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Exploration on the Clinical Medication Pattern and Mechanism of Psoriasis Vulgaris Based on Data Mining and Network Pharmacology

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Abstract: *In order to explore the clinical medication law and mechanism of unusual psoriasis based on data mining and network pharmacology. We collected and screened the prescription data of Shaanxi Traditional Chinese Medicine Hospital Skin Disease Hospital Specialized Clinic patients with psoriasis vulgaris from 1 September 2022 to 1 March 2023, and entered them into Excel software to establish a standardised case database of psoriasis vulgaris by two persons alternately, and then carried out the drug association rule analysis on the case data by using the Chinese medicine inheritance computing platform (V3.0) and IBM SPSS Modeler 18.0 to obtain the core drugs and construct a network of "disease-core drug-component-target", and then analyse the core drugs and the drug association rules. We constructed a "disease-core drug-component-target" network and analysed the protein interaction network and enrichment of intersecting targets. Resultsly, 189 prescriptions and 134 flavours of traditional Chinese medicines were obtained through screening, with a cumulative frequency of 3020 times, of which 38 flavours were used ≥20 times; The analysis of drug-association rules (support degree of the Apriori algorithm ≥65%, confidence degree ≥85%) showed that the core medicines had the same effect as the core medicines ≥85%) showed that the core drug Lonicera japonica-Lianqiao-Angelica sinensis-Paeonia lactiflora- Glycyrrhiza glabra medicinal group had a high degree of support. After excluding licorice, the core drug was subjected to network pharmacological analysis of the core drug components. A total of 192 active ingredients of the core drug components were associated with the disease targets of psoriasis vulgaris. Then GO enrichment analysis and KEGG pathway enrichment analysis were performed. In conclusion, according to the psoriasis clinic based on the database to obtain the key active ingredients and main targets of the drugs, it was found that the core group of drugs may alleviate the clinical symptoms of psoriasis by inhibiting the pro-inflammatory pathway and restricting the function of intracellular nuclear factors. It is of reference value for the study of the law of medication and mechanism for the prevention and treatment of psoriasis of the common type of traditional Chinese medicine.*

Keywords: *Data mining; cyberpharmacology; psoriasis vulgaris; medication patterns; mechanism study*

1. Introduction

Psoriasis Vulgaris (PV) is a refractory chronic inflammatory dermatosis characterised by maculopapular rash or polymorphic red plaques with silvery-white scales, accounting for more than 80% of the total incidence rate of psoriasis; recent studies have shown that exogenous factors or excessive stress of the immune system in vivo lead to the formation of unusual psoriasis caused by the abnormal differentiation of keratinocytes [1,2]. The disease is divided into progressive, quiescent and regressive phases according to the scaly skin lesions, and is prone to recurrent clinical episodes of increased hyperpigmentation, etc. Modern treatments are based on the use of topical corticosteroids, vitamin D derivatives, or biologics. Currently, the promotion of biological inhibitors to improve the singularity of the traditional programme, but at the same time, drug antibodies or insufficient amount of drug administration, sensitivity decreased, resulting in a decline in clinical efficacy; and the combined application of immunosuppressants, increase the dose or improve the drug interval of the programme, the long-term application of not only cause liver and kidney function damage, but also there are a number of unknown factors and uncertainty [3]. Traditional Chinese medicine (TCM) classifies this disease as "leukoderma pigmentosum", which is mostly caused by the deficiency of Ying and blood, blood heat and internal disturbance of wind and evil in the skin. TCM has advantages in repairing the skin barrier and regulating the immune status, and its clinical efficacy is remarkable, which has played a positive role in improving the clinical symptoms of the patients and decreasing the recurrence rate [4]. In this study, we summarised the clinical medication rules and mechanism characteristics of psoriasis vulgaris through data mining and network pharmacological analysis, in order to provide reference for the clinical identification and pharmacological analysis of medication.

2. Information and Methods

2.1. Prescription collection

The clinical Chinese medicine prescriptions involved were selected from the cases of Psoriasis Specialized Clinic patients with psoriasis of the common type who attended the Dermatology Hospital of Shaanxi Provincial Hospital of Traditional Chinese Medicine from 1 September 2022 to 1 March 2023. Screening was performed to determine the completeness of medical record information, including personal information, chief complaint, current medical history, past history, Chinese and Western medicine diagnosis, and prescription, among which there were 89 cases (47.0%) of female patients and 100 cases (53.0%) of male patients, with ages ranging from 18 to 82 years old. A total of 189 valid first consultation cases, 189 prescriptions, and 134 flavours of traditional Chinese medicine were included in the two-person alternating audit.

2.2. Case collection

2.2.1. Inclusion criteria

(1) The diagnostic criteria for psoriasis of the common type refer to the Chinese Medical Association Dermatological and Venereal Diseases Branch issued the "China Psoriasis Diagnosis and Treatment Guidelines (2018 full version)" [2]; (2) General information (age $\geq$ 18 years old patients, region, gender is not limited), clinical manifestations, prescription of traditional Chinese medicines, and other medical record information were recorded completely; (3) Treatment is led by the application of herbal prescriptions received by the specialized psoriasis clinic of the Dermatology Institute.

2.2.2. Exclusion criteria

(1) Outpatient medical record system data information is incomplete or missing, the composition or dosage of drugs in the case prescription is incomplete display; (2) exclude pregnant and lactating women, patients with psychiatric disorders, and patients with the combination of other important organs with serious primary diseases.

2.3. Data standardisation

The names, properties and functions of the Chinese medicines involved in the cases were standardised with reference to the 2020 edition of the Pharmacopoeia of the People's Republic of China [5] and the names of the Fourteenth Five-Year Plan textbook "Traditional Chinese Medicines" [6], which distinguish between the same medicines with different concoctions and efficacies, such as "raw dihuang" and "ripened dihuang". The names of different methods of preparation and different efficacy of the same drug, such as "Sheng Di Huang" and "Shu Di Huang", were standardised.

2.4. Data entry

The data entry work was carried out under the system of two-person alternating audit responsibility. The 189 valid cases were entered into the Microsoft Office Excel standardised psoriasis case database by a special person, and the data were reviewed and corrected by two persons alternately to ensure that the data source was reliable.

2.5. Data analysis

After screening, the data were uploaded to the Traditional Chinese Medicine Inheritance Calculation Platform V3.0, and then the "Data Analysis" module was selected to enter the "Statistical

Analysis" function to derive the analysis of drug frequency and category. After obtaining the high-frequency drugs, IBM SPSS Modeler 18.0 software was used to analyse the association rules (Apriori algorithm setting support ≥ 65%, confidence level ≥ 85%).

2.6. Network Pharmacology Analysis

2.6.1. Target screening of core drug components

Through the Traditional Chinese Medicine Systems Pharmacology Database and Analysis Platform (TCMSP) (http://lsp.nwu.edu.cn/tcmsp.pHp) (https://bidd.group/TCMID/), the traditional Chinese medicine integrated database (TCMID) (https://bidd.group/TCMID/), the encyclopedia of traditional Chinese medicine (ETCM) (https://bidd.group/TCMID/), and the Chinese medicine database (ETCM) (https://bidd.group/TCMID/). Chinese medicine (ETCM), the encyclopedia of traditional Chinese medicine (ETCM), the Chinese medicine compounds were collected and imported into the PubChem database (https://pubchem.ncbi.nlm.nih.gov/), the Canonical SMILES numbers were found, and then the active ingredients that met the requirements were imported into the SwissADME database and screened according to the principle of the five principles of drug-like properties. Then these active ingredients were imported into Swiss Target Prediction database (http://swisstargetprediction.ch/) (probability>0) for target prediction. After the target screening, the protein targets of the compounds were standardised in the Uniprot Protein Database (https://www.uniprot.org) in order to standardise the protein target information.

2.6.2. Disease target screening

We used "Psoriasis Vulgaris" as the keyword, DisGeNET (https://www.disgenet.org/), Genome Annotation Database Platform (GeneCards) (http://https://www.disgenet.org/), and the Uniprot Protein Database (https://www.disgenet.org/) were used to standardise the protein target information. DisGeNET (www.genecards.org/), Genome Annotation Database Platform (GeneCards) (https://www.genecards.org/) and online mendelian inheritance in man (OMIM) (https://omim.org/) databases were used to obtain the disease targets, and after combining the three disease databases, duplicate values were removed to obtain the target of Psoriasis Vulgaris. After combining the three disease database targets, duplicates were deleted to obtain the disease target of psoriasis vulgaris. The core drug active ingredient target and disease intersection target information was imported into Cytoscape 3.9.1 software to construct a "disease-core drug-ingredient-target network diagram".

2.6.3. Protein interaction network construction

The intersecting targets were imported into the STRING database (https://string-db.org/) with a confidence level of ≥0.400, and the results were visualised by Cytoscape 3.9.1 to obtain the key active ingredients according to the value of degree.

2.6.4. GO and KEGG enrichment analysis

Gene ontology (GO) function of core targets and Kyoto encyclopedia of genes and genomes (KEGG) pathway enrichment analysis Common core targets of core drugs and diseases were imported into Metascape database (https://metascape.org/gp/index.html#/main/step1) for GO and KEGG enrichment analysis, and the results were screened and imported into the Microbiotics Cloud Platform (http://www.bioinformatics.com.cn/) as well as the Cytoscape 3.9.1 software results for visualisation.

3. Results

3.1. Drug frequency analysis

A total of 189 prescriptions (including 134 flavours) were included. 134 flavours of Chinese medicines were used a total of 3020 times. Thirty-eight medicines were used ≥20 times, and the top 10 Chinese medicines were, in descending order of frequency, forsythia (7.93%), angelica sinensis (7.93%), liquorice (7.93%), Lonicera japonica (6.15%), Paeonia lactiflora (6.06%), Semen aristolochiae (5.96%), Mudanpi (5.91%), Cortex chennii (5.86%), Radix et rhizoma shengdi (5.81%), and safflower (4.92%), saffron (4.92%). See Table 1.

Table 1: Frequency analysis of medication administration (frequency ≥ 20)

No.	Medicine	Frequency	Percent(%)	No.	Medicine	Frequency	Percent(%)
1	forsythia	161	7.93	20	castor seed	50	2.46
2	angelica	161	7.93	21	windbreaks	49	2.41
3	liquorice	161	7.93	22	mustard	45	2.22
4	honeysuckle	125	6.15	23	chamomile	42	2.07
5	paeonia lactiflora	123	6.06	27	pueraria lobata	32	1.58
6	water lily	121	5.96	28	rhus chinensis	30	1.48
7	peony bark	120	5.91	29	peach kernel	30	1.48
8	tangerine peel	119	5.86	30	paeonia lactiflora	29	1.43
12	cape jasmine	87	4.29	31	chantui	28	1.38
13	scutellaria	82	4.04	32	humulus lupulus	27	1.33
14	chamomile	69	3.40	33	reevesia cordifolia	26	1.28
15	persimmon	69	3.40	34	Imperata cylindrica	26	1.28
16	wolfiporia extensa	59	2.91	35	viola mandsurica	26	1.28
17	schizonepeta	54	2.67	36	atractylodes macrocephala	23	1.13
18	acacia bark	52	2.57	37	white lentil	21	1.03
19	achyranthes bidentata	52	2.57	38	coix lacryma	20	0.99

3.2. Analysis of drug categories

The drug categories were divided into 17 categories in total, of which the top 5 in terms of frequency of use were, in order: clearing heat 1306 times (43.8%), tonifying deficiency 410 times (13.7%), invigorating blood and removing blood stasis 296 times (9.92%), resolving exterior symptoms (9.18%), and dispelling wind and removing exterior symptoms (7.41%), which, in combination with the frequency of the drugs and the information on the cases, involved the efficacy of drugs that were mainly used to clear heat and diarrhea, tonifying blood and nourishing blood, activating blood and removing blood stasis, dispelling wind and removing exterior symptoms, and so on. The efficacy of the drugs involved in combining the frequency of the drugs and the information of the cases was mainly clearing away heat and fire, tonifying blood and nourishing blood, activating blood circulation and removing blood stasis, and dispelling wind and relieving epidemics. See Table 2.

Table 2: Analysis of Chinese medicine categories (17 categories in total)

No.	Drug category	Frequency	Percent(%)	No.	Drug category	Frequency	Percent(%)
1	category of birdsong	1306	43.8	10	hemostatic	34	1.14
2	take care of weak points	410	13.7	11	anti-toxic, anti-insect and anti-itch	27	0.9
3	promote blood circulation and eliminate blood stasis	296	9.92	12	hepatic and wind-relieving drugs	23	0.74
4	antipyretic	274	9.18	13	digestive class	22	0.74
5	salubriousness	221	7.41	14	wenrich class	19	0.64
6	water-inducing and dampness-permeating	168	5.46	15	relieve dampness	9	0.30
7	resolving phlegm, relieving cough and asthma	63	2.11	16	astringent	6	0.20
8	tranquilizers	56	1.88	17	laxative	2	0.07
9	rheumatoid	53	1.78				

3.3. Association analysis of high-frequency traditional Chinese medicines IBM SPSS

Modeler 18.0 software was used to carry out the association analysis of the above high-frequency traditional Chinese medicines, and the calculation results were imported into cytoscape3.9.1. The Apriori algorithm was used to set the degree of support ≥65% and the confidence level ≥85%. Arranged by the support degree from high to low, there were 8 pairs of drug pairs with the support degree of 85% or more, and the resulting gains were all >1, indicating that the drug pairs derived from the screening were all statistically significant, among which the pair consisting of Lonicera japonica-Lianqiao-Angelica sinensis-Paeonia lactiflora-Glycyrrhiza glabra had a high support degree. See Table 3 and Figure 1.

Table 3: Analysis of drug pairs off rules

No.	Drug-pair combination	Degree of support(%)	Confidence level(%)	Gain
1	Lonicera japonica, forsythia	66.31	94.35	1.103
2	Radix Paeoniae Alba, angelicae	65.76	93.50	1.189
3	Radix Paeoniae Licorice, forsythia	65.76	90.24	1.055
4	Licorice, angelica	75.94	89.44	1.138
5	Licorice, glycyrrhiza glabra	65.76	88.62	1.167
6	Angelica sinensis, licorice	78.61	86.40	1.138
7	Angelica, forsythia	78.61	86.40	1.01
8	Licorice, forsythia	75.94	85.21	0.996

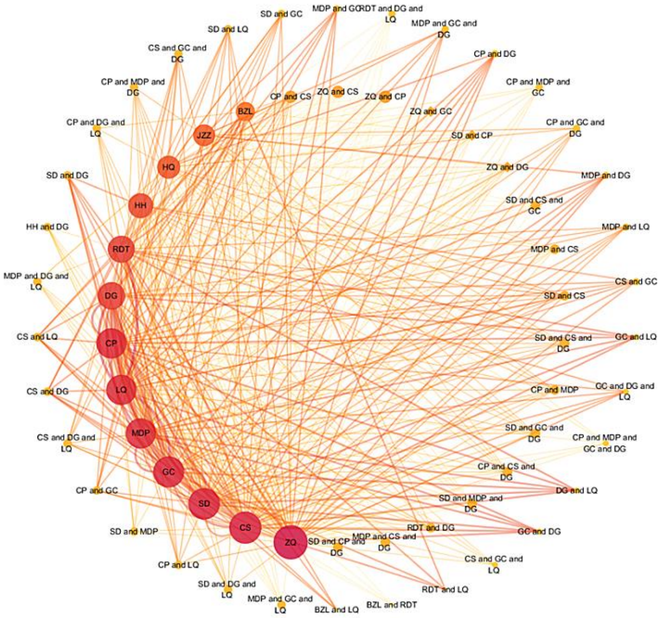


Figure 1: Associated network diagram of high-frequency Chinese medicines

3.4. Network pharmacological analysis

Through the above results, the core drug was screened as Lonicera japonica - Lianqiao - Angelica sinensis - Radix Paeoniae Alba (remove the liquorice of reconciliation), and it was analysed by network pharmacological analysis.

3.4.1. Target screening of core drug components

The TCMSP database was searched and screened to obtain 780 active ingredients of forsythia, 560 active ingredients of Lonicera japonica, 977 active ingredients of Angelica sinensis and 544 active ingredients of Paeonia lactiflora, and 1113 active ingredients were de-emphasised. By combining the results of each database search and deleting the duplicate values, we obtained 1310 targets related to psoriasis vulgaris and 1113 targets related to core drugs.

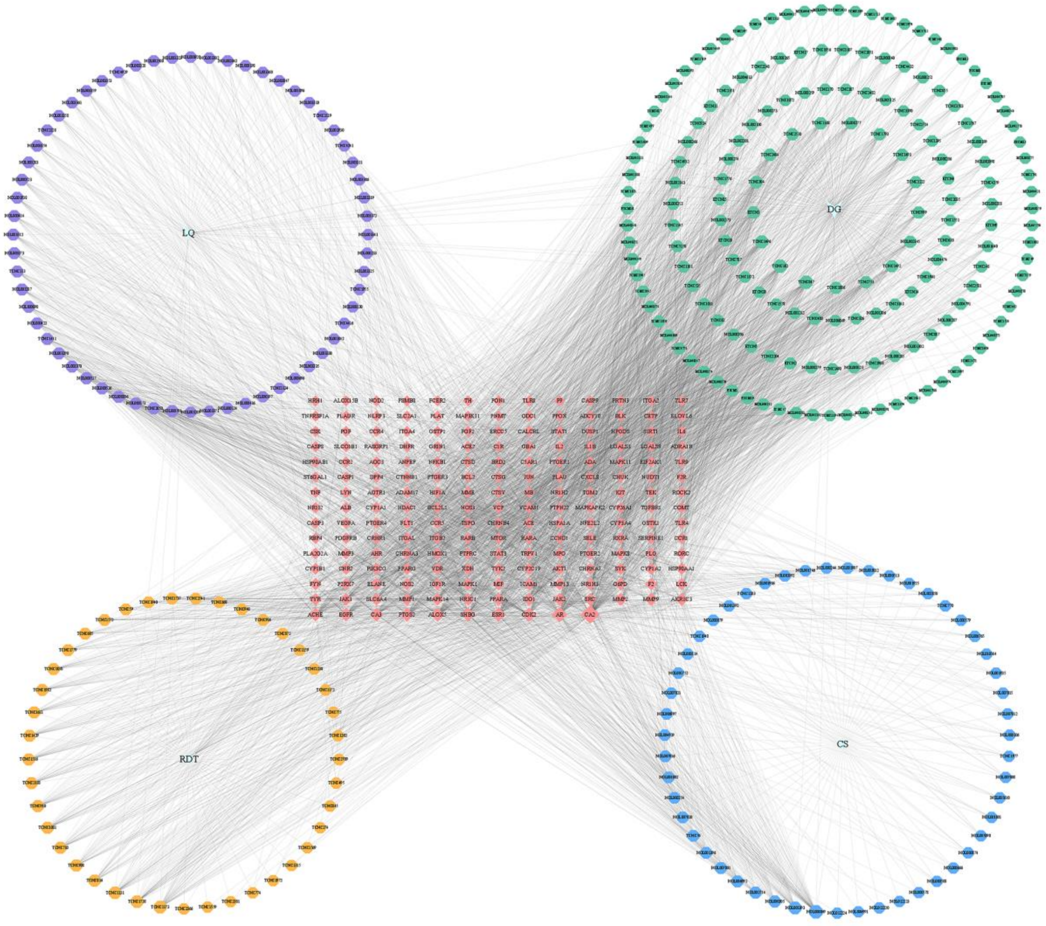
3.4.2. Construction of "Disease-core drug-component-target network diagram"

The target information of drugs and diseases were imported into InteractiVenn (http://www.interactivenn.net/) for plotting to get the disease-drug target Wayne diagram. The data were imported into R language to take the intersection, and 192 intersection targets were obtained, see Figure 2. The target of the active ingredients of the core drug and the target of the disease were imported into Cytoscape 3.9.1 software to construct the "Disease-core drug-ingredient-target" network diagram. The network diagram showed that there were 326 active ingredients related to the targets of Lonicera japonica, Lonicera japonica, Angelica sinensis and Paeonia lactiflora, including 60 Lonicera japonica, 41 Lonicera japonica, 174 Angelica sinensis, and 51 Paeonia lactiflora (including 8 common ingredients), which were ranked according to the value of the degree of the active ingredient (ranked in the top 5), as shown in Table 4 and Figure 3.

Figure 2: Disease-drug target Wayne diagrams

Table 4: Top 5 active ingredients in terms of degree value

ID	Molecule name	Herb name	Degree
MOL000069	Palmitic Acid	paeonia lactiflora	67
TCMC847	Caffeic Acid	angelica	64
TCMC182	(Z)-3-(3, 4-Dihydroxyphenyl)Prop-2-Enoic Acid	angelica	63
TCMC1496	Linolenic Acid	angelica	55
MOL001393	Myristic Acid	paeonia lactiflora	46



Note: Lianqiao (LQ), Lonicera japonica (RDT), Angelica sinensis (DG), Paeonia lactiflora (CS)

Figure 3: Disease-core drug-component-target network diagram

3.4.3. Protein Interaction Network Construction

Protein Interaction (PPI) Network Construction The 192 intersecting targets obtained were imported into the STRING website, and the confidence level ≥ 0.400 was selected, and the resultant files were imported into Cytoscape 3.9.1 software for plotting. Then the cytoHubba plug-in was used to extract the key targets based on the degree value, and five key targets were obtained, which were albumin (ALB), interleukin-1 beta (interleukin-1 beta, IL-1β) , interleukin-6 (interleukin-6, IL-6), serine/threonine protein kinase 1 (Serine/threonine-protein kinase AKT, AKT1), tumour necrosis factor (TNF). See Figure 4.

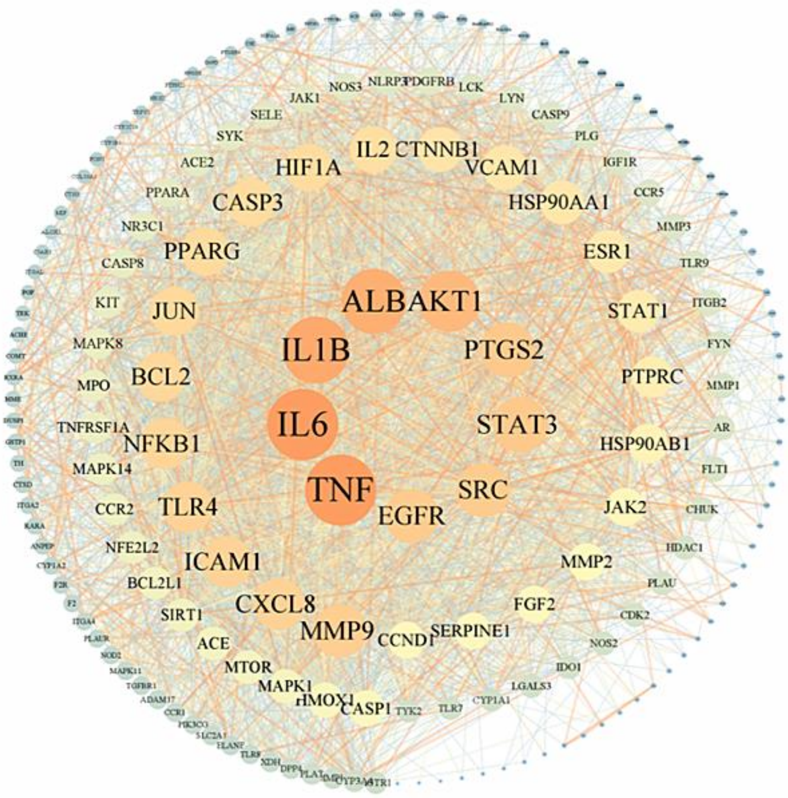


Figure 4: PPI network diagram

3.4.4. GO enrichment analysis

GO enrichment analysis was performed on the core targets (p<0.05), and the results were obtained as 2111 biological process (BP), 106 cellular component (CC), and 207 molecular function (MF). The resultant data were sorted by p-value from smallest to largest, and the first 10 pieces of information for each of the three entries of GO analysis were taken. BP mainly included response to molecules of bacterial origin, response to lipopolysaccharide, inflammatory response, response to bacteria, response to hormones, cellular response to lipids, positive regulation of response to external stimuli, positive regulation of cytokine production, regulation of inflammatory response, and positive regulation of cell migration, etc; CC mainly included membrane rafts, membrane microregions, lateral side of the membrane, receptor complex, outer side of the plasma membrane, plasma membrane rafts, and adhesion spots, cell-substrate binding, side of the cytoplasmic membrane, vesicle lumen, etc. ; MF, on the other hand, mainly exhibits protein structural domain specificity, kinase binding, protein kinase binding, nuclear receptor activity, ligand-activated transcription factor activity, RNA polymerase II-specific DNA-binding transcription factor binding, transcription factor binding, DNA-binding transcription factor binding, transcriptional co-regulator binding, and nuclear receptor binding. See Figure 5.

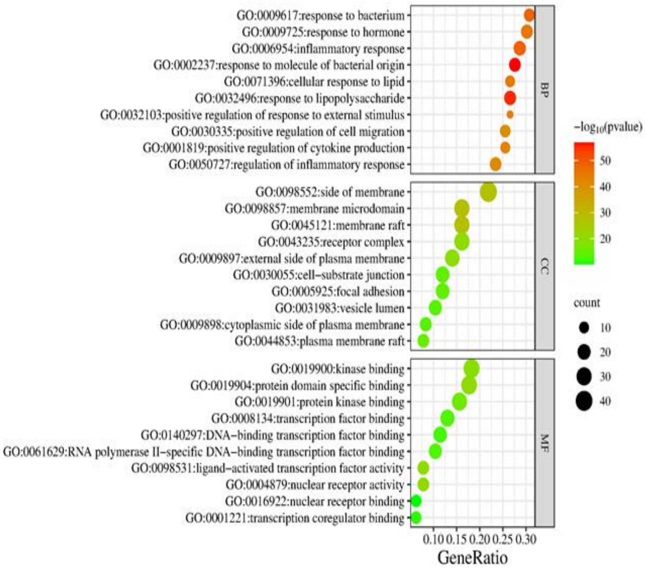


Figure 5: GO analysis

3.4.5. KEGG pathway analysis

KEGG pathway enrichment analysis was performed on the core targets ($p<0.05$), and 188 pathways were obtained from KEGG pathway enrichment analysis. The results of KEGG pathway enrichment analysis included cancer pathway, lipid and atherosclerosis, Kaposi's sarcoma-associated herpesvirus infection, AGE-RAGE signalling pathway diabetic complications, coronary artery virus disease-COVID-19, fluid shear and atherosclerosis, Th17 cell differentiation, toxoplasmosis, human cytomegalovirus infection, chemogenicity-receptor activation, PI3K-Akt signalling pathway, and PI3K-Akt signalling pathway. sclerosis, Th17 cell differentiation, toxoplasmosis, human cytomegalovirus infection, chemical carcinogenesis-receptor activation, PI3K-Akt signalling pathway, tuberculosis, measles, hepatitis B, prostate cancer, Chagas' disease, IL-17 signalling pathway, Epstein Barr virus (EBV) infection, TNF signalling pathway, NOD-like receptor signalling pathway. The top 20 information of KEGG analysis results were taken for visual analysis imported into Cytoscape 3.9.1 software to draw KEGG core pathway-gene maps, in which the five targets with the highest degree values were nuclear factor NF-κB (Nuclear factor NF-kappa-B p105, NF-κB1), serine/threonine protein kinase 1 (Serine/threonine-protein kinase AKT , AKT1), Inhibitor of nuclear factor κ B kinase subunit alpha (CHUK), Mitogen- activated protein kinase 1 (Mitogen- activated protein kinase 1, Mitogen-activated protein kinase 1, Mitogen- activated protein kinase 1, Mitogen- activated protein kinase 1, Mitogen- activated protein kinase 1, Mitogen- activated protein kinase 1, Mitogen- activated protein kinase 1, Mitogen- activated protein kinase 1). activated protein kinase 1 (MAPK1), interleukin-6 (IL-6). See Figures 6 and 7.

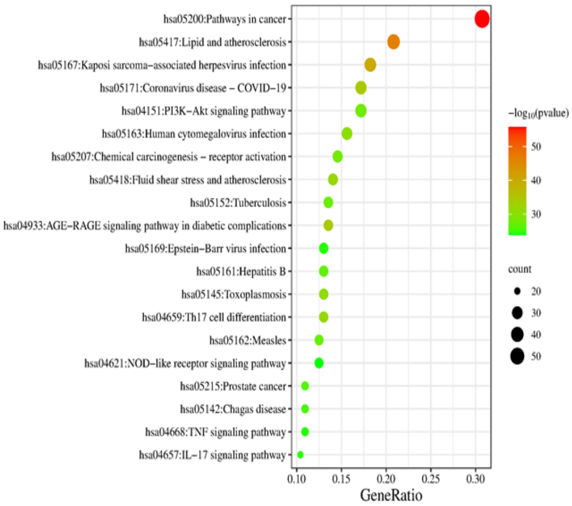


Figure 6: KEGG analysis

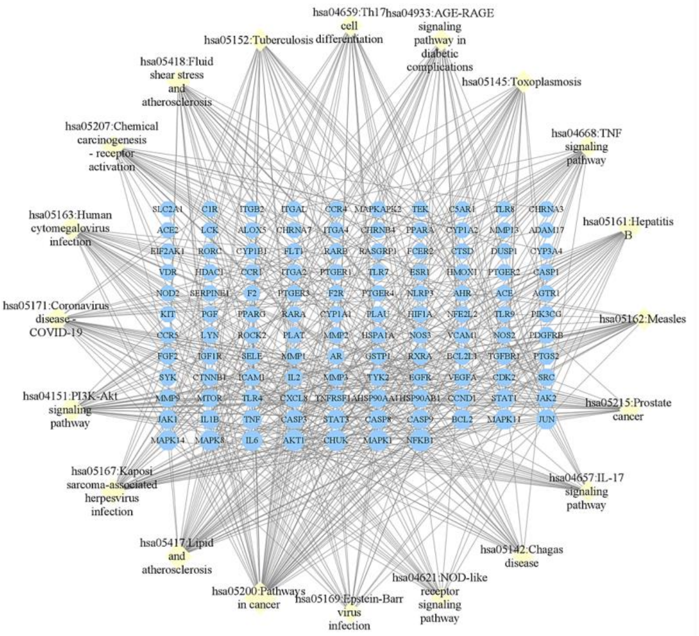


Figure 7: KEGG core pathway-gene map

4. Discussion

The complexity of psoriasis vulgaris only 1990 to 2019 global psoriasis incidence increased by 26.53%, male and female ratio in the 50-54 years age group reached the peak, in addition to genetic factors and environmental factors, caused by the recurrence of the disease by the role of multi-factors to the current public health and safety pose many challenges [7,8]. The clinical deterioration and onset of psoriasis vulgaris is often combined with a variety of diseases, the use of Chinese medicine multi-effective overall regulation of the advantages of metabolic diseases, such as the use of blood circulation and stasis of the use of traditional Chinese medicine, the use of a more effective clinical effect [9,10]. The symptoms of this disease are caused by the blood, or heat and wind in the skin that does not dissipate, or loss of nourishment of the skin due to prolonged Yin injury and blood loss. This study relies on the Chinese medicine inheritance computing platform (V3.0) and network pharmacology to analyse the prescription medication of psoriasis vulgaris, and extract the core drugs for the clinical treatment of psoriasis vulgaris, so as to systematically and comprehensively analyse the law of clinical use of medication and the mechanism of action of this disease.

Data mining analysis of this study showed that forsythia, licorice and angelica had the highest frequency among the top 10 Chinese medicines in descending order, followed by Lonicera japonica, Paeonia lactiflora, Semen aristolochiae, Mudanpi, Pericarpium Citri Reticulatae, Shengdi and Safflower, and that forsythia was able to dissipate knots and drain the heat of collaterals as recorded in Justice of the Materia Medica, forsythia is bitter in nature and slightly cold, and it is attributed to the meridians of the lungs, the heart, and the small intestines. It can propagate and disperse wind-heat in the Wei division, dispel stagnant heat in the surface, transmit heat to the gas, reach the evil in the outside, and dissolve the heat evil in the camp division through the gas division. "Red peony and safflower help to remove blood stasis, and mudanpi and chenpi help to move qi and blood. From the analysis of the frequency of medicines, we believe that heat, deficiency and blood stasis are the basis for the treatment of psoriasis. In the category of Chinese medicines, heat-clearing medicines accounted for about 43.8% of the total, followed by those that tonify the deficiency and those that invigorate blood circulation and remove blood stasis. According to the analysis of the frequency of medication can be roughly divided into three categories, clearing heat and removing toxins (forsythia, licorice, lonicera, sempervivum), nourishing yin and nourishing blood to move qi (Radix et rhizoma, Radix Angelicae Sinensis, Pericarpium Citri Reticulatae), cooling blood to activate blood circulation and remove blood stasis (Radix Paeoniae Alba, Paeoniae Mutansi, safflower). From this, it can be seen that it emphasizes the importance of nourishing yin and nourishing blood in replenishing the deficiency, and also fully reflects the principle of the medicine of normal type of psoriasis of clearing heat to cool blood, nourishing yin to nourish blood and activating blood circulation to remove blood stasis. They are independent and interrelated. Among the two or more pairs of drugs in the high-frequency Chinese medicine correlation analysis, the pair of Lonicera japonica - Lianqiao - Angelica sinensis - Paeonia lactiflora - Glycyrrhiza glabra has a high degree of support, and the pair of drugs often appears in the clinical dermatological formulas, so it can be found that the correlation of the composition of the drugs with the frequency of the use of medication and the category of traditional Chinese medicine has a strong correlation, and it further explains the frequency of traditional Chinese medicine, the category of traditional Chinese medicine, the formation of the law of the prescription, as well as the use of medication in the treatment of psoriasis. The principle of psoriasis treatment was further explained.

In this study, we found that a total of 326 active ingredients from the core group of Lonicera japonica-Lianqiao-Angelica sinensis-Paeonia lactiflora had a modulating effect on psoriasis vulgaris by using high-frequency drug association rules and network pharmacology, of which the top 5 of the DEGREE active ingredients were palmitic acid, caffeic acid, acrylic acid, linoleic acid, myristic acid, and so on. Studies have shown that palmitic acid, for example, can control the inflammatory response in psoriasis by inhibiting the STING-IRF3 activation pathway, and myristic acid is an important component in suppressing autoimmune inflammatory responses [11,12]. In addition, it has been found that acrylic acid can be isolated from caffeic acid in herbal tonics. These two components may be the main active ingredients for improving the repair of the skin barrier in psoriasis [13]. A linoleic acid-containing ceramide moisturiser was found to be effective in improving the dry, flaky skin manifestations of mild-to-moderate psoriasis vulgaris [14]. In this study, 192 intersecting targets were obtained by constructing a protein PPI network, in which five key targets were obtained as albumin (ALB), interleukin-1β (IL-1β) , interleukin-6 (IL-6), serine/threonine protein kinase 1 (AKT1), and tumour necrosis factor (TNF), among which ALB synthesized by the liver is the stabilisation of plasma colloid osmotic balance, ALB, synthesised by the liver, is an important protein for stabilising plasma colloid osmotic balance, maintaining capillary permeability and possessing anti-inflammatory properties. Currently, psoriasis has been proved to be an autoimmune inflammatory disease in which the inflammatory storm releases pro-inflammatory factors such as TNF, IL-1β, IL-6 and other pro-inflammatory factors, which disrupts the immune homeostasis, and the potential pathogenesis of psoriasis involves interactions between multiple immune cells such as T cells, macrophages and keratinocytes. In 2020, JAMA indicated that in plaque psoriasis, which has a high relapse rate, the use of biological inhibitors that inhibit pro-inflammatory processes is still the first-line recommendation [15,16]. However, the application of biological inhibitors alone still has the option of poorer control of local inflammation and higher cost, and the combination of Chinese medicine characteristic treatment can help to improve the clinical performance of psoriasis patients [17].

In this study, the GO and KEGG enrichment analyses showed that BP includes multi-link response to e. g. molecules of bacterial origin, lipopolysaccharides, hormones, lipids, and the regulation of the whole process of inflammatory response; CC includes a variety of cellular membrane regions, etc. ; and MF is shown to be involved in the structural domain-specificity of proteins, binding of kinases to protein kinases, and the ligand-activated activity of transcription factors, etc. , which suggests that the effect of traditional Chinese medicines is related to the regulation of the biological process of psoriasis. The biological process of psoriasis mainly focuses on the regulation of inflammatory response, transcription factor activity, etc. KEGG enrichment showed that the key pathways are involved in psoriasis inflammatory response through the differentiation of Th17 cells as well as IL-17 signalling pathway, TNF signalling pathway, and NOD-like receptor signalling pathway.

5. Summary

In summary, this study collated, mined and analysed the data of patients with unusual psoriasis XX, which is based on the pathogenesis of heat, deficiency and blood stasis, and used the medication principle of clearing heat and cooling the blood, nourishing yin and nourishing the blood, and activating blood circulation and removing blood stasis. Based on the database to obtain the key active ingredients and main targets of the drugs, it was found that the core group of Lonicera japonica - Lianqiao - Angelica sinensis - Radix Paeoniae Alba may alleviate the clinical symptoms of psoriasis by inhibiting the pro-inflammatory pathway, restricting the function of the intracellular nuclear factor, exerting the modulation of immune response and regulating the transcription factors and other multi-pathways, which is of reference value for the study of the medication pattern and mechanism of Chinese medicine to prevent and control the unusual type of psoriasis.

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