowest free energy is selected as the docking sample, and it is visualized by PyMol.

and 26 kinds of active components of Tripterygium wilfordii were obtained. The structures of the obtained components were verified by Pubchem database, and finally 21 components with complete information were obtained, as shown in Table 1. And its effective active ingredients were input into TCMSP platform to search for 148 targets of active ingredients of Tripterygium wilfordii.

# III. Results

a) Search the Active Ingredients and Targets of Tripterygium Wilfordii

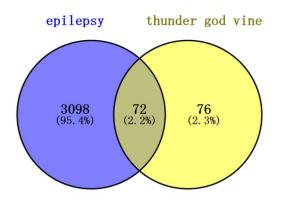
According to the search conditions, the active components of Tripterygium wilfordii were searched,

ID	Ingredient	OB%	DL
MOL000296	hederagenin	36.91	0.75
MOL000449	Stigmasterol	43.83	0.76
MOL003184	81827-74-9	45.42	0.53
MOL003185	(1R,4aR,10aS)-5-hydroxy-1-(hydroxymethyl)-7-isopropyl-8-	48.84	0.38
	methoxy-1,4a-dimethyl-4,9,10,10a-tetrahydro-3H-phenanthren-2-		
	one		
MOL003196	Tryptophenolide	48.50	0.44
MOL003229	Triptinin B	34.73	0.32
MOL003231	Triptoditerpenic acid B	40.02	0.36
MOL003245	Triptonoditerpenic acid	42.56	0.39
MOL003248	Triptonoterpene	48.57	0.28
MOL003280	TRIPTONOLIDE	49.51	0.49
MOL000358	beta-sitosterol	36.91	0.75
MOL000422	<u>kaempferol</u>	41.88	0.24
MOL004443	Zhebeiresinol	58.72	0.19
MOL002058	<u>40957-99-1</u>	57.20	0.62
MOL003209	Celallocinnine	83.47	0.59
MOL003217	Isoxanthohumol	56.81	0.39
MOL005828	nobiletin	61.67	0.52
MOL003187	triptolide	51.29	0.68
MOL003208	Celafurine	72.94	0.44
MOL003224	Tripdiotolnide	78.72	0.72
MOL003225	Hypodiolide A	76.13	0.49

#### Table 1: Active Ingredients of Tripterygium Wilfordii

b) Potential Targets of Tripterygium Wilfordii in the Treatment of Epilepsy

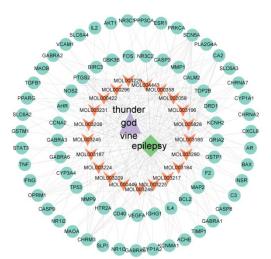
6007 targets related to epilepsy were retrieved. 3170 epileptic targets with a probability greater than or equal to 0.5 were selected, and the acquired tripterygium wilfordii targets and epileptic targets were standardized in Uniprot database. Using software venny2.1, 148 targets with tripterygium wilfordii active ingredients and 3170 epileptic-related targets were mapped and crossed, and 72 potential targets with tripterygium wilfordii for epilepsy treatment were obtained as a result, as shown in Figure 1.



*Figure 1:* Map of Tripterygium wilfordii epilepsy target. Blue circle represents Tripterygium wilfordii epilepsy target, yellow circle represents epilepsy target, and gray ellipse represents potential tripterygium wilfordii epilepsy target.

#### c) Construction of "Drug-Ingredient-Disease-Target" Network

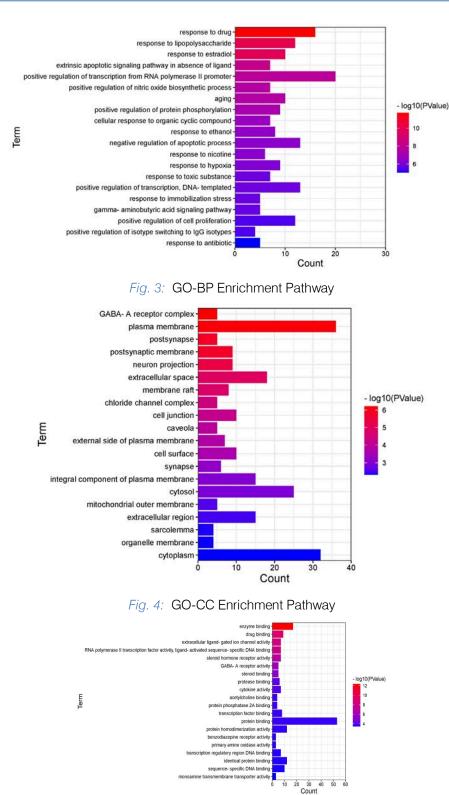
After the intersection, the potential targets were introduced into Cytoscape 3.9.0 software, and a "drugcomponent-disease-target" relationship network was constructed. It was found that each component was closely related to epilepsy through genes, as shown in Figure 2. The line segments among various factors represent the interaction relationship, and the more line segments, the stronger the interaction relationship.



*Figure 2:* Green circle represents the target, orange inverted V represents the active ingredient of Tripterygium wilfordii, green diamond represents epilepsy, and purple represents Tripterygium wilfordii.

d) GO Function Enrichment Analysis and KEGG Pathway Enrichment Analysis

The functional enrichment of GO is mainly divided into three parts: biological process (BP), cellular component (CC) and mo1ecular function (MF). According to the order of P value, the first 20 enrichment items are selected respectively. Among them, the mechanism of tripterygium wilfordii in treating epilepsy mainly involves biological processes such as GABA signaling pathway, cell composition such as synapse, mitochondria and plasma membrane raft, and molecular functions such as steroid binding, protease binding, protein binding, gated ion channel activity and GABA-A receptor activity. See Figure 3- Figure 5 for specific GO comments.





The enrichment results of KEGG pathway mainly include: cancer pathway, lipid and atherosclerosis signaling pathway, platinum resistance signaling pathway, Kaposi's sarcoma-associated herpes virus infection signaling pathway, chemical carcinogenesis-receptor activation signaling pathway, human cytomegalovirus infection signaling pathway, IL-17 signaling pathway, AGE-RAGE signaling pathway in diabetic complications, fluid shear stress and atherosclerosis signaling pathway, pulmonary tuberculosis signaling pathway, dopaminergic synapse and neuroactive ligand-. See Figure 6- Figure 7.

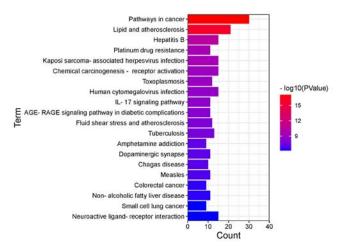
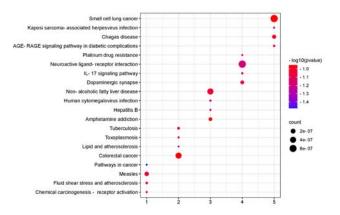


Fig. 6: The enrichment of KEGG pathway and the gradual change from red to blue represent the increasing P value

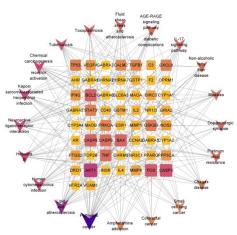


*Fig. 7:* KEGG bubble diagram. The larger the circle, the more genes are enriched, and the darker the red color, the lower the P value.

### e) Build KEGG Channel Relationship Network

Calculate the degree values of the first 20 enriched KEGG pathways and potential targets by using Cytoscape3.9.0 software, and adjust the size and color of the nodes with the degree values to construct the

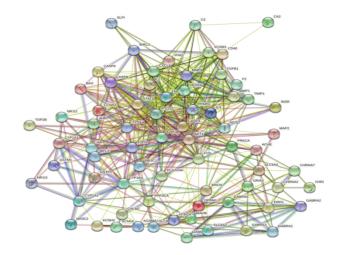
"target -KEGG pathway" relationship network diagram, as shown in Figure 8. Results It was found that Tripterygium wilfordii might play a therapeutic role on epilepsy through multiple active ingredients, multiple targets and multiple ways.



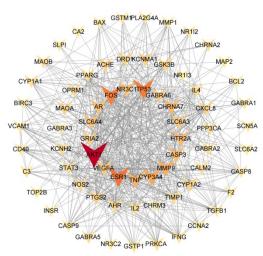
*Fig. 8:* Purple represents KEGG pathway, the larger the inverted V, the darker the color, the more enrichment pathways, and the larger the square, the darker the color, the more participating pathways.

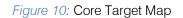
#### f) PPI Network Construction and Core Target Prediction

The 72 potential targets of tripterygium wilfordii and epilepsy are entered into the String database, and the PPI relationship network diagram is shown in Figure 9. The results showed that there were direct or indirect interactions among potential targets. The PPI network consisted of 72 nodes and 562 edges, with an average node degree of 15.8. The interaction results of PPI protein showed that protein domain and GABA receptor were found in its features, and it was speculated that Tripterygium wilfordii might play a role in epilepsy through GABA receptor system. Use Cyto hubba plug-in to screen out the core targets among potential targets and obtain the core sub-network. See figure 10. There are eight core targets in the core network, such as AKTI, ESR1, TP53, FOS, CYP3A4, MMP9, TNF and CASP3. These targets are also important targets in KEGG relationship network, and they play an important role not only in KEGG relationship network, but also in PPI network.



*Fig. 9:* PPI protein interaction network diagram, the sphere represents the target, the connection between the targets represents the interaction, and the more line segments, the stronger the effect.





### g) Component-Target Molecule Docking

According to the above screening steps, the related core genes were obtained, and the core genes were molecular docked with the components. The results are shown in Table 2. It was found that all the

other core genes can be docked except CASP3 gene, and the binding energy is less than-5 kcal mol-1, which indicates that the core targets have good binding activity with the corresponding active components. The smallest binding energy of the core target is the docking of CYP3A4 with kaempferol, and the binding energy isYear 2022

8.39 kcal mol-1. The results show that tripterygium wilfordii can treat epilepsy through gene regulation components and action pathways. The docking mode was visualized by PyMol, and it was found that there were hydrogen bonding forces in these docking

structures, which also indicated that the spatial matching degree of components and proteins was good. As shown in Figure 11.

Table 2: Docking information of	core target molecules, in which	ch the binding energy unit is kcal mol-1.

Number	Gene name	Ingredient	Docking position	Binding energy
1	AKT1	kaempferol	SER-56、GLN-61、GLN-59	-6.8
2	ESR1	Isoxanthohumol	ASP-21	-7.95
		nobiletin	HIS-206、TYR-213	-7.43
3	MMP9	nobiletin	ALA-191、GLN-227	-7.58
4	TP53	triptolide	ARG-267	-7.57
		nobiletin	GLY-154	-6.61
5	TNF	kaempferol	ALA-134、ASN-46、TRP-	-6.78
			28、GLY-24、ILE-136	
		trintalida	ALA-134、TRP-28、LEU-	-7.46
		triptolide	26	
6	FOS	triptolide	DA-5010、DC-5011	-8.32
7	CYP3A4	kaempferol	GLU-234、ARG-106	-8.39

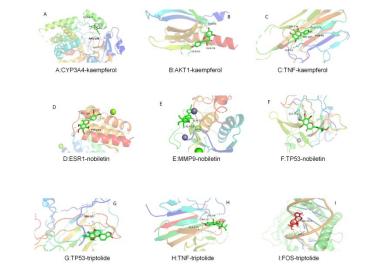


Fig. 11: Molecular Docking Diagram

## IV. DISCUSSION

Epilepsy is a serious neurological disease caused by the disorder of the physiological structure or function of the brain. More than half of the patients with epilepsy have one or more complications [12]. Mental diseases (such as depression, anxiety, psychosis, autism) and physical diseases (such as type 1 diabetes. arthritis, peptic ulcer, chronic obstructive pulmonary disease) are all related to long-term seizures [2]. However, the long-term use of antiepileptic drugs has great adverse reactions, and about 50% of patients can't control seizures well by using only one antiepileptic drug [13]. A large number of experiments and clinical studies show that the effect of integrated traditional Chinese and western medicine on epilepsy is better than that of chemical medicine alone [14]. Chinese medicine believes that epilepsy is closely related to pathological factors such as wind, blood stasis, phlegm and fire. The treatment should distinguish the attack period from the recovery period, and grasp the principle of "treating the target when it is urgent, and treating the root when it is slow". In the recovery period, the treatment is mainly to soothe the liver and regulate gi, strengthen the spleen and soothe the nerves, and replenish gi and nourish yin [15]. Finding new drugs to treat epilepsy is our constant pursuit. In recent years, network pharmacology of traditional Chinese medicine (TCM) with "multicomponent targeted network" as its main research mode has become increasingly popular, which mainly reveals the drug-gene-disease network relationship by predicting the targeted distribution and pharmacological effects of TCM compounds. Based on the concept of multi-component, multi-target and multi-way action of traditional Chinese medicine, this study studied the main components, targets, biological functions and signal

pathways of Tripterygium wilfordii through network pharmacology technology, in order to reveal its mechanism of action in treating epilepsy.

In this study, 21 kinds of active components and 72 potential anti-epileptic targets of Tripterygium wilfordii were screened by network pharmacology technology, and the network of "drug-componentdisease-target", "target -KEGG" and "PPI network" were constructed. Eight core targets including AKTI, ESR1, TP53, FOS, CYP3A4, MMP9, TNF and CASP3 were screened out. The same active ingredient of Tripterygium wilfordii can act on multiple targets; The same signal pathway can enrich multiple targets; The same target can correspond to multiple active ingredients and participate in multiple signal pathways.

The results of network analysis show that tripterygium wilfordii mainly includes kaempferol, βsitosterol, lignan, triptolide, tripterygium wilfordii polyglycoside and other active components as potential components for treating epilepsy. Studies have shown that flavonoids have antioxidant effect and can protect cells from oxidative stress. This study includes kaempferol, a flavonoid compound. Kaempferol can combine with benzodiazepines on GABA-A receptor to protect the brain from oxidative stress and has antiepileptic effect [16]. Tripterygium wilfordii can protect neurons from apoptosis induced by kainic acid in rats by inhibiting the expression of MHC- i, ii molecules in microglia and immune response [17]. Tripterygium wilfordii can also down-regulate the expression of caspase-3 and caspase-9 proteins in hippocampus of epileptic rats induced by kainic acid, thus inhibiting neuronal apoptosis [18]. Tripterygium wilfordii can inhibit neuronal apoptosis in epileptic rats by up-regulating Bcl-2 and down-regulating Bax protein expression [19]. Triptervolum wilfordii extract can inhibit the activation and proliferation of microglia, and its molecular mechanism may be related to the down-regulation of NF-KB protein and mRNA expression in microglia [20]. According to related research,  $\beta$  -sitosterol has obvious anticonvulsant effect among the main active components of Tripterygium wilfordii [21-22]. Experiments have proved that  $\beta$  -sitosterol has neuroprotective effect on hippocampal neurons with epileptic discharge [23]. The latest research found that the mechanism of tripterygium wilfordii polyglycoside inhibiting inflammatory factors may be related to MAPK signal transduction pathway and VEGF signal transduction pathway. Neuroinflammation and oxidative stress are closely related to epilepsy. Some effective anti-inflammatory and antioxidant drugs in animal models have been applied clinically, and have shown therapeutic effects on epilepsy patients.

Both PPI core targets and enrichment pathways confirm that the main components of Tripterygium wilfordii may be related to target regulation. Neuronactivated biomarker protein kinase subtype B 1(Aktl) is a serine/threonine kinase activated by oxidative stress, which is closely related to seizures [24-25]. It can participate in protein synthesis in hippocampal synaptic plasticity and control many pathological signal processes of epilepsy. Therefore, intervention of Akt/MTOR pathway with AKT subtype specific inhibitors may provide a way for the treatment of epilepsy. In addition, the level of interleukin-6(IL-6), a proinflammatory cytokine, was confirmed to increase significantly after epilepsy [27-29]. The level of cysteine aspartic protease 3 (Caspas3) encoded by CASP3 was also confirmed to be significantly increased in the serum of epileptic patients [30]. It was found that the expression of miRNA-141 in epileptic patients was upregulated, which induced neuronal apoptosis and increased the expression level of Caspase-3/9 and p53 protein. miRNA-141 was involved in epilepsy by targeting p53 to inhibit apoptosis [31]. VEGFA is overexpressed in patients with drug-resistant temporal lobe epilepsy, suggesting that it is involved in the pathological process of epilepsy [32]. Seizures significantly inhibit the plasticity of synapses, and the short-term plasticity mainly depends on the fluctuation and steady state of calcium levels in synapses [33]. The neuroprotective effect of ESR1 is mainly through its influence on synaptic plasticity [34]. ZHANG et al. [35] found that mice lacking FOS expression had more severe seizures, increased neuronal excitability and neuronal cell death, and FOS regulated the expression of GLUR6 and brain-derived neurotrophic factor (BDNF) in vivo and in vitro. As an important factor of apoptosis after brain injury, HIF-1a may provide a new target for the treatment of epilepsy [36]. Under hypoxia, HIF-1a is widely expressed in neurons, glial cells and ependymal cells in the central nervous system. Li Yanmei [37] and others found that the homozygous mutation of CYP3A4\*1G may be related to drug resistance in children with epilepsy with hereditary or unknown etiology. Screening CYP3A4\*1G genotype is one of the important methods to guide the selection of antiepileptic drugs and to judge and predict the therapeutic effect of antiepileptic drugs in children with hereditary or unknown etiology. Liu Dandan [38] studies have shown that seizures in the acute stage of viral encephalitis are related to the increased levels of IL-1 $\beta$ , IL-6 and TNF- $\alpha$ in cerebrospinal fluid. Therefore, the core target of this study is closely related to regulating the occurrence and treated development of epilepsy by effective components of Tripterygium wilfordii.

In order to further analyze the signal pathways and biological processes involved in tripterygium wilfordii therapeutic targets, the KEGG signal pathways and GO biological processes of tripterygium wilfordii therapeutic targets were enriched. Among them, oxidative stress and neuronal apoptosis are both related to seizures. There is evidence that in some animal epilepsy models, antioxidant therapy can reduce the nerve damage caused by oxidative free radicals, thus plaving an anti-epileptic role [39-40]. At present, most antiepileptic drugs play an antiepileptic role mainly by regulating voltage-gated ion channels, enhancing Caminobutyric acid-mediated inhibition, regulating synaptic release, or blocking ionic glutamate receptors. Therefore, the function of synapses is closely related to epilepsy [41]. It has also been reported that the level of catecholamine in striatum decreased during the incubation period in the seizure model induced by sodium glutamate [42]. The activity of neurotransmitter receptor is also closely related to the occurrence of epilepsy. It has been found that stimulating vagus nerve can enhance the activity of inhibitory neurotransmitter receptor a- aminobutyric acid receptor, thus inhibiting the occurrence of epilepsy [43]. The results of GO bioaccumulation analysis in this paper provide bioinformatics basis for potential target therapy of epilepsy predicted by Tripterygium wilfordii. The results of KEGG enrichment analysis showed that Tripterygium wilfordii might be related to epilepsy through IL-17 signaling pathway, human cytomegalovirus infection and tumor necrosis factor signaling pathway. The above reports on the effective active ingredients of Tripterygium wilfordii are basically consistent with the predicted results of the enrichment analysis of Tripterygium wilfordii target and KEGG signal pathway and GO biological process in this study.

# V. Conclusion

The selected targets, their biological functions and enriched signal pathways are closely related to the regulation of biological changes of epilepsy. However, many components selected from Tripterygium wilfordii are regulated by the core targets, which play a role in treating epilepsy. Further, it is suggested that the active ingredients of Tripterygium wilfordii may exert its therapeutic effect by acting on a variety of biological changes in the development of epilepsy. Its core target is closely related to the development of epilepsy, and the biological functions and enriched signal pathways of potential targets are also closely related to the mechanism of epilepsy. This study preliminarily expounded the molecular mechanism of tripterygium wilfordii in treating epilepsy, which provided a theoretical basis for new drug research and a new idea for treating epilepsy with traditional Chinese medicine. However, further experimental verification is still needed.

#### Author Contributions

X.L.and Y.W. participated in the design of this study, and they both performed the statistical analysis. X.L.carried out the study and collected important background information. Y.W.drafted the manuscript. All authors read and approved the final manuscript. X.L.and Y.W. carried out the concepts, design.

#### Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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#### Data availability

The data used to support the findings of this study is available from the corresponding author upon request.

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