

Research Article

Systems Pharmacology-Based Research on the Mechanism of Danzhi Xiaoyao San in the Treatment of Depression

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Received: May 09, 2023

Accepted: June 08, 2023

Published: June 15, 2023

Abstract

Depression is a common and serious mental disorder characterized by persistent feeling of sadness and loss of interest in activities. Despite conventional treatments can improve depression symptoms and prevent a recurrence, complementary and alternative therapies are necessary to be involved because of the detrimental effects of the current therapy. Traditional Chinese Medicine (TCM) formulas are considered to be a potential complementary method with special advantages for treating the multiple pathogenesis of depression in a holistic way. However, the underlying pharmacological mechanism of TCM formula on depression therapy remained elusive. Therefore, in current study, a systems pharmacology approach integrating Absorption, Distribution, Metabolism, and Excretion (ADME) filtering, target fishing, gene enrichment analysis, network pharmacology, and pathway analysis was developed to comprehensively explore the multiple therapeutic mechanisms of Danzhi Xiaoyao San (DZXYS) for the treatment of depression. Finally, 111 active components and 112 potential targets of DZXYS were identified through ADME filtering and target fishing. Gene enrichment analysis found that DZXYS played a significant role in treating depression through the regulation of multiple pathogenesis including neurotransmitter systems imbalance, brain derived neurotrophic factor, hypothalamic-pituitary-adrenal axis dysregulation, inflammation, and immune. Moreover, the compound-target and target-pathway networks were constructed to elucidate the therapeutic mechanism of DZXYS from the system perspective. This study proposes a promising way for facilitating in-depth understanding of the complicated therapeutic mechanism of TCM on depression.

Keywords: Danzhi xiaoyao san; Systems pharmacology; Active compounds; Depression; Mechanisms

Introduction

Depression is a multifactorial psychiatric disorder, characterized by specific symptoms including listlessness, interest drops, extreme of inferiority, hopelessness or guilt and a reduced ability to enjoy life [1]. According to the report released by World Health Organization (WHO), more than 350 million people worldwide are affected by depression, leading to a tremendous public health burden [2]. Evidence showed that depression is a systemic disease rather than a mental disorder, which always involves different pathophysiology mechanisms including neurotransmitter systems imbalance, decreased Brain Derived Neurotrophic Factor (BDNF), abnormal gene expression, Hypothalamic-Pituitary-Adrenal (HPA) axis dysregulation, impaired inflammatory response and immune regulation.

Antidepressant drugs are commonly used to help alleviate the symptoms of depression and prevent relapse of the illness. The current available clinical antidepressant medications mainly act on monoamine transmitters including serotonin and norepinephrine [3]. However, these drugs often cause detrimental effects, such as lagging, low compliance and failed treatment, which will lead to the intolerant or refractory responses of many patients [4,5]. Therefore, it is urgent to develop antidepressant drugs based on multiple pathogenesis against depression. Traditional Chinese medicine (TCM) as one of the major complementary and alternative medicine therapies featured as multi-components and multiple targets have been shown to possess special advantages for the treatment of complex pathogenesis of depression [6,7].

Danzhi Xiaoyao San (DZXYS), recognized as a classical prescription from Abstract for Chinese Internal Medicine (Nei Ke Zhai Yao) has been widely used to treat depression for many years. This herbal formula is composed of *Radix Bupleuri* (Chai-Hu), *Paeoniae Radix Alba* (Bai-Shao), *Angelica Sinensis Radix* (Dang-Gui), *Fu-Ling*, *Atractylodes macrocephala Koidz.* (Bai-Zhu), *Licorice* (Gan-Cao), *Moutan Cortex* (Mu-Dan-Pi), and *Gardeniae Fructus* (Zhi-Zi). A previous clinical study suggested that DZXYS played a significant role in lowering the Hamilton depression scale (HAMD), reducing the scores of anxiety/somatization, reversing cognitive impairment and feeling of despair in depressive patients [8]. Although DZXYS exhibit multiple therapeutic effects for relieving the symptoms of depression, its active compounds, related targets, pathways and underlying pharmacological mechanism remain elusive.

Systems pharmacology has been suggested as a promising approach to shift away from the traditional “one-drug, one-target, one-disease” towards the “multi-component, multi-target” strategy, which will shed light on a comprehensive investigation to systemically dissect the relationship between drugs, targets, pathways and diseases, as well as the potential pharmacological mechanisms of herbal formulae on disease therapy. Growing evidence revealed that systems pharmacology method is capable of uncovering the complicated pharmacological mechanisms of TCM herbs and formulas on the treatment of various diseases. For example, the combinatorial rule and the pharmacological mechanisms of Qing-Luo-Yin and Liu-Wei-Di-Huang Pill for the treatment of rheumatoid arthritis and various diseases were elucidated from a network/systemic perspective [9,10]. In our previous work, systems pharmacology has been successfully used to explore the potential mechanisms of the single herb and herb pairs for various diseases therapy [11,12]. In addition, a series of systems pharmacology frameworks have been developed to disclose the underlying mechanisms of TCM formulas for stroke, asthma and obesity [13-15].

Therefore, in current study, an integrative systems pharmacology strategy, which combines ADME (absorption, distribution, metabolism, and excretion) filtering, target fishing, gene enrichment analysis, network pharmacology and pathway analysis is proposed to reveal the multiple mechanisms of DZXYS in treating depression based on a holistic and systemic way. The detailed work flowchart is shown in Figure 1. The systems pharmacology framework constructed in our study not only sheds light on providing a probe to explore the complex therapeutic mechanism of DZXYS for depression at the system level, but also promotes the modernization and internationalization of TCM formulas.

Materials and Methods

Building the Compound Database of DZXYS

The chemical constituents of DZXYS were extracted from the TCMSP (Traditional Chinese Medicine Systems Pharmacology Database and Analysis Platform, <https://tcmssp.com/tcmssp.php>) database, and then manually supplemented from abundant literatures of CNKI and PubMed databases. All structures of these constituents were downloaded from TCMSP and NCBI PubChem databases, and then subjected to full geometry optimization using GUASS package with the same parameters as our previous work [16,17]. Considering that compounds with glycosyls cloud undergo glycosidase hydrolysis reaction before being absorbed, in this section, their corresponding aglycones were also added into the compound database of DZXYS for further research.

Active Compounds Screening

Predicting ADME properties of drug candidate molecules plays an important role in drug development, because of the fact that the failure of 60% of drug molecules is related to poor ADME properties [18]. Therefore, early ADME prediction of a candidate compound can significantly reduce the cost of drug research. For herbal medicine, it usually contains hundreds of constituents, but only a few bioactive compounds provide physiological benefits for human health. Identifying the active ingredients with favorable ADME properties is a fundamental step to uncover the therapeutic effects of DZXYS. In the present work, three *in silico* models, i.e., Drug-Likeness (DL), Oral Bioavailability (OB), and Blood-Brain Barrier (BBB) were employed to screen the potential active compounds of DZXYS.

Drug-likeness calculation: Drug-likeness is a qualitative profile used in drug design to optimize pharmacokinetic and pharmaceutical properties, such as solubility, and chemical stability. Therefore, for deciphering the molecular mechanism of functional food, it is first necessary to apply drug-likeness filter to remove non-drug-likeness compounds from the molecule database, and then just focus on the drug-likeness molecules [19]. In the present work, a robust *in silico* model was employed to screen the molecules with drug-likeness features from compound database of DZXYS. In this model, Tanimoto coefficient (as shown in Equation (1)) was used to calculate the DL index of each compound of DZXYS.

In which, A is the molecular descriptors of constituents of DZXYS, and B is the average molecular properties of 6511 small drug-like and drug molecules in DrugBank database (<http://www.drugbank.ca>). The DL threshold is ultimately set to 0.18, which is based on the average DL value in the DrugBank database.

$$T(A, B) = \frac{A \cdot B}{|A|^2 + |B|^2 - A \cdot B} \quad (1)$$

Oral bioavailability evaluation: Being an important ADME parameter, oral bioavailability indicates the fractional extent of the oral bioactive molecule dosage which finally reaches its target site to exhibit the pharmacological activity [20]. In present work, OB value was also employed to screen the active constituents from DZXYS, and the values were computed through a reliable *in silico* model OBioavail 1.1 [21]. This model was built using metabolism (P450 3A4) and transport (P-glycoprotein) information of 805 drug and drug-like molecules. The linear (i.e., Partial Least Square (PLS), Multiple Linear Regression (MLR)), and nonlinear (support vector machine (SVR)) methods were used to construct this model, ending up with an optimal model holding a determination coefficient (R^2) of 0.80 and a Standard Error of Estimate (SEE) of 0.31 for test sets. Finally, herbal constituents with proper OB values (OB \geq 30%) were screened as the candidate compounds for further research.

BBB penetration: Blood-brain barrier is a highly selective semipermeable membrane that regulates the passage of small and large molecules into the Central Nervous System (CNS) [22]. Therefore, being the chief obstacle to the delivery of drugs to the CNS, BBB permeability was selected to identify the candidate ingredients that targeted the patient's CNS involved in the damp depression. Here, a reliable *in silico* BBB model constructed in our previous work [23] was employed to predict the BBB permeabilities of all compounds in DZXYS databases. Finally, the compounds with BBB values greater than -0.3 were identified as favorable BBB permeabilities, since molecules with less than -0.3 is not permeable.

Target Fishing and Gene Ontology Enrichment Analysis

Identifying compound-target interaction is a crucial task in drug discovery and elucidating the mechanism of drug action [24]. Here, a combinatorial method enriched with chemogenomic, similarity ensemble and data-mining approaches was employed to identify the compound-target interaction. First, the filtered active compounds were sent to the TTD (Therapeutic Targets Database <http://bidd.nus.edu.sg/group/ttd/>) and DrugBank databases to mine the compound-target interactions supported by abundant literatures. Second, two robust *in silico* models for identifying compound-target interaction, i.e., omics-based Ligand-Target Chemogenomic model (LTC) [25] and Similarity Ensemble Approach (SEA, <http://sea.bkslab.org/>) [26], were implemented to obtain the target proteins of filtered active compounds. Subsequently, all target information from the above two steps was sent to the database of Uniprot database (<https://www.uniprot.org/>) to eliminate the overlaps and noise. Finally, we mapped all target genes of DZXYS to the databases of Drug Bank, TTD, OMIM and DisGeNET to build the connections with depression.

Gene Ontology (GO) analysis was employed to reveal how active compounds of DZXYS acted on the multiple pathological mechanisms of depression. All depression-related target proteins of DZXYS were inputted into ClueGO plugin of Cytoscape 3.8.2 using $p\text{-values} \leq 0.05$ as the restriction, and GO enriched terms for cellular components, biological process and molecular functions were identified.

Network Construction and Analysis

Abundant experimental and clinical evidence has demonstrated that the pathological mechanism of depression mainly implicated in disorder of neurotransmitter, dysfunction of nervous system (BDNF, brain-derived neurotrophic factor), disorder of signal transduction (HPA (Hypothalamic Pituitary Adrenal) axis), metabolism imbalance, as well as dysregulation of inflammatory and immune responses. All target proteins of DZXYS were mapped onto these different pathological mechanisms of depression. Subsequently, Compound-Target network (C-T network) implicated in six individual pathological mechanisms were constructed to further discover the underlying mechanism of DZXYS in the treatment of depression. Pathway enrichment was employed to obtain the representative pathways of six pathological mechanism involved in depression based on Metascape databases [27]. Afterwards, these pathways and their linked target genes of DZXYS were used to construct T-P network. All visualized network graphs were constructed by Cytoscape 3.8.2 [28].

Results and Discussion

Filtering Active Components from DZXYS

A total of 1078 DZXYS candidate molecules were finally extracted from abundant literatures and TCMSP database, including 1036 ingredients from these 8 herbal medicines and 42 aglycones (Supplementary Table S1). Among them, Chai-Hu owned the largest number of constituents (347 molecules), as followed by Gan-Cao with 280 components and Dang-Gui with 126 chemicals. Other herbal medicines, Zhi-Zi, Bai-Shao, Mu-Dan-Pi, Bai-Zhu, and Fu-Ling contained 97, 84, 57, 55 and 33 compounds, respectively.

In general, an oral administrated medicine must overcome several *in vivo* obstacles like bioavailability, chemical and physi-

cal stabilities, before exhibition of the pharmacological effect at the binding site. Therefore, to identify the active molecules from DZXYS, we employed three classical *in silico* ADME parameters (including DL, OB and BBB). As a result, 106 active molecules from these eight herbal medicines in the DZXYS were found meeting the screening thresholds with satisfactory ADME profiles. For example, liquiritigenin, a flavonoid compound in Gan-Cao, displayed the favorable pharmacokinetic profiles (OB=32.76%, DL=0.18 and BBB=-0.29), and this compound was proved alleviating depressive-like behavior via inhibiting p-phosphatidylinositol 3-kinase (PI3K)/Akt/p-Mammalian Target of Rapamycin (mTOR) pathway and improving BDNF/p-tropomyosin-related kinase B (TrkB) pathway in mice model of depression [29]. A phytosterol compound beta-sitosterol (OB=36.91%, DL=0.87 and BBB=0.75) which is shared by Bai-Shao, Dang-Gui, Gan-Cao, Mu-Dan-Pi and Zhi-Zi also displayed anti-depressant-like activity in mice model. Betulinic acid (OB=55.38%, DL=0.78 and BBB=0.22), a pentacyclic triterpenoid shared by Bai-Shao, Gan-Cao and Mu-Dan-Pi, also reduced depressant-like behavior in tail suspension test [30]. A stigmastane-type phytosterol in Chai-Hu, α -spinasterol (OB=42.98%, DL=0.76 and BBB=0.79), which is a multitarget transient receptor potential cation channel subfamily V member 1 (TRPV1) antagonist and cyclooxygenase (PTGS1 (prostaglandin G/H synthase 1) and PTGS2 (prostaglandin G/H synthase 2)) inhibitor, exhibited anti-depressant-like effect in mice model [31,32]. Hederagenin (OB=36.91%, DL=0.75 and BBB=0.96), a triterpenoid saponin in Chai-Hu, also exhibited the anti-depression activity via regulating the expression of monoamine neurotransmitters and 5-hydroxytryptamine (serotonin) 1A receptor mRNA in rat model of depression [33]. α -Amyrin (OB=39.51%, DL=0.76 and BBB=1.28) was a pentacyclic triterpenoid from Bai-Zhu, and also exhibited the potent anti-depression effect through increasing the activities of amine oxidase [flavin-containing] A (MAOA) and Gamma Aminobutyric acid (GABA) in mice hippocampus [34]. Isoimperatorin (OB=45.46%, DL=0.23 and BBB=0.66), an active furocoumarin in Zhi-Zi, had a dual PTGS2 selective/5-lipoxygenase inhibitory property, making it possible for a novel anti-inflammatory drug. All these results convincingly proved the reliability and feasibility of our filter model.

As we know, different from the allopathy of western medicine, herbal formula featured as a holistic treatment regulates multiple therapeutic pathways to maintain the balance of human body. Factually, the pathological factors implicated in depression not only focus on the central nervous system, but also correlate with the cytokine hypothesis, oxidative stress and NO pathway [35]. Therefore, some major ingredients which possessed pharmacokinetic and pharmacological properties, but low BBB indexes, were also added into the active compound database, including paeoniflorin (OB=53.87%, DL=0.79, BBB=-1.86) and pachymic acid (OB=33.63%, DL=0.81, BBB=-0.57). For instance, paeoniflorin, the major active constituent found in Bai-Shao and Mu-Dan-Pi, had been reported to modulate HPA axis, via up-regulating serotonergic (serotonin and 5-hydroxyindoleacetic acid) and noradrenergic (noradrenaline) systems, ameliorating neuroinflammation and depressive-like behaviors, which contributed to a candidate molecule for the treatment of depression [36,37]. The other compound pachymic acid, a predominant triterpenoid in Fu-Ling, also had multiple pharmacological properties, such as anti-inflammation, anti-cancer and anti-vomiting [38].

To avoid the missed active constituents, a few active molecules were also manually added into the active molecules da-

tabase of DZXYS based on text-mining in literature databases. For example, geniposide (OB=14.64%, DL=0.44, BBB=-2.61), as one of the main active molecules (73.44±2.62mg/g) in Zhi-Zi with both medicinal and nutritional effects [39], produced the antidepressant-like property via regulating HPA axis in chronic unpredictable mild stress-induced depressive rats [40], and this compound also ameliorated the depression-like behavior through up-regulating BDNF expression in streptozotocin-evoked diabetic mice [41]. In addition, albiflorin (OB=12.09%, DL=0.77, BBB=-2.19) had a high concentration (12.61±3.09 mg/g) in Bai-

Shao [42], exhibited obvious anti-depressant-like effect via up-regulating the expression levels of hippocampal serotonin (5-HT)/Norepinephrine (NE) and BDNF in mice model of depression [43]. Ferulic acid (OB=39.56%, DL=0.06, BBB=-0.03) in Dang-Gui is a marker for evaluating the quality of this herb, because of relative high concentration (0.21~1.75mg/g dry weight) and abundant pharmacological effects, like antidepressant-like, anti-inflammatory, anti-microbial, and anti-hyperlipidemic properties [44]. Therefore, these molecules were manually added into the active molecule database of DXP, although they obtained the low DL values or OB indexes.

By combining the results of filter model and text-mining, finally, 120 molecules were screened as the candidate active ingredients of DZXYS, and their ADME parameters were displayed in Table 1. Among them, Gan-Cao has the largest number of active ingredients (72 molecules), as followed by Chai-Hu and Mu-Dan-Pi both with

11 active molecules. In addition, Bai-Shao, Bai-Zhu, Mu-Dan-Pi, Dang-Gui and Bai-Shao contained 7, 6, 5, 4 and 4 active ingredients, respectively.

Target Identification and Gene Ontology Enrichment Analysis

To further decode the therapeutic targets of DZXYS, a comprehensive range of target identification was provided. As a result, 431 targets were collected for 119 active ingredients, while only one compound (octalupine, CH234) had no related target protein. In order to focus on depression-related genes, 850 depression-related targets were collected based on the search engine results from four gene-disease databases. And then 431 targets and 119 active compounds of DZXYS were mapped to these 850 depression-related targets to build the connections with depression. Finally, 111 active compounds of DZXYS were identified interacting with 112 depression-related proteins (as displayed in Table S2).

As shown in Table S2, the overwhelming majority of those active ingredients (105 out of 111 compounds) were connected with more than one target proteins, displaying their multiple mechanisms of action. For example, ferulic acid, the main active compound of Dang-Gui, not only inhibited MAOA selectively [45], but also prevented the activity of ornithine decarboxylase (ODC1) by 46% [46]. Glycyrrhizic acid, which is the major sweet-tasting ingredient of Gan-Cao, not only suppressed the activity of caspase-3 (CASP3) [47], but also inhibited corticosteroid 11-beta-dehydrogenase isozyme 1 (HSD11B1) activity in rat [48]. Paeoniflorin, the major active compound of Bai-Shao and Mu-Dan-Pi, exerted a neuroprotective effect through activating adenosine receptor A1 (ADORA1) in rat [49], and also inhibited TNF (tumor necrosis factor), IL6 (Interleukin-6) to improve the cardiac function in rat model with ventricular remodeling

[50]. Enoxolone, also called as glycyrrhetic acid, was a pentacyclic triterpenoid derivative of Gan-Cao, and inhibited the expression of cytochrome P450 2E1 (CYP2E1) to attenuate the acetaminophen-induced liver injury in mice [51]. Additionally, as the major active ingredient of Zhi-Zi, geniposide upregulated HMOX1 (heme oxygenase 1) expression to improve the capacity of anti-oxidant effect in primary hippocampal neurons [52]. All these results documented that the bioactivity compounds in herbal medicines exhibited the promiscuous actions.

In order to explore the underlying molecular mechanism of these 112 targets DZXYS, GO enrichment analysis, including biological process, molecular function, and cellular component were carried out. As shown in Figure 2A, the top 5 enriched GO molecular processes included G protein-coupled amine receptor activity, regulation of blood vessel diameter, cellular response to catecholamine stimulus, chemical synaptic transmission, postsynaptic, and neurotransmitter biosynthetic process, which have been suggested to implicate in the pathological mechanism of depression. For example, G protein-coupled amine receptor, which is the largest human membrane protein family, is involved in numerous physiological functions such as parasympathetic and

sympathetic nervous functions, immune regulation and metabolism, and has been found to be major therapeutic targets in various human diseases like psychiatric diseases and neurodegeneration [53].

In term of GO molecular function (Figure 2B), the candidate chemicals were mainly enriched in postsynaptic neurotransmitter receptor activity, G protein-coupled amine receptor activity, and steroid hormone receptor binding, etc. These molecular functions are linked with the pathological pathways of depression. For example, anti-depression drugs, such as Selective Serotonin Reuptake Inhibitors (SSRIs), Tricyclic Antidepressants (TCA), and Serotonin-Norepinephrine Reuptake Inhibitors (SNRIs), primarily inhibited the reuptake of monoamine neurotransmitters (like dopamine, noradrenaline, and serotonin) in an attempt to enhance the persistence of these neurotransmitters in the synaptic space to trigger postsynaptic neurotransmission receptors [54,55]. For GO cellular component (Figure 2C), the major enriched GO ontologies were post-synapse, membrane raft, dendritic spine, and so on, which are closely related with depressive disease. For example, the postsynaptic release of endocannabinoids played an important role in long-term depression in striatum [56].

Network Analysis to Explore the Therapeutic Mechanisms of DZXYS

Compound-Target network analysis: Modulation of Neurotransmitter Systems Plenty of experimental and clinical studies documented that neurotransmitter systems play the fundamental roles in the pathological mechanism of depression [57,58]. Actually, the petroleum ether soluble fraction and water-EtOH soluble fraction of DZXYS displayed anti-depressive effects through regulating the monoamine neurotransmitters (like 5-HT, dopamine and noradrenaline) and amino acid neurotransmitters in the hippocampus of rat models with Chronic

Unpredictable Mild Stress (CUMS) [59]. Therefore, the C-T network of DZXYS implicated in neurotransmitter systems was constructed as displayed in Figure 3.

Figure 3 showed that 43 target proteins are implicated in disorder of neurotransmitter secretion. Among them, ESR1 (es-

Table 1: The active ingredients and ADME parameters of DZXYS.

MOL ID	Molecule Name	CAS	DL	OB(%)	BBB	Herbs
CH257	(+)-Anomalin	73069-28-0	0.66	46.06	0.00	Chai-Hu
BZ016	(24S)-24-Propylcholesta-5-ene-3beta-ol	64997-52-0	0.78	36.23	1.09	Bai-Zhu
GC200	(2R)-7-Hydroxy-2-(4-hydroxyphenyl) chroman-4-one	41680-09-5	0.18	71.12	-0.25	Gan-Cao
GC173	1,3-Dihydroxy-9-methoxy-6- benzofurano[3,2-c]chromenone	-	0.43	48.14	-0.19	Gan-Cao
GC218	1-Methoxyphaseollidin	65428-13-9	0.64	69.98	0.48	Gan-Cao
CH205	3',4',5',3,5,6,7-Heptamethoxyflavone	17245-30-6	0.59	31.97	0.08	Chai-Hu
ZZ053	3-Epioleanolic acid	25499-90-5	0.76	32.03	0.39	Zhi-Zi
GC225	3'-Hydroxy-4'-O-Methylglabridin	-	0.57	43.71	0.73	Gan-Cao
GC233	3'-Methoxyglabridin	74046-05-2	0.57	46.16	0.47	Gan-Cao
BZ032	3β-Acetoxyatractylone	61206-10-8	0.22	54.07	1.08	Bai-Zhu
GC237	4'-Methoxyglabridin	-	0.52	36.21	0.61	Gan-Cao
MDP040	4-O-methylpaeoniflorin_qt	-	0.43	67.24	-0.15	Mu-Dan-Pi
GC247	6-Prenylated eriodictyol	-	0.41	39.22	-0.29	Gan-Cao
GC249	7-Acetoxy-2-methylisoflavone	3211-63-0	0.26	38.92	0.16	Gan-Cao
GC057	7-Methoxy-2-methyl isoflavone	19725-44-1	0.20	42.56	0.56	Gan-Cao
BZ055	8β-Ethoxy atractylenolide	113269-35-5	0.21	35.95	1.12	Bai-Zhu
ZZ062	Ammidin	482-44-0	0.22	34.55	0.92	Zhi-Zi
CH216	Areapillin	83162-82-7	0.41	48.96	-0.29	Chai-Hu
BS007	Beta-sitosterol	83-46-5	0.75	36.91	0.87	Bai-Shao
DG021	Beta-sitosterol	83-46-5	0.75	36.91	0.87	Dang-Gui
GC011	Beta-sitosterol	83-46-5	0.75	36.91	0.87	Gan-Cao
MDP010	Beta-sitosterol	83-46-5	0.75	36.91	0.87	Mu-Dan-Pi
ZZ014	Beta-sitosterol	83-46-5	0.75	36.91	0.87	Zhi-Zi
BS002	Betulinic acid	472-15-1	0.78	55.38	0.22	Bai-Shao
GC007	Betulinic acid	472-15-1	0.78	55.38	0.22	Gan-Cao
MDP005	Betulinic acid	472-15-1	0.78	55.38	0.22	Mu-Dan-Pi
ZZ069	Corymbosin	18103-41-8	0.41	51.96	-0.21	Zhi-Zi
FL028	Dehydroeburicoic acid	6879-05-6	0.83	44.17	-0.16	Fu-Ling
GC278	Dehydroglyasperins C	199331-35-6	0.37	53.82	-0.12	Gan-Cao
FL015	Eburicoic acid	560-66-7	0.81	38.70	-0.04	Fu-Ling
FL010	Ergosta-7,22e-dien-3beta-ol	1105-11-9	0.72	43.51	0.91	Fu-Ling
FL011	Ergosterol peroxide	2061-64-5	0.81	40.36	0.34	Fu-Ling
ZZ068	Ethyl oleate (NF)	111-62-6	0.19	32.40	1.10	Zhi-Zi
GC068	Euchrenone	-	0.57	30.29	0.39	Gan-Cao
GC175	Eurycarpin A	166547-20-2	0.37	43.28	-0.06	Gan-Cao
GC013	Formononetin	485-72-3	0.21	69.67	0.02	Gan-Cao
GC254	Gadelaidic acid	506-31-0	0.20	30.70	0.94	Gan-Cao
GC116	Gancaonin A	27762-99-8	0.40	51.08	0.13	Gan-Cao
GC117	Gancaonin B	124596-86-7	0.45	48.79	-0.10	Gan-Cao
GC258	Gancaonin G	126716-34-5	0.39	60.44	0.23	Gan-Cao
GC259	Gancaonin H	126716-35-6	0.78	50.10	-0.14	Gan-Cao
GC123	Gancaonin L	129145-50-2	0.41	66.37	-0.13	Gan-Cao
GC124	Gancaonin M	129145-51-3	0.41	30.49	0.21	Gan-Cao
GC126	Gancaonin O	129145-53-5	0.41	44.15	-0.28	Gan-Cao
GC170	Glabranin	41983-91-9	0.31	52.90	0.31	Gan-Cao
GC171	Glabrene	60008-03-9	0.44	46.27	0.04	Gan-Cao
GC168	Glabridin	59870-68-7	0.47	53.25	0.36	Gan-Cao
GC172	Glabrone	60008-02-8	0.50	52.51	-0.11	Gan-Cao
GC089	Glepidotin A	42193-83-9	0.35	44.72	0.06	Gan-Cao
GC090	Glepidotin B	87440-56-0	0.34	64.46	-0.09	Gan-Cao
GC070	Glyasperin B	142488-54-8	0.44	65.22	-0.09	Gan-Cao
GC073	Glyasperin C	142474-53-1	0.40	45.56	0.07	Gan-Cao
GC072	Glyasperin F	145382-61-2	0.54	75.84	-0.15	Gan-Cao
GC265	Glyasperins M	-	0.59	72.67	-0.04	Gan-Cao
GC139	Glycyrin	66056-18-6	0.47	52.61	-0.13	Gan-Cao
GC045	Glycyrol	23013-84-5	0.67	90.78	-0.20	Gan-Cao
GC096	Glypallichalcone	146763-58-8	0.19	61.60	0.23	Gan-Cao
GC167	Glyzaglabrin	65242-64-0	0.35	61.07	-0.20	Gan-Cao
FL024	Hederagenin	465-99-6	0.75	36.91	0.96	Fu-Ling
GC243	Icos-5-enoic acid	7329-42-2	0.20	30.70	1.09	Gan-Cao
GC034	Inermine	2035-15-6	0.54	75.18	0.40	Gan-Cao
GC239	Inflacoumarin A	158446-33-4	0.33	39.71	-0.24	Gan-Cao
GC204	Isobavachin	31524-62-6	0.32	36.57	-0.04	Gan-Cao
GC216	Isoformononetin	486-63-5	0.21	38.37	0.25	Gan-Cao
GC207	Isoglycyrol	23013-86-7	0.84	44.70	0.05	Gan-Cao
ZZ063	Isoimperatorin	482-45-1	0.23	45.46	0.66	Zhi-Zi
GC076	Isotrifoliol	329319-08-6	0.42	31.94	-0.25	Gan-Cao
GC008	Jaranol	3301-49-3	0.29	50.83	-0.22	Gan-Cao

GC077	Kanzonol B	-	0.35	39.62	-0.12	Gan-Cao
GC246	Kanzonol F	-	0.89	32.47	0.56	Gan-Cao
GC099	Kanzonol U	178330-48-8	0.38	58.44	0.34	Gan-Cao
GC082	Kanzonol W	184584-82-5	0.52	50.48	0.04	Gan-Cao
GC261	Licoagrocarpin	202815-29-0	0.58	58.81	0.61	Gan-Cao
GC270	Licoagroisoflavone	-	0.49	57.28	0.09	Gan-Cao
GC110	Licoarylcoumarin	125709-31-1	0.43	59.62	-0.23	Gan-Cao
GC022	Licochalcone a	58749-22-7	0.29	40.79	-0.21	Gan-Cao
GC109	Licochalcone G	1261240-29-2	0.32	49.25	-0.04	Gan-Cao
GC142	Licocoumarone	118524-14-4	0.36	33.21	0.06	Gan-Cao
GC145	Licoisoflavanone	66067-26-3	0.54	52.47	-0.22	Gan-Cao
GC143	Licoisoflavone	66056-19-7	0.42	41.61	-0.27	Gan-Cao
GC144	Licoisoflavone B	66056-30-2	0.55	38.93	-0.18	Gan-Cao
GC115	Licoricone	51847-92-8	0.47	63.58	-0.14	Gan-Cao
CH122	Linoleyl acetate	5999-95-1	0.20	42.10	1.08	Chai-Hu
GC040	Liquiritigenin	578-86-9	0.18	32.76	-0.29	Gan-Cao
CH230	Longikaurin A	75207-67-9	0.53	47.72	0.09	Chai-Hu
GC054	Lupiwighteone	104691-86-3	0.37	51.64	-0.23	Gan-Cao
ZZ044	Mandenol	544-35-4	0.19	42.00	1.14	Zhi-Zi
GC047	Medicarpin	607363-34-8	0.34	49.22	0.53	Gan-Cao
CH234	Octalupine	6809-89-8	0.28	47.82	0.30	Chai-Hu
GC274	Odoratin	53948-00-8	0.30	49.95	-0.24	Gan-Cao
GC275	Phaseol	88478-02-8	0.58	78.77	-0.06	Gan-Cao
GC094	Phaseolinisoflavan	40323-57-7	0.45	32.01	0.46	Gan-Cao
GC050	Pinocembrin	480-39-7	0.18	64.72	0.12	Gan-Cao
CH249	Sainfuran	90664-32-7	0.23	79.91	0.23	Chai-Hu
GC067	Shinflavanone	157414-03-4	0.72	31.79	0.25	Gan-Cao
GC151	Shinpterocarpin	157414-04-5	0.73	80.30	0.68	Gan-Cao
CH051	Stigmasterol	83-48-7	0.76	43.83	1.00	Chai-Hu
DG026	Stigmasterol	83-48-7	0.76	43.83	1.00	Dang-Gui
ZZ020	Stigmasterol	83-48-7	0.76	43.83	1.00	Zhi-Zi
ZZ083	Sudan III	85-86-9	0.59	84.07	0.10	Zhi-Zi
ZZ046	Supraene	111-02-4	0.42	33.55	1.73	Zhi-Zi
FL004	Trametenolic acid	24160-36-9	0.80	38.71	-0.14	Fu-Ling
GC023	Vestitol	20879-05-4	0.21	74.66	0.30	Gan-Cao
GC276	Xambioona	82345-36-6	0.87	54.85	0.52	Gan-Cao
BZ011	α -Amyrin	638-95-9	0.76	39.51	1.28	Bai-Zhu
CH318	α -Spinasterol	481-18-5	0.76	42.98	0.79	Chai-Hu
BZ026	Atractylenolide I	73069-13-3	0.15	37.37	1.29	Bai-Zhu
BZ029	Atractylone	6989-21-5	0.13	41.10	1.85	Bai-Zhu
FL017	Pachymic acid	29070-92-6	0.81	33.63	-0.57	Fu-Ling
DG022	Ferulic acid	537-98-4	0.06	39.56	-0.03	Dang-Gui
MDP017	Paeonol	552-41-0	0.04	28.79	0.84	Mu-Dan-Pi
BS068	Paeoniflorin	23180-57-6	0.79	53.87	-1.86	Bai-Shao
MDP022	Paeoniflorin	23180-57-6	0.79	53.87	-1.86	Mu-Dan-Pi
BS071	Albiflorin	39011-90-0	0.77	12.09	-2.19	Bai-Shao
DG056	(Z)-Ligustilide	4431-01-0	0.07	51.30	1.24	Dang-Gui
ZZ080	Geniposide	24512-63-8	0.44	14.64	-2.61	Zhi-Zi
CH240	Saikosaponin a	20736-09-8	0.09	32.39	-2.93	Chai-Hu
CH242	Saikosaponin D	20874-52-6	0.09	34.39	-2.89	Chai-Hu
GC066	Enoxolone	471-53-4	0.74	22.05	-0.53	Gan-Cao
GC136	Glycyrrhizic acid	1405-86-3	0.11	19.62	-2.86	Gan-Cao

trogen receptor), ESR2 (estrogen receptor beta), PPARG (peroxisome proliferator activated receptor gamma), ODC1, ADRB2 (beta-2 adrenergic receptor), ADRA1B (alpha-1B adrenergic receptor), MAOB (amine oxidase [flavin-containing] B), and TYR (tyrosinase), which linked with 69, 61, 51, 40, 36, 25, 21 and 21 active ingredients of DZXYs, respectively, were the hub targets of DZXYs for regulating neurotransmitter systems. For example, ESR1 played a certain role in etiology of postpartum depression probably via regulating the signaling of neurotransmitters [60]. Additionally, the researches of electrophysiology and microdialysis proved that the activation of PPARG weakened the ability of drug abuse to mediate dopaminergic neurons of the ventral tegmental area, and then decreased the level of dopamine (one type of neurotransmitter) released in the nucleus accumbens [61,62].

As displayed in Figure 3, five ingredients, including MDP017 (paeonol), DG022 (ferulic acid), GC057 (7-methoxy-2-methyl isoflavone), DG056 ((Z)-ligustilide), and GC023 (vestitol), were the main active ingredients of this formula to regulate neurotransmitter system, because of their hub roles in C-T network and/or high contents in the herbal medicine of DZXYs. For instance, paeonol was the main ingredient isolated from Mu-Dan-Pi, and interacted with 15 target proteins in C-T network (Figure 3), such as MAOA, MAOB, TNF (tumor necrosis factor), and ADRB1 (beta-1 adrenergic receptor), et al. In fact, this phenol compound was documented not only inhibiting MAOA and MAOB in a dose-dependent manner with IC50 values of 54.6 and 42.5 μ M [63], respectively, but also dose-dependently suppressing TNF formation [64].

Regulation of BDNF, HPA axis and metabolism: Based on the

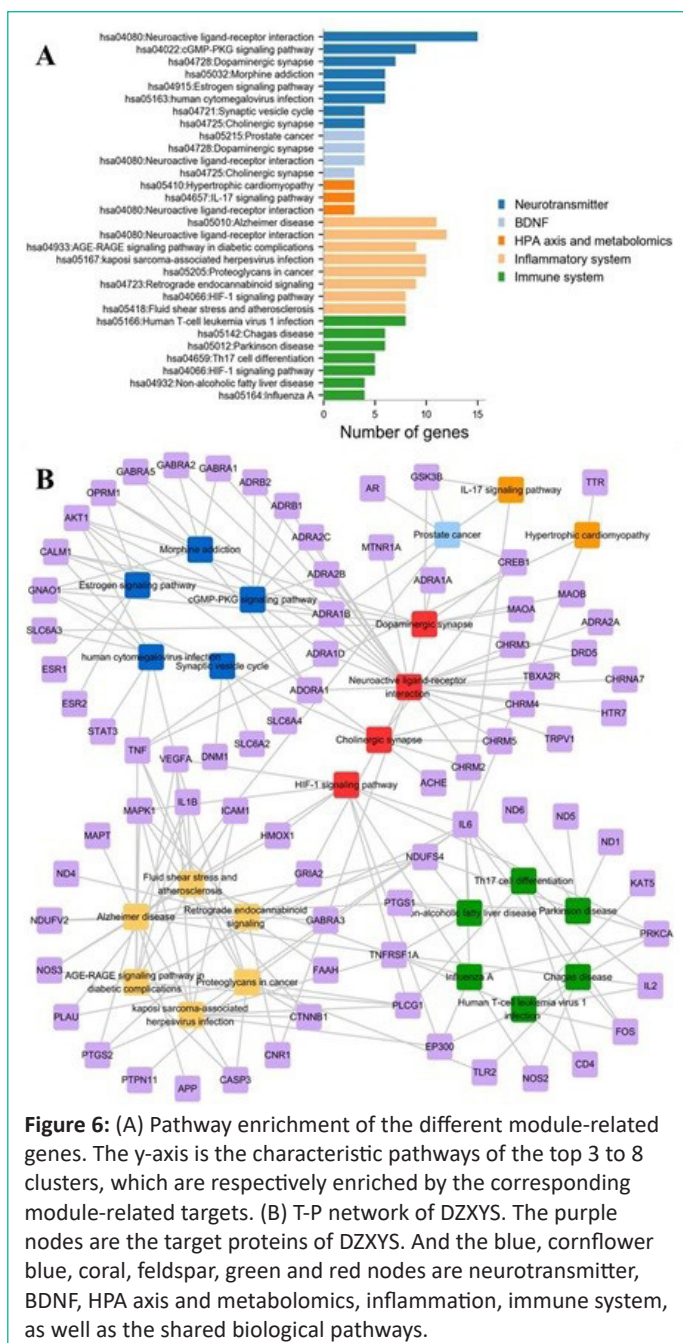


Figure 6: (A) Pathway enrichment of the different module-related genes. The y-axis is the characteristic pathways of the top 3 to 8 clusters, which are respectively enriched by the corresponding module-related targets. (B) T-P network of DZXYS. The purple nodes are the target proteins of DZXYS. And the blue, cornflower blue, coral, feldspar, green and red nodes are neurotransmitter, BDNF, HPA axis and metabolomics, inflammation, immune system, as well as the shared biological pathways.

beta (GSK3B), were

implicated in the regulation of BDNF to display the anti-depression effect. For instance, the hub target AR, targeted by 64 active ingredients of DZXYS, was proved to modify the BDNF expression through modulating the expression of miR-204-5p, and then ameliorated the depressive-like behavior in the Chronic Mild Stress (CMS) mice model of depression [67]. Besides AR, several other targets, including ESR2, GSK3B and MAOB, which displayed a high number of interactions with the active compounds, were considered as the hub proteins to regulate BDNF to exhibit anti-depressive effects. For example, the weakened ESR2 signaling gave rise to down-regulated transcription of BDNF gene, which resulted in the low levels of BDNF in the hippocampal region [68]. All the evidence suggested that DZXYS may regulate multiple BDNF-related targets (like, AR, ESR2, GSK3B and MAOB) to exhibit the therapeutic effects on depression.

Dysregulation of HPA axis activity in patients with major depressive disorder is among the unanimous and powerful biological discoveries in psychiatry, which has been found to restore with efficacious treatment, although inconsistencies ex-

ist [69,70]. Factually, several researches had been proved that DZXYS could suppress the abnormal hyperactivity of HPA axis via acting on the arginine vasopressin to display anti-depressant property [59,71]. Some active ingredients of DZXYS in Figure 4, like paeoniflorin (MDP022, one of the major monoterpene glycosides in Bai-Shao) and glycyrrhizic acid (GC136, one of the major bioactive triterpene glycosides in Gan-Cao), also had been proved to exhibit anti-depressant effect through reducing HPA activity [72,73]. Taking paeoniflorin as an example, this compound ameliorated the depression-like behavior in male offspring rats, at least partially through restoring the HPA axis hyperfunction [73]. All these results indicated that several active ingredients of DZXYS (like paeoniflorin and glycyrrhizic acid) exhibited synergic anti-depressant effect through reducing the HPA axis dysfunction.

With the development of analytical technologies, several key metabolites, such as malonate, formate, glutamate, glucose, fructose, m-hydroxyphenylacetate, alanine, lipid/protein complexes, and amino acids were closely related to depressive disorder [74-76], and these metabolites were found mainly involved in energy metabolism, gut microbial metabolism, lipid metabolism and amino acids metabolism [57]. As displayed in Figure 4, 9 target proteins, like GSK3B, ADRB2, ABCB1 and ADRB1, have significant relationships with the pathological mechanism of depression via metabolomics. For example, the hub protein GSK3B, a serine threonine kinase, targeted by 48 active ingredients, was regarded as one of central regulators in the regulation of glucose metabolism [77]. Moreover, this protein was suggested to be involved in the pathogenetic mechanism of major depressive disorder, and to be a therapeutic target as an improver of anti-depressant action [78]. Therefore, all these findings proposed that DZXYS could regulate several metabolites to exhibit anti-depressant effects.

Inflammation and immune regulation: There is growing evidence that depression and inflammation have strong bidirectional links, fueling one another [79]. Specifically, all cardinal features of an inflammatory response were discovered in patients with major depression, such as enhanced expression of both pro-inflammatory cytokines and their receptors [80]. Therefore, the target proteins of DZXYS implicated in inflammatory response were also discussed in details. The C-T network (Figure 5) showed that 58 targets such as PTGS2, NOS2, PPARG, SCN5A and DPP4 related to inflammatory response. For example, PTGS2 was targeted by the 83 active ingredients of DZXYS, such as paeonol, glabrone, (Z)-ligustilide, ferulic acid, and kanzonol B. In rat models of depression, PTGS2 inhibition ameliorated the depression-like behaviors through suppressing neuroinflammation, neural apoptosis, and oxidative stress [81]. Besides, 15 active ingredients were experimentally validated to exhibit anti-inflammatory properties through inhibiting PTGS2 at mRNA and/or protein levels, such as (z)-ligustilide [82], ferulic acid [83], stigmasterol [84], hederagenin [85], formononetin [86], licochalcone A [87], liquiritigenin [88], glycyrol [89], pinocembrin [90], isotrifoliol [91], glabridin [92], paeonol [64], imperatorin [93], isoimperatorin [94], and α -spinasterol [95]. Another hub target, NOS2 linked with 56 target proteins were involved in the pathological mechanism of major depressive disorder. Recent studies showed that NOS2 inhibition was used as an adjuvant therapy to improve the therapeutic efficacy of serotonergic antidepressants [96], and the inhibition of NOS2 induced antidepressant-like properties in rodents [97,98]. In addition, several compounds like glycyrol [89], formononetin [99], licochalcone A [100], isotrifoliol [91], and glabridin [101], were

experimentally confirmed to down-regulate the expression of NOS2, resulting in anti-inflammatory effects.

Several animal models of depression revealed that a cell-mediated immune response induced depression-like behavior, blocking of which reversed the development of depression-like behavior [102-104]. Therefore, the target proteins of DZXYS implicated in the immune system were also discussed in Figure 5. It is worth noting that the expression of NOS2 was induced in several cell types by inflammatory and immunological stimuli, therefore, the hub target NOS2 implicated in the pathophysiology of depression not only through inflammatory system (as mentioned above), but also by regulating immune system. Additionally, IL-2 (interleukin-2), a central regulator of immune responses, had been displayed to directly modulate dopaminergic activity and neuronal excitability in mesolimbic pathway, which is implicated in the pathological outcomes of depression [105]. As displayed in Figure 5, IL-2 was targeted by 18 active ingredients of DZXYS, and was identified as the

hub target for the anti-depression property of DZXYS. All these results indicated that DZXYS exhibited the anti-depression effects via regulating multiple immune-related target proteins.

Pathway Analysis of DZXYS

To further decipher the underlying mechanism of DZXYS in the treatment of depression, we enriched the targets of DZXYS with KEGG signaling pathway based on Metascape tool. The top 3 to 8 clusters (one pathway per cluster) distributed in the modules of neurotransmitter, BDNF, HPA axis, metabolomics, inflammatory and

Immune systems were shown in Figure 6A. These pathways and linked genes were used to build T-P network as displayed in Figure 6B. As displayed in Figure 6A and 6B, the pathway of neuroactive ligand-receptor interaction had the highest number of linked targets, including 15 neurotransmitter-related genes, 12 inflammation-related targets, 4 BDNF-related proteins, and 3 targets implicated in HPA axis and metabolomics.

Subsequently, HIF-1 signaling pathway showed the higher number of connections with 8 inflammation-related and 5-immune-related genes, followed by the pathway involved in Alzheimer disease with 11 inflammation-related genes.

All these pathways were closely related to the pathological mechanism of depression. For example, in the pathway of neuroactive ligand-receptor interaction, several neuroactive receptors were implicated in the therapeutic mechanism of depression, such as epinephrine and norepinephrine receptors (ADRA1D, ADRA2A,

ADRA1B, ADRA2B, ADRA2C, ADRB1 and ADRB2), GABA receptors (GABRA1, GABRA2 and GABRA5), and dopamine receptors (DRD1 and DRD5), *et al.* In fact, the α -adrenergic receptors (ADRA2A, ADRA2B and ADRA2C), which regulated the release of norepinephrine, serotonin and other neurotransmitters, have been proved to be the promising targets for the treatment of depression [106]. Additionally, Hypoxia Inducible Factor-1 (HIF-1), which driven transcriptional response in hypoxia, might have a favorable effect on depression. The target genes of HIF-1, like vascular endothelial growth factor and erythropoietin, had been documented to exhibit antidepressant properties in several models [107]. All these findings made HIF-1 signaling pathway a potential target of anti-depressive agents. The pathways involved in Alzheimer disease also showed the higher

topological property in the T-P network of DZXYS, becoming the major therapeutic pathway in treatment of depression. In fact, depression is one of the most common neuropsychiatric disturbances in Alzheimer disease, with estimated prevalence ranging from 25% to 74.9% [108,109].

Conclusion

Depression is a multifactorial psychiatric disorder which involved various pathological mechanisms. DZXYS as a TCM formula plays a significant role in treating multiple pathogenesis against depression through multi-compounds, multi-target, and multi-pathway method. However, it remains unclear about the active compounds, potential targets, related pathways and complex therapeutic mechanisms of DZXYS in the treatment of depression. Therefore, a systems pharmacology method is developed to explore the pharmacological mechanisms of DZXYS on depression therapy.

In current study, 111 active compounds and 112 related protein targets were obtained by ADME evaluation system and target fishing. Then GO enrichment analysis was used to reveal the relationships between potential targets and multiple pathogenesis to further explore the therapeutic mechanism of DZXYS for the treatment of depression. Finally, C-T and T-P networks were established to exhibit the therapeutic effects of DZXYS against depression via regulating the neurotransmitter systems imbalance, BDNF, HPA, inflammation, and immune response. The present work will not only accelerate the in-depth understanding of the complicated therapeutic mechanism of DZXYS on depression therapy from a systematic perspective, but also will provide a way to promote TCM modernization and internationalization.

Author Statements

Acknowledgment

The research is supported by the Key Science and Technology Program of Henan Province (No. 192102310439), Joint Youth Fund for Basic and Applied Basic Research of Guangdong Province (No. 2019A1515111095), International Cooperative Research Project of Shenzhen Collaborative Innovation Program (No. GJHZ20190821173801659), and the Key Scientific Research Projects of Higher Education Institutions in Henan Province (No. 20B180006).

Conflict of Interest

The authors declare no conflict of interest.

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