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Multi-Target Regulation Mechanisms of Systemic Lupus Erythematosus: A Network Pharmacology and Molecular Docking Study on Active Compounds from Artemisia argyi

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Article

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Abstract

As a complex autoimmune condition, Systemic Lupus Erythematosus (SLE) features aberrant immune responses and multi-system involvement. Current therapeutic strategies face limitations such as drug resistance and adverse effects, necessitating novel therapeutic approaches. This study aimed to investigate the therapeutic potential and molecular mechanisms of active compounds from Artemisia argyi in SLE treatment using network pharmacology and molecular docking techniques.

Materials and Methods: Active constituents of Artemisia argyi were identified from the TCMSP database using screening criteria of oral bioavailability (OB ≥ 30%) and drug-likeness (DL ≥ 0.18). Potential targets of these compounds were identified using the PharmMapper server and UniProt database. SLE related targets were retrieved from OMIM and GeneCards databases. The intersection of compound and disease targets was identified using Venny 2.1, a protein-protein interaction (PPI) network was then constructed via STRING, and GO and KEGG pathway enrichment analyses were carried out with DAVID. Key active compounds were validated for target binding using molecular docking via Auto Dock Vina. Select the high binding energy as the key active genes and find its downstream target genes through the JASPER database and Ensembl database. Quantitative Real-Time PCR (qRT-PCR) analysis was performed to corroborate the pharmacological results obtained from the network.

Results: Nine active compounds of Artemisia argyi were identified, associated with 380 protein targets. Intersection analysis with 218 SLE related genes revealed 19 key targets, including CASP3, HSP90AA1, and PPARG. GO analysis indicated significant enrichment in biological processes such as leukocyte activation and immune response. KEGG pathway analysis highlighted 18 pathways. Molecular docking demonstrated strong binding affinities (binding energy < -5.5 kcal/mol) of quercetin and naringenin with core targets, suggesting their potential to modulate inflammatory and apoptotic pathways. The qRT-PCR results showed that the extract of Artemisia argyi could activate PPARG and bind to promote the transcription of downstream genes ($P<0.05$).

Conclusion: This study reveals the active ingredients and potential molecular mechanism of Artemisia argyi in the treatment of SLE, and provides a reference for subsequent basic research.

1. Introduction

Systemic Lupus Erythematosus (SLE) is a complicated chronic autoimmune disorder, distinguished by its involvement of multiple organs and systems, as well as pronounced immune system abnormalities. Although current therapeutic strategies, including immunosuppressants and biologics, are effective for some patients, issues such as individual variability in efficacy, long-term adverse effects, and drug resistance severely limit their widespread application[1]. Hence, it is crucial to develop new therapeutic approaches, especially those that can modulate multiple targets. With the rapid development of systems biology and bioinformatics, network pharmacology and molecular docking techniques have emerged as powerful tools for investigating the molecular mechanisms of complex diseases and multi-component drugs. These approaches integrate diverse data resources to elucidate multi-target interactions between diseases and active drug components, while predicting potential mechanisms of action[2]. By incorporating molecular docking techniques, researchers can validate the binding affinities of active compounds with critical targets, providing a foundation for subsequent experimental and clinical studies[3].

Artemisia argyi, a traditional Chinese medicinal herb, has long been used for its anti-dampness, anti-inflammatory, and immunomodulatory effects. Modern pharmacological studies have confirmed that flavonoid and essential oils

in Artemisia argyi exhibit potent antioxidant, anti-inflammatory, and immunomodulatory properties. For instance, the essential oil of Artemisia argyi (AAEO), rich in monoterpenes and sesquiterpenes, demonstrates significant antioxidant capacity, inhibits a variety of pathogens, and reduces oxidative damage caused by free radicals[4]. Furthermore, Artemisia argyi modulates the activity of immune cells, such as macrophages and T cells, suggesting its potential for use in autoimmune diseases[5]. Nevertheless, comprehensive research into the molecular pathways through which the active components of Artemisia argyi exert therapeutic effects on SLE is still limited. Despite the widespread application of network pharmacology and molecular docking techniques in studying active compounds of traditional Chinese medicine, certain limitations persist. For example, the multi-target nature of active compounds makes it challenging to comprehensively elucidate their mechanisms of action. Additionally, experimental data on the specific interactions between Artemisia argyi's active compounds and SLE related targets and signaling pathways remain insufficient. This research is designed to employ network pharmacology and molecular docking methods to comprehensively in vestigate the potential molecular mechanisms underlying the therapeutic effects of active compounds from Artemisia argyi on SLE and conduct experimental verification. The goals of this study are to build a compound-target-disease network to uncover the multi-target regulatory features and to confirm the binding affinities of key active compounds with critical targets via molecular docking, and revealing potential mechanisms by which Artemisia argyi regulates SLE associated signaling pathways, thus providing a theoretical basis for establishing novel treatment strategies.

2. Materials and Methods

2.1 Identification of Active Constituents and Their Targets in Artemisia argyi

Using "Artemisia argyi" as the search keyword, we queried the Traditional Chinese Medicine Systems Pharmacology Database and Analysis Platform (https://tcmspw.com/tcmsp.php) to obtain its chemical constituents and pharmacokinetic parameters. Active compounds were identified using the criteria of OB at least 30% and DL at least 0.18. The selected compounds were uploaded to the PharmMapper (https://www.lilab-ecust.cn/pharmmapper/index.html) server, which predicts potential targets using a pharmacophore target library. The predicted protein targets were further processed using the UniProt database (https://www.uniprot.org/uniprotkb) to retrieve their PDB IDs, ensuring compatibility with downstream molecular docking analysis.

2.2 Identification of Systemic Lupus Erythematosus (SLE) Targets

The identification of targets related to SLE was achieved through keyword searches in the GeneCards (https://www.genecards.org/) and OMIM (https://www.omim.org/) databases using the term "systemic lupus erythematosus". Relevant disease-associated genes were retrieved and compiled for further analysis.

2.3 Formulation of a Protein-Protein Interaction Network

The intersection of drug targets and disease targets was determined using Venny 2.1. Utilizing the STRING database (https://cn.string-db.org/), a PPI network was established, where Homo sapiens was designated as the species and the minimum interaction confidence score was established at 0.4. The network visualization was generated using the STRING online tool to display interactions between proteins.

2.4 Constructing and Analyzing the Network of Active Substances and Their Targets

The active compound-target network was visualized using Cytoscape software (v3.10.1). Core target genes were identified and analyzed using the Degree algorithm, which calculates the connectivity of nodes within the network. This analysis facilitated the establishment of a comprehensive network model linking drugs, diseases, active compounds, and targets, pinpointing key nodes that may be crucial for the treatment of SLE.

2.5 GO Functional Profiling and KEGG Pathway Overrepresentation Assessment

GO and KEGG enrichment analyses of the potential targets were conducted using the DAVID (https://davidbioinformatics.nih.gov/). The significance of enrichment was assessed using a threshold of $P < 0.05$. The results illuminate the potential biological processes and pathways involved in the therapeutic mechanisms of Artemisia argyi.

2.6 Molecular Docking

The three-dimensional structures of key active compounds such as β-sitosterol, stigmasterol, quercetin, and naringenin were obtained from the UniProt and PDB databases, and subsequently processed using Chem3D (version 18.1). The 3D structures of the core protein targets were obtained from the PDB database. Using PyMOL software, target proteins were preprocessed, including removal of water molecules and ligands. AutoDockTools (version 1.5.6) was employed to locate the active binding sites of the targets. Molecular docking simulations were carried out using AutoDock Vina. The binding energy was calculated, and interactions with binding energy < -5.0 kcal/mol were considered reliable for further analysis and prediction.

2.7 Analysis of Key Target Genes

Based on the binding energy in molecular docking, the key functional gene PPARG was obtained.We assume that the active substances in Artemisia argyi activate PPARG, and in combination, promote the transcription of downstream genes. The downstream target genes of PPARG were identified using the hTF and GTRD databases. Meanwhile, genes related to the disease SLE were retrieved from MalaCards. The intersection of the three datasets was taken. The intersection genes were screened using the JASPER database and the Ensembl database to identify the downstream target genes of PPARG and these genes were related to SLE.

2.8 Artemisia argyi Water Extract Preparation

The dried aerial parts of Artemisia argyi were purchased as a finished commercial product from Nanyang Xingwantang Wormwood Products Co., Ltd. (Zhouwan Village, Pushan Town, Nanyang City, Henan Province, China). The place of origin was Nanyang, Henan, China. The product was manufactured according to the enterprise standard Q/NXWT 005-2024, with the production batch number XWT1105. The plant material was identified and quality-controlled by the manufacturer before commercial supply. Because the material was purchased as a finished commercial product rather than collected directly from the wild by the authors, no additional voucher specimen was deposited in a publicly available herbarium, and no field collection permit was required. The use of this commercial plant material complied with relevant institutional, national and international guidelines and legislation concerning plant materials.

A total of 150 g of these leaves was subjected to reflux in 1.5 L of double-distilled water until the volume was reduced to 250 ml. The resulting crude extract was centrifuged (8,000 rpm, 12 min, 4°C) and subsequently filtered to remove residual particulate matter. The clarified extract, referred to as AAW, had a concentration of 50 mg/ml and was stored at -20°C for later use.

2.9 Cell Culture and Treatment

THP-1 cell lines were purchased from Pricella Biotechnology (Wuhan, China, Cat. No. CL-0233). THP-1 Cell Complete Medium was used for cell culture. THP-1 cells were placed in 37℃, 5% CO_2 constant temperature incubator for culture. THP-1 monocytes (1×10^6 cells/ml) were stimulated with 100 ng/ml phorbol 12-myristate 13-acetate (PMA; MedChemExpress, Cat. No. HY-18739) for 24 hours. The cells were categorized into the control group, the group with 200μg/ml AAW added, and the group with 200μg/ml AAW combined with 15μm of PPARG inhibitor, and stay for 24h.

2.10 Isolation of Ribonucleic Acid and Quantitative Polymerase Chain Reaction Analysis

Cellular total RNA was isolated using Chloroform substitute (Servicebio, Cat. G3014). Reverse transcription of RNA to cDNA. Oligo (dT), nuclease-free ultrapure water was added, mixed, centrifuged briefly, incubated at 65℃ for 5min, cooled on ice, and centrifuged. 5X Reaction Buffer was added and incubated at 42℃ for 60min, then heated at 70℃ for 5min, and stored at -80 ℃. The primers for the downstream targets of PPARG are presented in Table 1. Power SYBR Green PCR Master Mix (Thermo Fisher Scientific, NY, USA). The thermal cycling conditions were as follows: Initial steps consisted of 50°C for 2 min and 95°C for 2 min. The amplification process consisted of 45 cycles, each maintained at 95°C for 15 seconds. For normalization, GAPDH was utilized as the reference gene, and the relative quantification of mRNA expression was assessed via the comparative quantification cycle ($2^{-\Delta\Delta ct}$) technique.

Table 1
The qRT-PCR primers of the downstream genes of PPARG

Gene	Primer sequence(5’-3’)
PPARG-FP	GGGATCAGCTCCGTGGATCT
PPARG-RP	TGCACTTTGGTACTCTTGAAGTT
IL-13-FP	CCTCATGGCGCTTTTGTTGAC
IL-13-RP	TCTGGTTCTGGGTGATGTTGA
TLR9-FP	TGGGACCTCTGGTACTGCTT
TLR9-RP	TCGTTGTACACCCAGTCTGC
CD72-FP	ATCTGAGGTTTGTGAAGGCTCC
CD72-RP	AACATTCTCGTAGGTGATTTCCC
LTF-FP	ATGGTGGTTTCATATACGAGGCA
LTF-RP	CTTTCGGTCCCGTAGACTTCC
CHI3L1-FP	AAGCAACGATCACATCGACAC
CHI3L1-RP	TCAGGTTGGGGTTCCTGTTCT

2.11 Statistical analysis

Statistical evaluations were conducted utilizing GraphPad Prism 8.0.1 software. One-way ANOVA was applied to compare multiple groups, whereas unpaired t-tests were utilized for comparisons between two groups. P-value less than 0.05 was considered to indicate a statistically significant difference.

3. Results

3.1 Integration of Artemisia argyi active compounds with SLE-associated Genes

From the TCMSP database, 9 active compounds were screened from 135 reported consituents of Artemisia argyi (Table 2). Target prediction mapped these active compounds to 380 non-redundant protein targets after deduplication.

Table 2
Active components of Artemisia argyi (TCMSP)

Mol ID	Molecule Name	*OB* (%)	*DL*
MOL000098	Quercetin	46.43	0.28
MOL000358	Beta-sitosterol	36.91	0.75
MOL000449	Stigmasterol	43.83	0.76
MOL001040	(2R)-5,7-dihydroxy-2-(4-hydroxyphenyl)chroman-4-one	42.36	0.21
MOL001494	Mandenol	42.00	0.19
MOL002883	Ethyl oleate (NF)	32.4	0.19
MOL005720	24-methylenecyloartanone	41.11	0.79
MOL005735	Dammaradienyl acetate	44.83	0.83
MOL005741	Cycloartenol acetate	41.11	0.80

A total of 2,699 genes associated with "SLE" were retrieved from the GeneCards database, of which 180 with a relevance score ≥ 4.15 were retained for further analysis. An additional 51 SLE-related genes were obtained from the OMIM database. Merging and removing duplicates from the two datasets yielded 218 SLE-associated targets. Intersection of these 218 targets with the 380 predicted active targets of Artemisia argyi identified 19 common key targets (Fig. 1A).

To characterize interactions among the 19 overlapping targets, a STRING-based PPI network was constructed. Nodes were ranked by degree, and the top genes are shown in Fig. 1B. Among them, IL2, CASP3, ACE, PPARG, HSP90AA1, and ANXA5 exhibited the highest connectivity and were consistently prioritized across network views. The compound–target–disease network assembled in Cytoscape (Fig. 1C), where node size and color scale with connectivity, further emphasized these hubs. Integrating the two analyses, IL2, CASP3, ACE, PPARG, HSP90AA1, and ANXA5 were designated as core targets with the greatest putative influence in the A. argyi–SLE axis (Fig. 1D).

3.2 GO Functional and KEGG Pathway Enrichment Analysis

Using DAVID, GO enrichment and KEGG pathway analysis were performed on the 19 key targets. For biological process (BP), enriched processes included leukocyte activation in immune response, assembly of telomerase holoenzyme complex, positive regulation of microtubule associated protein kinase activity, macrophage foam cell differentiation, negative regulation of protein metabolic processes, and positive regulation of leukocyte tethering or rolling. For cellular Components, targets were associated with dendritic growth cones, axonal growth cones, COP9 signalosome, brush border membranes, and secretory granule lumens. For molecular functions, enriched molecular functions comprised glycosphingolipid binding, nitric oxide synthase regulator activity, TPR domain binding, oligosaccharide binding, DNA polymerase binding, phospholipase binding, and sialic acid binding (Fig. 2A).

KEGG pathway analysis identified 18 significant pathways, including lipid and atherosclerosis (hsa05417), COVID-19 (hsa05171), pathways in cancer (hsa05200), IL-17 signaling (hsa04657), and Th17 cell differentiation (hsa04659) (Fig. 2B).

3.3 Molecular Docking

Molecular docking was conducted to validate interactions between key active compounds and core protein targets, using a binding-energy threshold of < − 5.0 kcal/mol to denote favorable binding. All compound–target complexes met this criterion, with docking energies − 5.5 kcal/mol (Fig. 3). Among the screened compounds, quercetin achieved the most favorable docking score, indicative of stable binding. Both quercetin and naringenin formed hydrogen bonds interactions with residues in the predicted binding pockets of the core proteins (Table 3).Representative three-dimensional binding poses are presented in Fig. 4.

Table 3
The interaction sites of key active ingredients and key target proteins

Component	Target protein	Bond type	Interaction position
Quercetin	CASP3	hydrogen bond	ARG−207
	ANXA5	hydrogen bond	ARG−227
	IL−2	hydrogen bond	ARG−83, SER−87, GLU−67
	ACE	hydrogen bond	GLY−404, LYS−118, GLU−123, TYR−213
	HSP90AA1	hydrogen bond	ASN−51, PHE−138
	PPARG	hydrogen bond	ARG−443, GLU−324
(2R)-5,7-dihydroxy-2-(4-hydroxyphenyl)chroman-4-one	CASP3	hydrogen bond	PHE−400, ASN−195
	ANXA5	hydrogen bond	GLN−235, THR−254, LYS−242, ARG−227
	IL−2	hydrogen bond	SER−87
	ACE	hydrogen bond	ARG−124, ASN−85
	HSP90AA1	hydrogen bond	ASP−54, LYS−58
	PPARG	hydrogen bond	THR−447, ARG−397
Stigmasterol	ANXA5	hydrogen bond	GLU−253
	IL−2	hydrogen bond	LYS−43, THR−41
	ACE	hydrogen bond	SER−298
	PPARG	hydrogen bond	THR−447
Beta-sitosterol	IL−2	hydrogen bond	GLU−67
	ACE	hydrogen bond	ASN−66

3.4 Analysis of PPARG-regulated target genes

We assume that the active substances in Artemisia argyi activate PPARG, and in combination, promote the transcription of downstream genes. Putative PPARG downstream targets were retrieved from the hTFtarget and GTRD databases and intersected with SLE-related genes, yielding 89 PPARG-regulated genes implicated in SLE (Fig. 5). Candidate direct targets were then prioritized using JASPAR, by scoring PPARG motif matches within promoter sequences; genes with a binding score > 0.7 were retained. This analysis identified five putative direct PPARG targets relevant to SLE: LTF, CD72, IL13, CHI3L1, and TLR9 (Table 4).

Table 4
Obtain the downstream target genes of PPARG through the JASPER databas

GENE	Matrix ID	Score	Relative score	Start	End	Strand	Predicted sequence
CD72	MA0065.1	12.357317	0.8035206	1954	1973	+	CAAGGGGTCAAACGCCCCCA
LTF	MA0065.1	13.616349	0.82135594	1613	1632	-	CTTGGGGTCAGGGTTCACCT
CHI3L1	MA0066.1	14.025682	0.81395733	1741	1760	-	GTAAGCCACAGTGCCCTAAA
TLR9	MA0065.1	8.6470375	0.75096124	1414	1433	+	TGAGGGGCCCGGGGTCACCC
IL13	MA0065.1	6.2349477	0.7167918	497	516	+	ACAAAGAAGAAAAGTCATAA

3.5 qRT-PCR Verification

qRT-PCR analysis showed that treatment with the Artemisia argyi active fraction significantly upregulated PPARG and its predicted downstream targets—LTF, CD72, CHI3L1, TLR9, and IL13—at the mRNA level (all $P < 0.05$). Co-treatment with a PPARG inhibitor significantly attenuated these inductions (all $P < 0.05$), supporting a PPARG-dependent transcriptional mechanism (Fig. 6).

4. Discussion

This study identified nine active compounds of Artemisia argyi associated with 380 potential protein targets. Through intersection analysis with 218 SLE related genes, 19 key targets were identified. These targets were further analyzed via a protein-protein interaction (PPI) network, with Degree-based ranking revealing core targets such as L2, CASP3, HSP90AA1, and PPARG, which are closely linked to the pathological processes of SLE. Previous studies have highlighted the critical role of CASP3 in apoptosis and immune regulation, particularly in tissue damage mechanisms associated with SLE[6]. Additionally, the drug-disease-active compound-target network validated the potential mechanisms of these targets in SLE treatment, offering novel insights for modernizing traditional Chinese medicine (TCM).

GO functional enrichment analysis revealed that these targets are significantly involved in leukocyte activation and immune responses, processes integral to SLE pathogenesis. SLE is characterized by immune system dysregulation, including autoantigen recognition defects and excessive inflammatory responses[7]. Leukocyte activation is a critical step in the inflammatory cascade, mediating leukocyte adhesion and migration to inflammation sites, thereby amplifying inflammatory responses. In SLE, this process may be exacerbated by abnormal expression of adhesion molecules such as SELE and VCAM-1, leading to heightened inflammation and tissue damage[2]. Furthermore, aberrant activation of immune cells, including T cells and monocytes, likely propagates inflammatory signaling. The upregulation of SELE, associated with endothelial cell activation, is

commonly observed in SLE patients and correlates with disease activity[3]. GO analysis of leukocyte activation provides valuable perspectives on how these molecular events drive SLE related inflammation.

KEGG pathway overrepresentation assessment pinpointed 18 noteworthy pathways, among which the IL-17 signaling pathway and Th17 cell differentiation pathway stand out as vital to the inflammatory and immune dysregulation in SLE[8] IL-17, a pro-inflammatory cytokine produced by Th17 cells, prompts diverse cell types to secrete inflammatory mediators like IL-6, TNF-α, and GM-CSF, thereby intensifying inflammatory responses[4]. IL-17 exerts its effects through interactions with its receptor (IL-17RA/RC), activating downstream NF-κB, JAK/STAT, and MAPK signaling pathways, which promote the expression of pro-inflammatory molecules. This inflammatory amplification mechanism may explain the hyperactive inflammation observed in SLE patients[9]. Th17 cells, the primary source of IL-17, play a pivotal role in SLE pathogenesis. Aberrant proliferation and differentiation of Th17 cells contribute to a positive feedback loop in inflammation via IL-17 signaling[1]. Th17 cell differentiation is regulated by critical factors such as IL-6, IL-23, and TGF-β, which activate transcription factors like STAT3 and RORγt, driving Th17 cell proliferation and IL-17 secretion[2]. In SLE patients, elevated levels of these signaling molecules lead to excessive Th17 cell differentiation and enhanced pro-inflammatory functions.

Quercetin, a natural flavonoid, is well-known for its anti-inflammatory, antioxidant, and immunomodulatory effects. In this study, quercetin exhibited the highest binding affinity (binding energy < -5.5 kcal/mol) and formed stable interactions with several core targets, including CASP3, STAT1, and HSP90AA1. These findings suggest that quercetin may exert therapeutic effects in SLE by modulating apoptotic and inflammatory signaling pathways, such as JAK/STAT and PI3K/AKT[1]. Previous studies corroborate the therapeutic potential of quercetin in autoimmune diseases, including SLE. A review summarized its role in reducing pro-inflammatory cytokine release, regulating immune cell function, and significantly mitigating SLE pathology in both in vitro and animal models[9]. Similarly, naringenin, another key active compound, also demonstrated high affinity with multiple SLE targets. Naringenin primarily modulates phospholipase binding and DNA polymerase activity, potentially impacting apoptosis and cytokine production. Existing research indicates that naringenin's antioxidant, anti-inflammatory, and immunomodulatory effects could be beneficial in treating immune-related diseases, including SLE[10]. Both quercetin and naringenin act through multi-target, multi-pathway mechanisms, playing essential roles in immune regulation. Specifically, they may alleviate SLE progression by suppressing inflammation and modulating T-cell functions within IL-17 signaling and Th17 differentiation pathways.

Upon activation, PPARG pairs with the retinoic acid X receptor (RXR) to form a hetero-dimer to modulate the transcription of target genes[11]. We hypothesize that the active substance of Artemisia argyi activates PPARG and binds to promote the transcription of downstream genes. Research has indicated a substantial reduction in the expression of LTF within B cells of female SLE patients[12]. The LTF gene encodes lactoferrin and has multiple functions such as antibacterial, antiviral and immune regulation[13–15]. Therefore, LTF may mainly be involved in disease progression in SLE by influencing immune regulation, inflammatory response and infection defense. In B cells, CD72 acts as an inhibitory receptor, suppressing the response of TLR7-dependent B cells to self-nucleic acid antigens (such as Sm/RNP) and preventing the development of SLE. The deletion or low expression of CD72 can promote the progression of SLE and lead to the activation of CD99 + CD72 B cell subsets[16, 17]. TLR stimulation is regarded as an additional signal that helps activate and/or regulate abnormal adaptive immune responses[18]. Data from mouse models indicate that TLR7 has a pathogenic effect in the pathogenesis of SLE, while TLR9 has a protective effect[19]. CHI3L1 participates in inflammatory responses by regulating the function of macrophages[20]. Research has demonstrated a strong correlation between CHI3L1 and macrophage polarization, with this interaction potentially influencing the progression of SLE[21].

5. Conclusion

This study elucidates the potential multi-target therapeutic mechanisms of Artemisia argyi against systemic lupus erythematosus through an integrated approach combining network pharmacology, bioinformatics, molecular docking and experimental verification. Key findings demonstrate that active compounds, particularly quercetin and naringenin, target core SLE associated proteins involved in critical pathological processes. The study further proposes specific mechanisms, such as PPARG activation promoting downstream gene transcription, While validated in part by qRT-PCR and supported by literature, the identified mechanisms and compound efficacious require further in vivo pharmacodynamic and toxicological evaluation. Nonetheless, this work provides a crucial scientific foundation for understanding Artemisia argyi anti-SLE effects and advances the modernization of traditional Chinese medicine for immune disorders.

Declarations

Conflicts of interest

All the authors declare no competing interests.

Author Contribution

Man Luo: Conceptualization, Writing-original draft, Visualization.Xianlei Zhou: Data curation, Software, Investigation.Zimo Yan: Writing-review & editing.Zhi Zhang: Visualization, Validation.Xuemei Zhang: Conceptualization, Resources, Supervision, Project administration.

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Data Availability

We hereby confirm that the official permission document issued by KEGG has been submitted via email to srep@nature.com, and we kindly ask you to review it.

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Figures

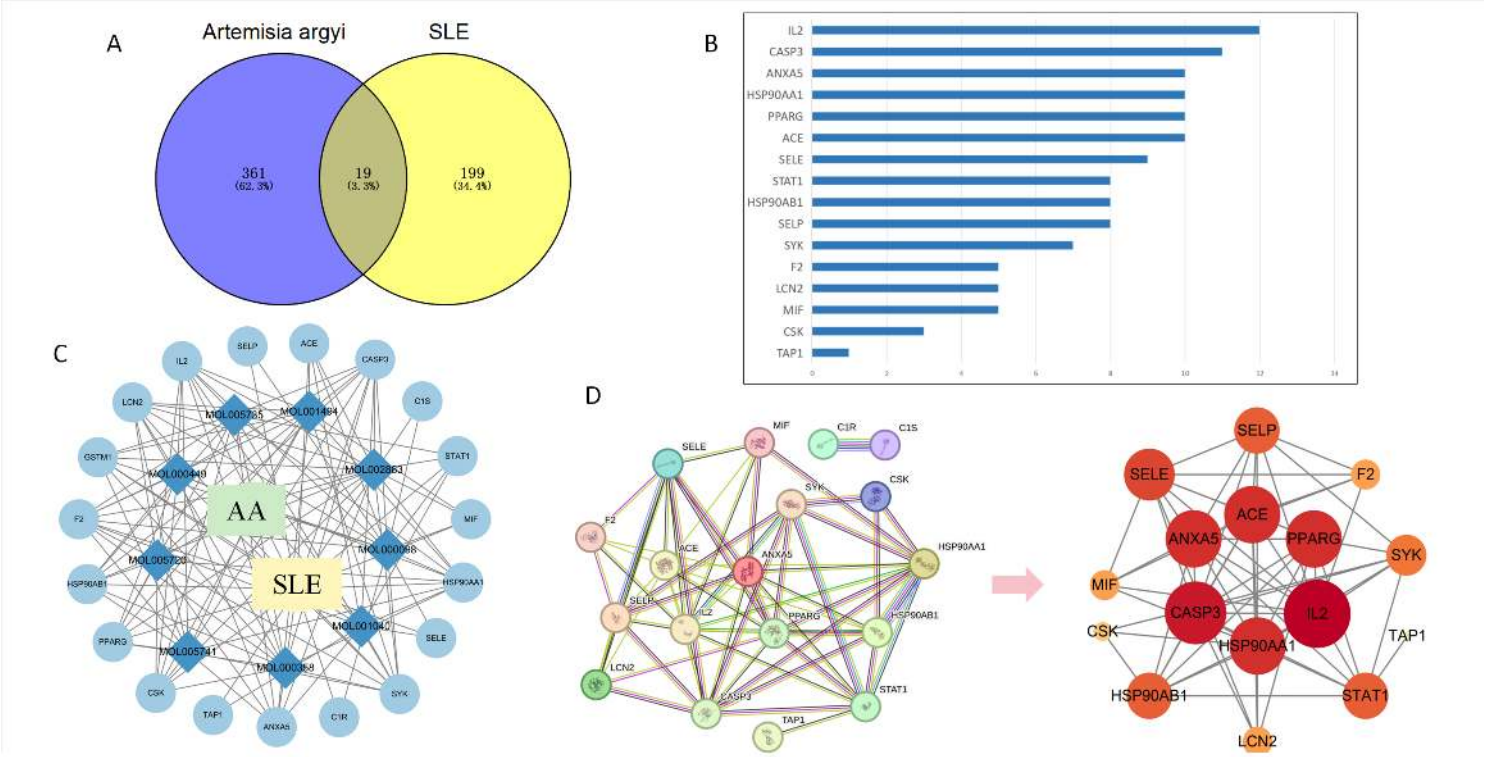

Figure 1

Artemisia argyi active substance is a key target in the treatment of systemic lupus erythematosus (A). The potential targets of Artemisia argyi were intersected with the SLE target genes, resulting in 19 overlapping key targets. (B). Based on the degree value ranking, The top 16 genes. (C). A comprehensive drug-disease-active compound-target network. (D). IL2, CASP3, ACE, PPARG, HSP90AA1, and ANXA5 identified as core targets with the highest impact

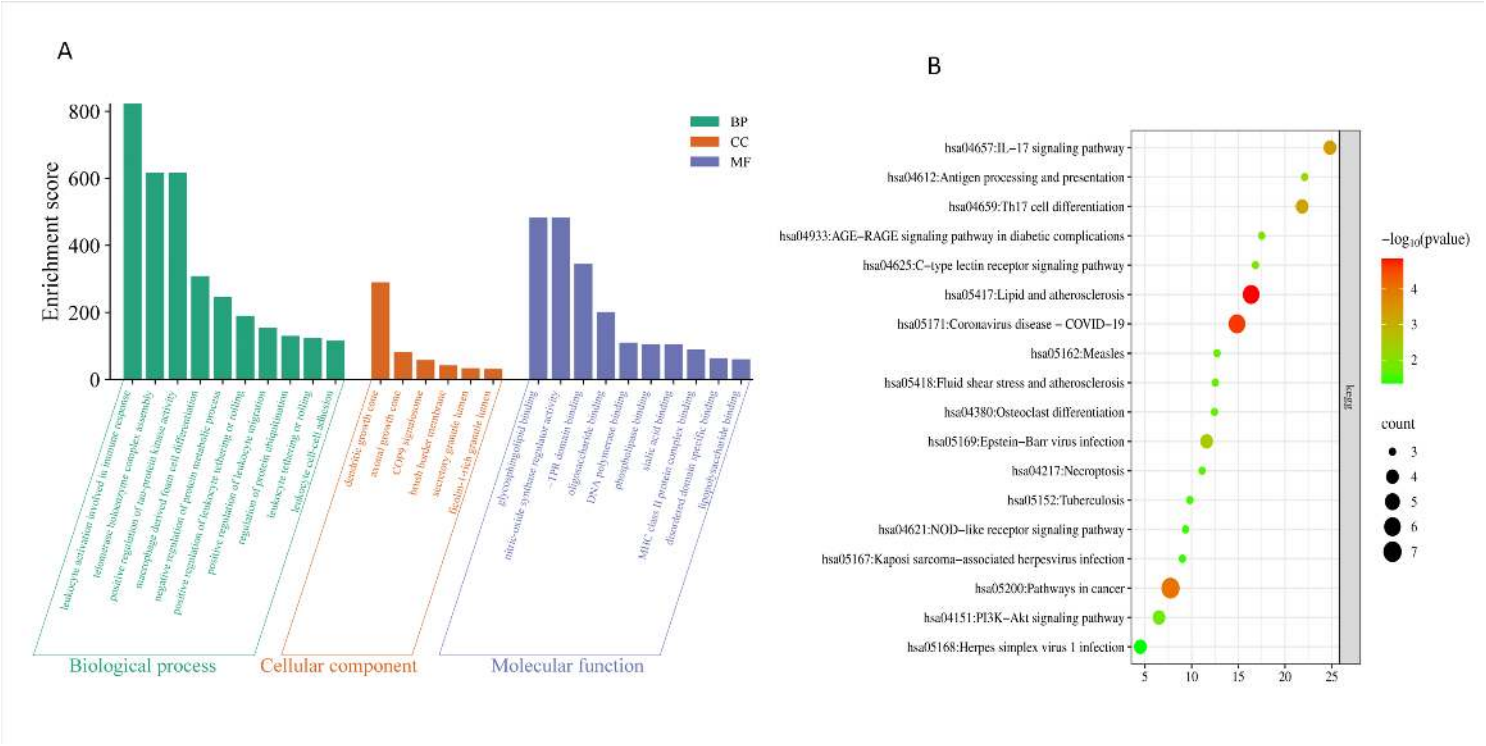

Figure 2

Top 10 GO terms and KEGG pathways of hub genes.

(A) GO enrichment analysis. (B) KEGG pathway enrichment analysis. Pathway information was obtained from the KEGG database (https://www.kegg.jp/kegg/

) and used in accordance with KEGG citation and copyright guidelines.

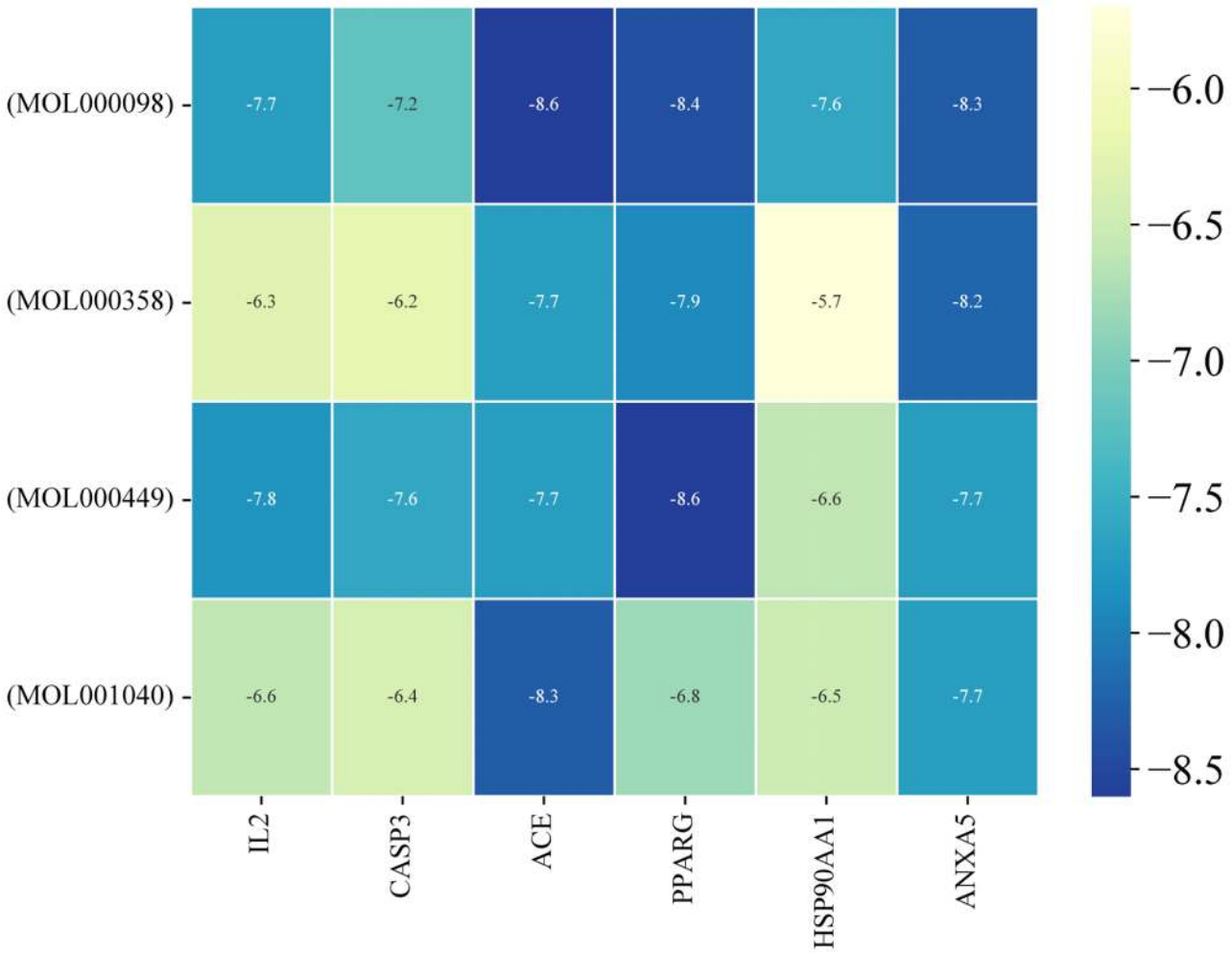

Figure 3

Binding capacity between key active ingredients and key targets.

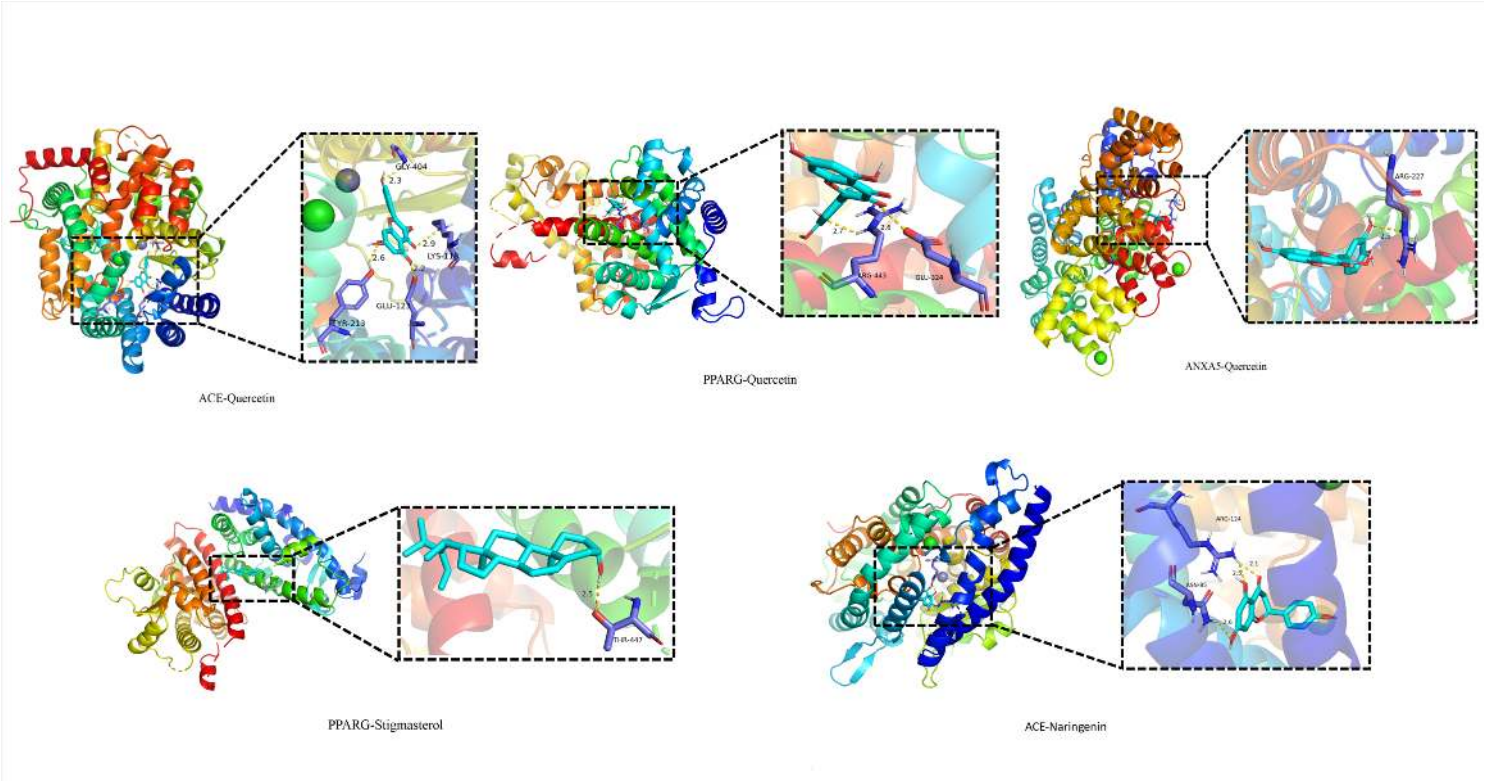

Figure 4

Molecular docking visualization results

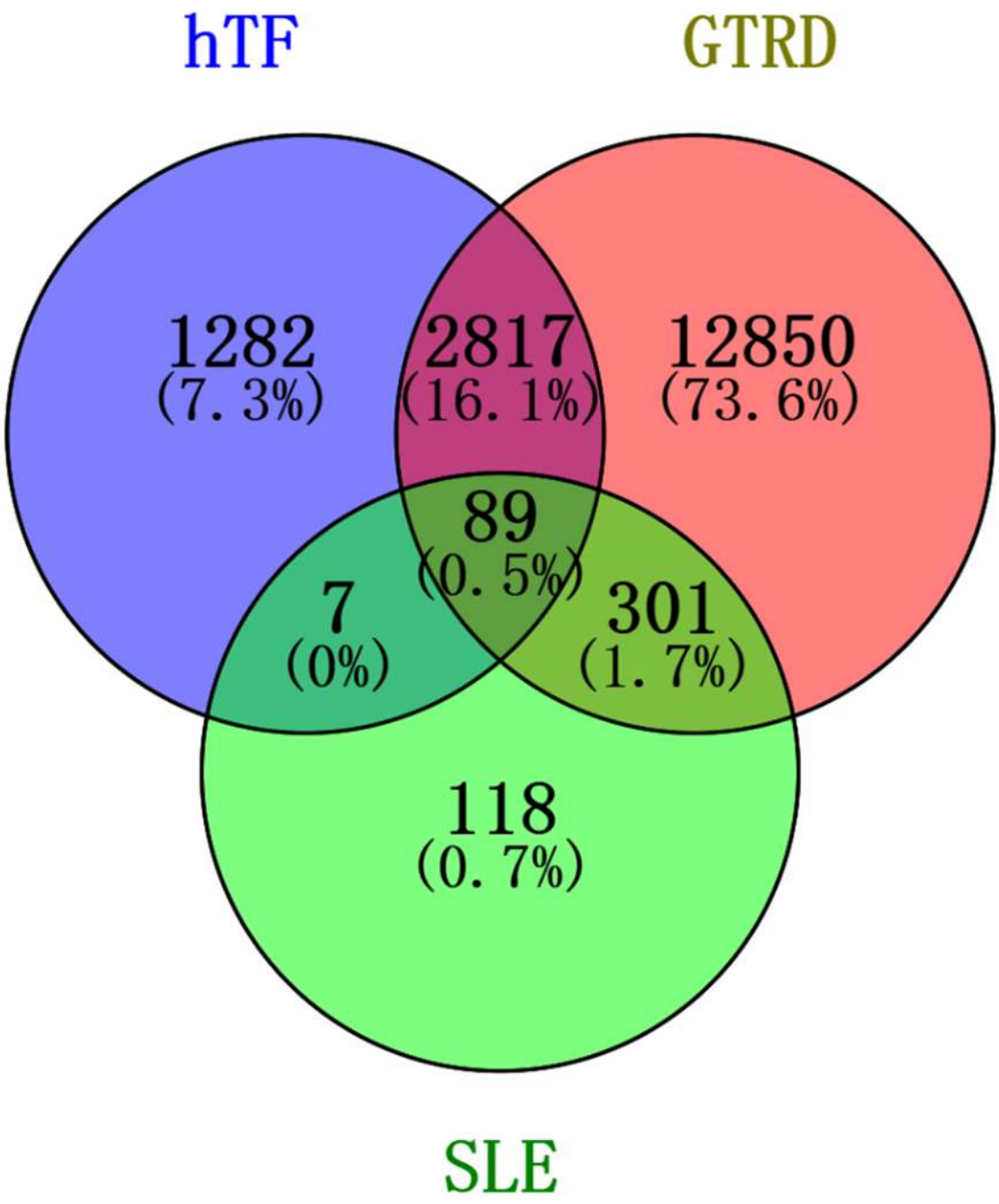

Figure 5

89 genes related to SLE and regulated by PPARG were obtained

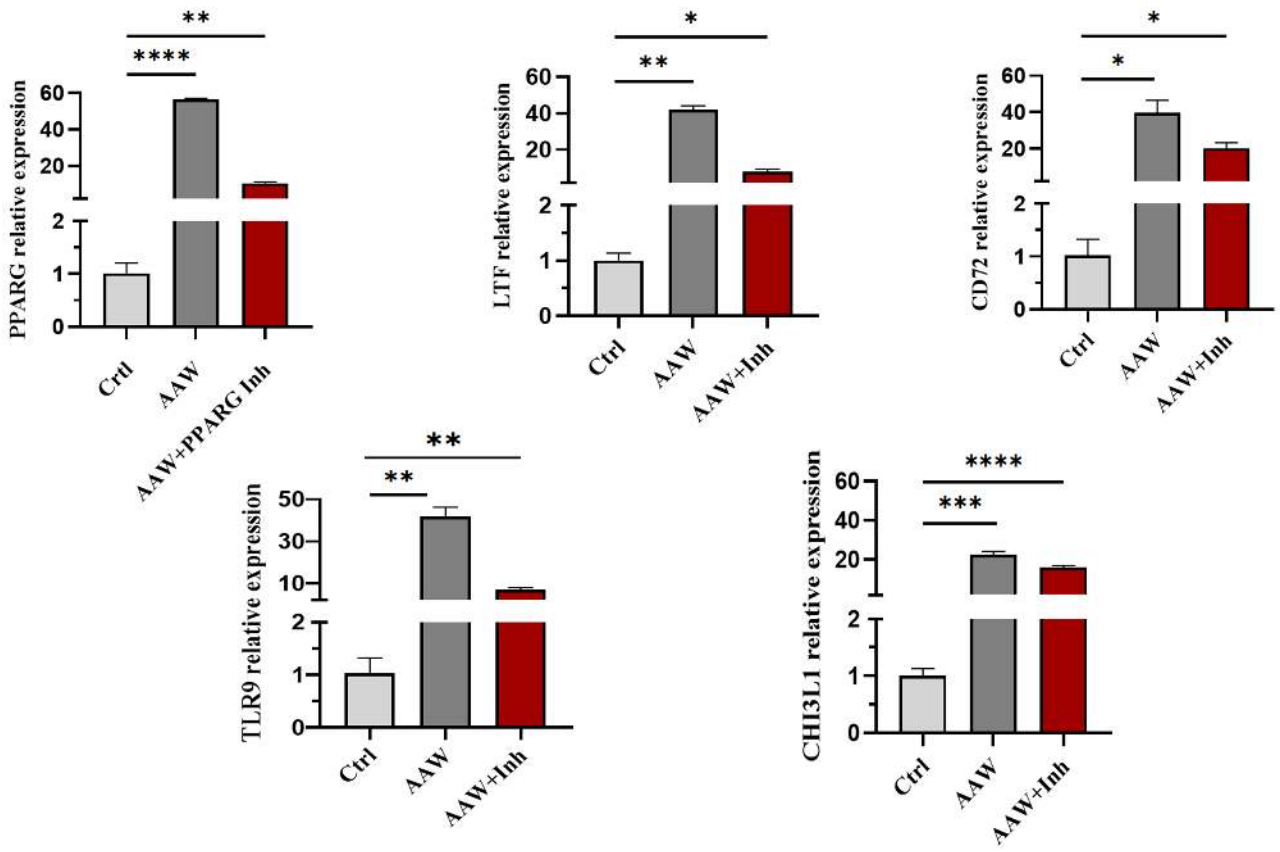

Figure 6

Expression of PPARG and downstream target genes after AAW and PPARG inhibitors