Anti-inflammatory and Deodorizing Effects and Mechanisms of Action of Traditional Chinese Medicine Formulations: A Network Pharmacology Approach

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Abstract [**Objectives**] To investigate the material basis and underlying mechanisms by which topical traditional Chinese medicine (TCM) alleviates odor issues in the vulvar region associated with inflammatory responses. [**Methods**] The active components and their corresponding targets were identified through screening using the TCMSP database, HIT 2.0 database, and NetInfer. The UniProt database was utilized to standardize the name of the collected targets. Subsequently, an intersection analysis was conducted with targets obtained from the GeneCards database to determine the anti-inflammatory targets of the TCM formulation under investigation. A network diagram illustrating the relationships among TCM, its bioactive components, and their corresponding targets was constructed using Cytoscape software, followed by topological analysis. Additionally, a protein-protein interaction (PPI) network was developed and analyzed utilizing the STRING database in conjunction with Cytoscape. Gene Ontology (GO) enrichment analysis of the targets was performed employing the DAVID database. [**Results**] A total of 76 active compounds were identified from the TCM formulation through screening, corresponding to 662 targets. Subsequent analysis revealed 62 core targets associated with vaginitis and urethritis. Network diagram analysis indicated that the principal Chinese herbs in this formulation were Sophorae Flavescentis Radix, Herba Leonuri, and *Eupatorium fortunei*. The formulation may exert anti-inflammatory and deodorizing effects via bioactive compounds such as quercetin, apigenin, and genistein, while simultaneously mitigating inflammatory responses by modulating target proteins including ALB, IL6, TNF, IL-1β, and IFNG. [**Conclusions**] The TCM formulation has the potential to mitigate inflammatory responses and diminish the odor of secretions through multi-component and multi-target mechanisms. Due to their capacity to mask flavors, inhibit bacterial growth, and reduce inflammation, medicinal plants hold significant research and practical value in the domain of odor control.

Key words Traditional Chinese medicine (TCM) formulation, Anti-inflammatory, Vulvar odor, Network pharmacology

1 Introduction

With the growing emphasis on personal hygiene and health management, body odor has garnered increasing public attention. Unpleasant odors arising from sweat, urine, and secretions of the reproductive organs not only impact individuals' social interactions and mental well-being but may also, in certain cases, indicate underlying medical conditions. Contemporary medical research suggests that the production of body odor is primarily associated with the metabolic byproducts of the microbial flora residing on the skin surface. In general, vulvar secretions from sensitive areas in a healthy state are nearly odorless. The presence of an unpleasant odor in these secretions may indicate infections such as bacterial vaginitis or symptoms associated with non-infectious conditions, including urinary incontinence, malignant ulcers, trimethylaminuria, and chronic constipation[1]. While the use of deodorants may temporarily mask or reduce the odor to an acceptable level, it remains essential to address and regulate the underlying causes of abnormal body odor at its source.

Among the conditions associated with vulvar odor, bacterial vaginitis is the most prevalent cause of malodor in vaginal discharge. This odor issue is frequently accompanied by infection and inflammatory responses[2]. Inflammation can result in increased secretions, and if these are not promptly cleaned, the moist environment of the vulva may promote bacterial proliferation, thereby exacerbating unpleasant odors. Consequently, when developing deodorizing treatments using medicinal plants, it is essential not only to focus on antibacterial properties and odor masking but also to address the regulation of inflammatory responses. This study employed network pharmacology techniques to screen medicinal plants with anti-inflammatory properties and to investigate their mechanisms of action, aiming to enhance therapeutic strategies for managing body odor. The components examined in this research, derived from the Fuyanjie® Snow Lotus Core Cleansing and Nourishing Sanitary Pad—known for its efficacy in mitigating odor issues—include *Saussurea involucrata*, Flos Carthami, Aloe, Angelicae Sinensis Radix, Fructus Cnidii, Stemonae Radix, Ramulus Cinnamomi, Angelicae Dahuricae Radix, *Eupatorium fortunei*, Sophorae Flavescentis Radix, Astragali Radix, Radix Rehmanniae, Fructus Kochiae, Herba Leonuri, and Borneolum Syntheticum. Therefore, this study employed the traditional Chinese medicine (TCM) formulation as a case example and utilized network pharmacology methods to investigate the material basis and potential mechanisms underlying the anti-inflammatory and deodorizing effects of medicinal plants.

2 Materials and methods

2.1 Screening of active components and targets The known compounds isolated and identified from the TCM formulation were compiled using the Herbal Ingredients' Targets Platform (HIT 2.0, http://www.badd-cao.net:2345/) database. Subsequently, these compounds were queried in the Traditional Chinese Medicine Sys-

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tems Pharmacology Database and Analysis Platform (TCMSP, https://www.tcmsp-e.com/index.php) to screen for those exhibiting drug-likeness (*DL*) values ≥ 0.18, indicating potential pharmacological activity. Additionally, active ingredients with a topological polar surface area (*TPSA*) ≤ 140, suggestive of the capacity to penetrate the skin or mucous membranes, were screened, and their corresponding molecular targets were identified. For bioactive compounds in the TCMSP database lacking recorded targets, NetInfer (https://lmmd.ecust.edu.cn/netinfer/) was employed to predict their potential targets. To enhance the reliability of these predictions, only targets with a score greater than 1 were selected. The identified targets were subsequently submitted to the UniProt database (https://www.uniprot.org) for standardization of target names. All target genes were humanized, and duplicate genes were eliminated.

2.2 Screening of anti-inflammatory targets Relevant targets were identified in the GenCards database using the keywords "Vaginal Inflammation" and "Urethritis". After summarizing and removing duplicate entries, these targets, along with the target information associated with the TCM formulation, were imported into the Hiplot biomedical data online visualization tool (https://hiplot.cn/) to generate a Venn diagram and identify potential anti-inflammatory targets of the formulation. Compounds lacking corresponding relationships with the aforementioned functional targets were subsequently excluded to isolate the effective components that may exhibit anti-inflammatory activity within this TCM formulation.

2.3 Construction and analysis of TCM-bioactive components-targets network The active components and their corresponding targets associated with the anti-inflammatory efficacy of the TCM formulation identified in Section **2.2** were visually analyzed using Cytoscape 3.10.3. A network diagram illustrating the relationships among TCM, active components, and their targets was constructed. In this network, nodes represented TCMs, active compounds, and their respective targets, while edges denoted the interactions between these nodes. Topological analysis of the network was performed, and the significance of each node was assessed using degree and betweenness centrality metrics.

2.4 Construction and analysis of protein-protein interaction (PPI) network The anti-inflammatory target genes identified in Section **2.2** were submitted to the STRING database (https://string-db.org) to construct a PPI network. Protein nodes lacking interaction relationships were excluded to facilitate the investigation of the pharmacological mechanisms at the protein interaction level. The resulting PPI network data were imported into Cytoscape software, where hub gene targets were identified using the MCC algorithm implemented in the cytoHubba plugin.

2.5 GO enrichment analysis of anti-inflammatory efficacy The gene information encoding the targets associated with the anti-inflammatory effects of the TCM formulation, as obtained in Section **2.2**, was submitted to the DAVID database (https://david.ncifcrf.gov). "Homo sapiens" was selected as the species for analysis, and Gene Ontology (GO) analysis was conducted using a significance threshold of $P < 0.01$. The resulting data were visualized with Hiplot to identify functional information potentially highly correlated with the anti-inflammatory effects of the TCM formulation.

3 Results and analysis

3.1 Bioactive components and anti-inflammatory targets In accordance with the screening criteria in Section **2.1**, a total of 76 bioactive compounds and 662 corresponding targets were identified from the TCMSP and HIT2.0 databases. The bioactive compounds obtained from the TCM formulation are presented in Table 1.

Utilizing the keywords "Vaginal Inflammation" and "Urethritis", relevant targets were retrieved from the GeneCards database and subsequently summarized to eliminate duplicates. An intersection analysis was then performed in conjunction with the target information of the TCM formulation, resulting in the identification of 62 potential anti-inflammatory targets associated with the formulation (Fig. 1).

3.2 TCM-bioactive components-targets network The bioactive components and their corresponding targets associated with the anti-inflammatory efficacy of the TCM formulation were visually analyzed using Cytoscape software, resulting in the construction of a TCM-bioactive components-targets network diagram (Fig. 2). Topological analysis revealed that this network comprised a total of 148 nodes and 459 edges. As illustrated in Fig. 2, the outermost circle represented the target site, while the two inner circles corresponded to the bioactive compounds. Based on the results of the network topology analysis, the average degree of the nodes within the established network was 6.2, with 42 nodes exhibiting a degree higher than this average. Additionally, the average betweenness centrality was 0.013 3, and 35 nodes demonstrated betweenness centrality values exceeding this average. A total of 30 nodes simultaneously satisfied both screening criteria, as presented in Table 2. This indicates that Sophorae Flavescentis Radix, Herba Leonuri, and *E. fortunei* may constitute the core TCMs within the formulation. Furthermore, quercetin, apigenin, and genistein are likely the principal active components responsible for the formulation's anti-inflammatory effects. PTGS2, ESR1, and NOS2 may be the primary targets mediating these anti-inflammatory effects.

The primary active components of Sophorae Flavescentis Radix are alkaloids, which exhibit anti-inflammatory and antibacterial pharmacological properties and are capable of inhibiting various inflammatory factors. In TCM, this herb is commonly employed to treat dermatological conditions and vaginal pruritus[3]. Wang *et al.*[4] developed a rat model of aerobic bacterial vaginitis through vaginal inoculation with *Escherichia coli* and *Staphylococcus aureus*. Subsequently, they administered a total alkaloid gel derived from Sophorae Flavescentis Radix and a placebo gel to evaluate the local therapeutic effects of the extract on vaginitis. The research team determined that the total alkali gel derived from Sophorae Flavescentis Radix not only suppressed the inflammatory response

Table 1 Bioactive components derived from the TCM formulation

No.	Compound	Source of TCM	No.	Compound	Source of TCM	No.	Compound	Source of TCM
1	Beta-sitosterol	1, 2, 4, 5, 7, 9, 10, 13, 14	27	Dammaradienyl acetate	6	53	Lupeol	14
2	Apigenin	1, 2, 4, 9, 14	28	Diosmetin	5	54	Maackiain	14
3	Quercetin	1, 4, 7, 9, 14	29	Dipterocarpol	12	55	Matairesinol	7
4	Calycosin	2, 10, 14	30	Ent-epicatechin	13	56	Matrine	14
5	Kaempferol	1, 4, 7	31	Erythrodio	12	57	Nodakenin	10
6	Luteolin	6, 9, 14	32	Eupaformonin	6	58	O-acetyl-beta-amyrin	6
7	Sitosterol	6, 11, 13	33	Eupaformosanin	6	59	Octacosanol	6
8	(+)-Catechin	1, 13	34	Eupatoriopicrin	6	60	Oleanolic acid	12
9	Biochanin	2, 14	35	Galeopsin	4	61	Oxymatrine	14
10	Formononetin	2, 14	36	Genistein	14	62	Peroxyergosterol	13
11	Isorhamnetin	2, 4	37	Heptacosane	13	63	Prehispanolone	4
12	Sitogluside	11, 13	38	Hesperetin	14	64	Preleoheterin	4
13	Stigmasterol	6, 10	39	Hispanolone	4	65	Pristimerin	8
14	Syringin	7, 9	40	Hispidulin	9	66	Rhein	1
15	(−)-Epicatechin	1	41	Iso-preleoheterin	4	67	Scopolin	3
16	2-(4-Hydroxyphenyl) ethyl hexacosanoate	11	42	Isoimperatorin	10	68	Sophocarpine	14
17	7-Acetoxy-8-hydroxy-9-isobutyryloxythymol	6	43	Isoleosibirin	4	69	Sophoramine	14
18	9-Acetoxy-8,10-epoxy-6-hydroxythymol-3-O-angelate	6	44	Isoquercetin_qt	4	70	Sophoridine	14
19	Amyrin palmitate	6	45	Isoxanthohumol	14	71	Taraxasteryl acetate	6
20	Arachic acid	11	46	Jaceosidine	9	72	Taxifolin	13
21	Arachidonic acid	4	47	Kurarinol	14	73	Tetracosane	13
22	Asiatic acid	12	48	Leojaponin	4	74	Tuberostemonine	8
23	Bronyl acetate	12	49	Leonurine	4	75	Wogonin	2
24	Byakangelicin	3	50	Leonuriside	4	76	Xanthohumol	14
25	Coumarin 343	13	51	Leosibiricin	4			
26	Daidzein	2	52	Liriodenine	8			

NOTE 1. Aloe; 2. Astragali Radix; 3. Angelicae Dahuricae Radix; 4. Herba Leonuri; 5. Fructus Cnidii; 6. *Eupatorium fortunei*; 7. Flos Carthami; 8. Stemonae Radix; 9. *Saussurea involucrata*; 10. Angelicae Sinensis Radix; 11. Radix Rehmanniae; 12. Borneolum Syntheticum; 13. Ramulus Cinnamomi; 14. Sophorae Flavescentis Radix.

but also exhibited a significantly greater antibacterial effect compared to the placebo. Besides, there was a marked increase in the population of beneficial bacteria, specifically *Lactobacillus*, which contributed to a protective effect on the vaginal mucosa[4]. The primary components of Herba Leonuri include flavonoids, terpenoids, and alkaloids. Studies demonstrated that the alcohol extract of Herba Leonuri exerted a moderate inhibitory effect on *Candida albicans* and displayed significant antimicrobial activity against methicillin-resistant *S. aureus*[5]. The primary active components of *E. fortunei* are volatile oils. Research indicated that the volatile oil extracted from *E. fortunei* exhibited inhibitory effects against *S. aureus* and *E. coli*[6]. Furthermore, Miao *et al.*[7] isolated and identified brachangobinan A from *E. fortunei* and demonstrated, through network pharmacology and experimental studies, that this compound exerted anti-inflammatory effects by inhibiting pro-inflammatory factors and blocking the NF-κB signaling pathway. These findings suggest that TCM formulations may possess anti-inflammatory and antibacterial properties, thereby contributing to the maintenance of microecological balance within the flora.

Quercetin is a flavonoid compound commonly found in medicinal plants. *In vitro* studies have demonstrated that quercetin can inhibit the production of tumor necrosis factor-alpha (TNF-α) induced by lipopolysaccharide (LPS) in macrophages and suppress the secretion of inflammatory cytokines, including interleukin-6 (IL-6) and interleukin-4 (IL-4)[8-10]. Quercetin exhibits antibacterial activity against *S. aureus* and *E. coli* and can potentiate the efficacy of other antibacterial agents against drug-resistant fungi[11]. Apigenin, a flavonoid compound with anti-inflammatory and antioxidant properties, is commonly present in various plants, including celery, chamomile, and *S. involucrata*[12]. Peng *et al.*[12] demonstrated that the topical application of apigenin is an effective treatment for skin diseases. Genistein, a natural phytoestrogen, can bind to estrogen receptors ERα and ERβ, thereby exerting a bidirectional regulatory effect analogous to that of estrogen or anti-estrogen agents[13]. Through animal experiments, Sun *et al.*[14] demonstrated that supplementation with genistein was beneficial in treating senile vaginitis characterized by estrogen deficiency. Consequently, topical application of TCM formulations may mitigate local inflammatory responses via the aforementioned active components.

Estrogen receptor 1 (ESR1) and its ligand, estrogen, contribute to the defense against pathogen invasion by maintaining the thickness of the vaginal epithelium and promoting the secretion of antimicrobial peptides, cytokines, and chemokines[15].

Studies have demonstrated that the absence of ESR1 can influence the proliferation and apoptosis of vaginal epithelial cells[15]. In the prostatitis model, agonists of estrogen receptor β have been shown to effectively reduce the expression of inflammatory cytokines, including TNF-α, nitric oxide synthase 2 (NOS2), and cyclooxygenase-2 (PTGS2), thereby mitigating inflammation[16]. Therefore, the primary targets of the TCM formulation indicate that its anti-inflammatory mechanism predominantly involves the reduction of inflammatory factor levels and the restoration of mucosal barrier function.

The primary cause of vulvar odor is abnormal secretions resulting from inflammation of the vagina or urethra. Once these secretions are expelled from the body, pathogenic bacteria metabolize them, producing amine compounds. The active components of TCM formulations may locally penetrate the affected area, targeting specific inflammatory pathways and concurrently inhibiting the activity of pathogenic bacteria, thereby reducing the production of odor-causing substances at their source.

Table 2 Key nodes of TCM-bioactive components-targets network and their topological characteristics

Node	Type of node	Degree	Betweenness centrality	Node	Type of node	Degree	Betweenness centrality
PTGS2	Target	52	0.303 0	Kaempferol	Compound	14	0.024 1
Quercetin	Compound	41	0.243 4	Beta-sitosterol	Compound	13	0.025 9
Apigenin	Compound	27	0.095 2	*Eupatorium fortunei*	TCM	13	0.024 7
ESR1	Target	24	0.072 8	(−)-Epicatechin	Compound	12	0.029 8
NOS2	Target	23	0.069 2	TNF	Target	12	0.021 5
Genistein	Compound	20	0.068 4	Calycosin	Compound	12	0.015 7
Sophorae Flavescentis Radix	TCM	19	0.060 2	F2	Target	11	0.024 6
Luteolin	Compound	19	0.045 2	TRPV1	Target	10	0.019 4
Wogonin	Compound	17	0.029 5	Formononetin	Compound	10	0.015 5
AR	Target	16	0.067 2	Ramulus Cinnamomi	TCM	10	0.014 7
NR3C2	Target	16	0.025 0	Octacosanol	Compound	9	0.040 4
Herba Leonuri	TCM	15	0.040 5	Erythrodio	Compound	9	0.019 5
DPP4	Target	15	0.024 9	Dipterocarpol	Compound	8	0.018 5
CASP3	Target	14	0.041 0	Peroxyergosterol	Compound	7	0.020 4
ESR2	Target	14	0.032 5	MMP1	Target	7	0.019 0

3.3 PPI network analysis The PPI network associated with the anti-inflammatory targets of the TCM formulation is illustrated in Fig. 3. This network comprised 62 protein nodes and 377 edges, with each edge representing an interaction between nodes. A higher number of edges connected to a node indicated greater significance of the corresponding target protein. The PPI network data were imported into Cytoscape software, and the MCC algorithm within the cytoHubba plugin was employed to identify hub gene targets within the network. As depicted in Fig. 4, the key target proteins identified were ALB, IL6, TNF, IL-1β, and IFNG.

Toll-like receptor 4 (TLR4) is expressed in vaginal epithelial cells and plays a crucial role in modulating the immune and inflammatory responses within the vaginal environment. LPS, a component of Gram-negative bacteria, can bind to TLR4, thereby triggering the inflammatory response and promoting the release of inflammatory mediators, including interleukin-1β (IL-1β), IL-6, and tumor TNF-α, which contribute to the exacerbation of inflammation[17]. Furthermore, research indicates that elevated expression levels of TNF-α and IL-1β contribute to increased neutrophil infiltration and subsequent tissue damage, thereby facilitating the development of urinary tract infections and urethritis[18]. Consequently, the modulation of IL-1β, IL-6, and TNF target proteins by TCM formulations may play a role in regulating inflammatory responses in the vaginal and urethral tissues.

Interferon-gamma (IFN-γ) is a key cytokine involved in the regulation of immune responses. Studies have demonstrated that in human vaginal epithelial cell models, TLR agonists can stimulate the production of IFNG, indicating a significant association with mucosal inflammatory responses[19]. Albumin (ALB) may be associated with damage to vaginal epithelial cell and is considered to play a crucial role in the pathogenesis of vulvovaginal candidiasis[20]. The concentration of ALB exhibits significant variability across diverse physiological and pathological states, but monitoring ALB levels in patients may facilitate the prediction of infection outcomes. PPI network analysis of TCM formulations indicates that the core bioactive compounds of these medicinal plants may modulate processes involved in odor secretion by affecting key cytokines associated with the inflammatory response.

3.4 GO enrichment analysis The obtained targets of 62 bioactive compounds associated with the anti-inflammatory efficacy of the TCM formulation were submitted to the DAVID database for GO analysis. Using a significance threshold of $P < 0.01$, a total of 1 267 GO terms were identified, comprising 1 178 biological process (BP) terms, 61 molecular function (MF) terms, and 28 cellular component (CC) terms. The resulting data were imported into Hiplot for further analysis. Comprehensive filtering was applied based on P values, Q values ($Q < 0.05$), and gene enrichment counts. Subsequently, the top 10 terms from each category (BP, MF, and CC) were selected to generate bar charts (Fig. 5).

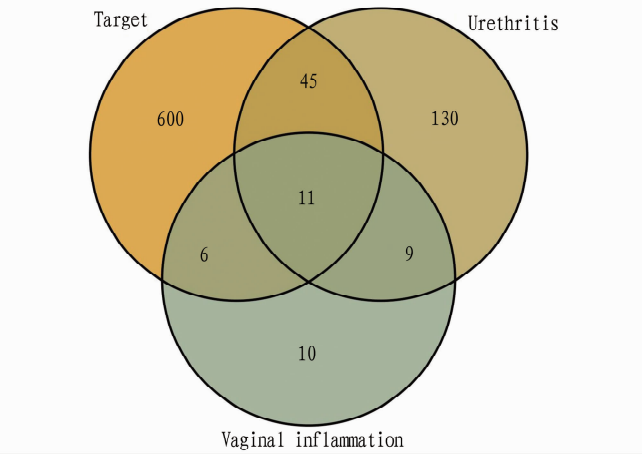
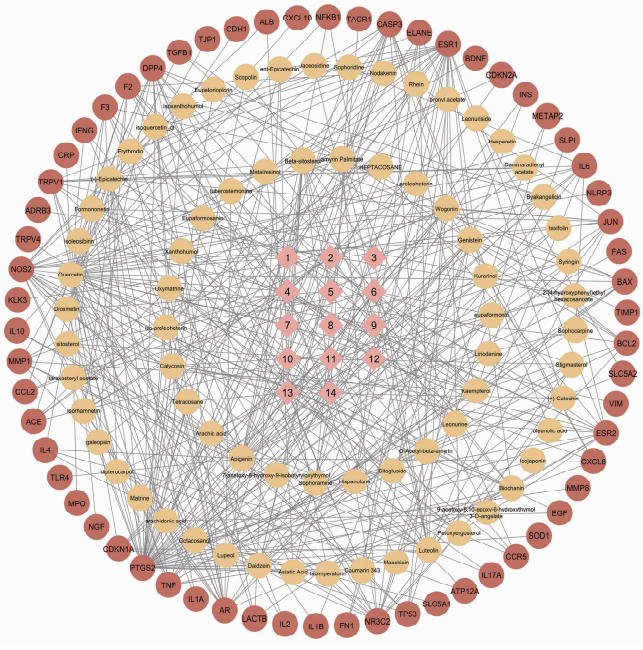


Fig. 1 Venn diagrams of inflammatory gene targets and the targets of the TCM formulation



NOTE Components 1 to 14 are the same as those in Table 1.

Fig. 2 TCM-bioactive components-targets network diagram

GO analysis indicated that the bioactive compounds in the TCM formulation may be potentially involved in biological processes related to the secretory granule lumen, cytoplasmic vesicle lumen, and vesicle lumen. These compounds may influence the secretion of signaling molecules, such as cytokines, by modulating responses to LPS and molecule of bacterial origin, as well as regulating inflammatory responses. Consequently, they may affect molecular functions including cytokine receptor binding, serine-type peptidase activity, and estrogen response element binding, thereby contributing to anti-inflammatory effects.

LPS is a distinctive constituent of the outer membrane of Gram-negative bacterial cells and can induce an inflammatory response in the host through the activation of TLR4[21]. LPS derived from uropathogenic *E. coli* is implicated in urinary tract infections and may contribute to the development of urethritis[22]. Therefore,

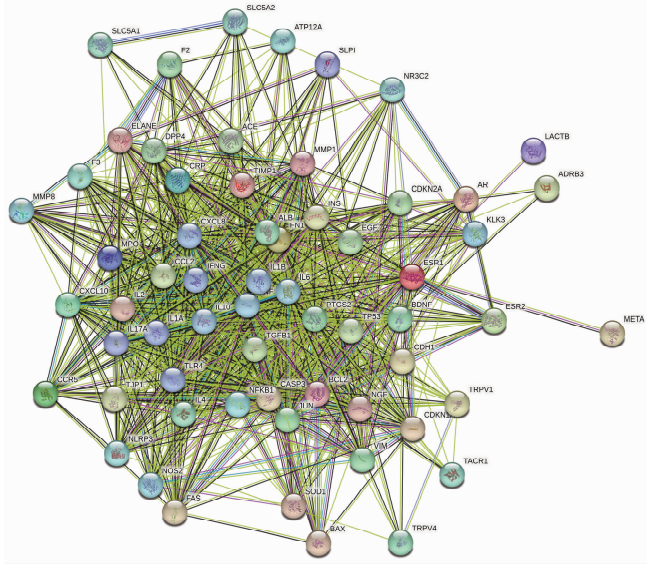


Fig. 3 PPI network diagram

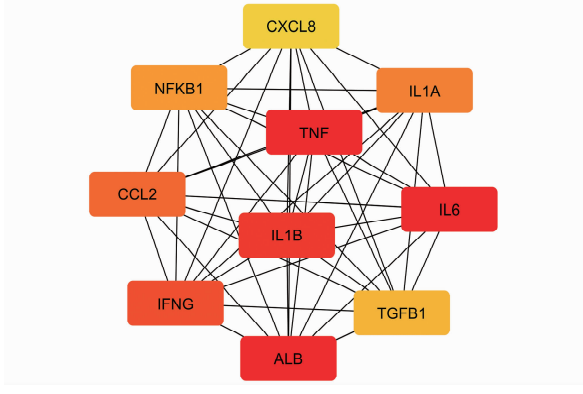
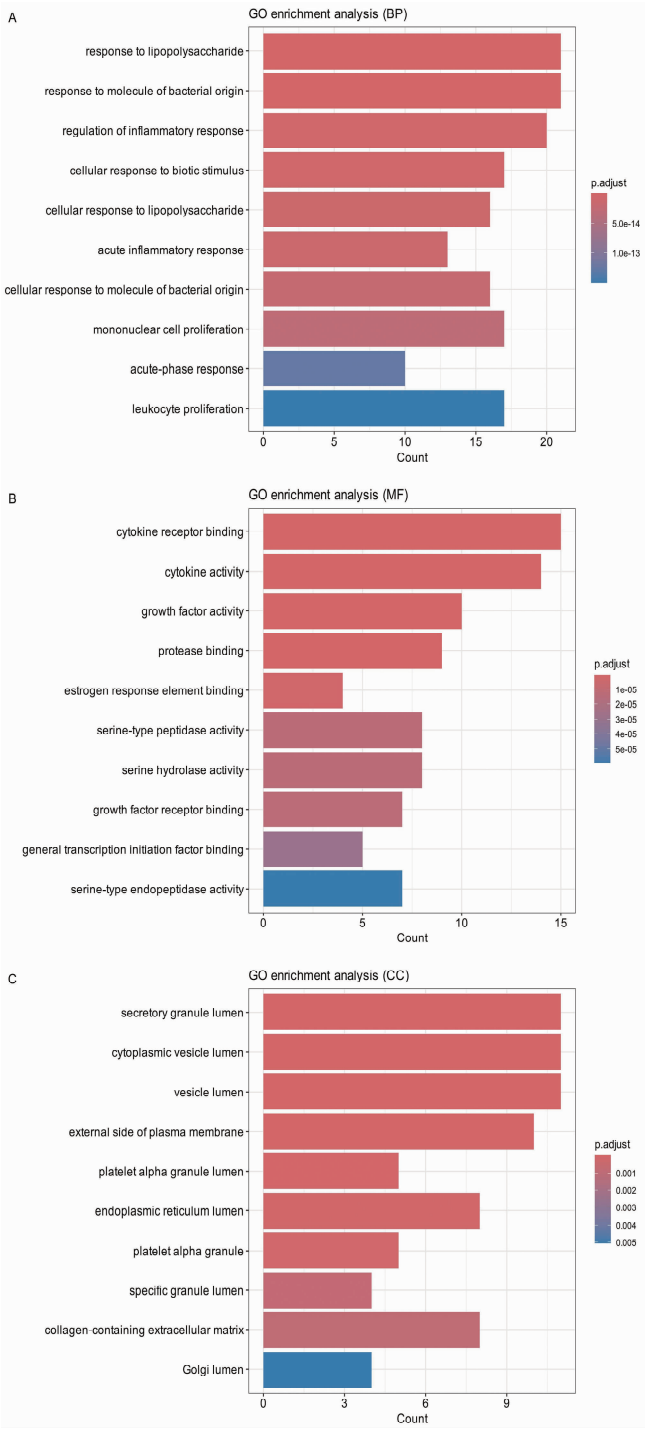


Fig. 4 Network diagram of hub genes

modulating the host's response to LPS may be advantageous in mitigating chronic inflammation.

Generally, the pathogenic bacteria responsible for bacterial vaginitis produce a range of virulence factors that suppress and overwhelm the host immune response. For example, *Gardnerella vaginalis* secretes haemolysin, which forms pores and fissures in the cell membrane, thereby compromising the integrity of the vaginal epithelial barrier and ultimately resulting in the dysfunction and death of vaginal epithelial cells[23]. Furthermore, *G. vaginalis* is capable of hydrolyzing mucosal glycans through the secretion of sialidase, which disrupts the protective mucus layer of the vaginal epithelium and thereby facilitates the adhesion of bacterial cells to the vaginal epithelium[24]. This indicates that the recognition and response of the vaginal mucosa to bacterial-derived molecules are associated with the onset and progression of vaginitis.

Cytokines are fundamental signaling molecules that play a critical role in the body's inflammatory and immune responses. Research has demonstrated that the highly active secreted aspartic protease of *C. albicans* can stimulate vaginal epithelial cells to produce increased levels of IL-1β and IL-18[25]. The overexpression



NOTE A. BP enrichment results; B. MF enrichment results; C. CC enrichment results.

Fig. 5 GO enrichment analysis diagram of bioactive compound targets

of these cytokines may initiate inflammatory responses or even induce cell death, thereby exacerbating local pathological damage within the vaginal tissue. Atrophic vaginitis is a form of vaginitis resulting from estrogen deficiency and may manifest clinically with symptoms such as abnormal vaginal secretions[26]. Estrogen plays a crucial role in promoting the proliferation and differentiation of vaginal epithelial cells, as well as enhancing the physical barrier function of the vaginal mucosa[27]. Moreover, it facilitates the synthesis and storage of glycogen necessary for epithelial cells, thereby enhancing lactic acid production, maintaining the acidic environment of the vagina, and inhibiting the proliferation of pathogenic bacteria[28]. Specifically, cytokines, estrogens, and their respective receptors play a crucial role in vaginal inflammation. The interplay of these biological pathways may elucidate the multichannel mechanisms through which TCM formulations mitigate inflammatory responses, ultimately addressing the underlying causes of body odor.

4 Conclusions and prospects

Microbial infections and inflammation can disrupt the body's homeostasis, subsequently leading to issues related to body odor. The management of odor in the vulvar region can be approached through three primary strategies: odor masking, bacterial inhibition, and anti-inflammatory treatment. Chen *et al.*[29] identified seven amine compounds in the vaginal secretions of patients with nonspecific vaginitis, including methylamine, isobutylamine, putrescine, cadaverine, histamine, tyramine, and phenylethylamine. These amines are likely responsible for the characteristic abnormal fishy odor. Botanical deodorants that effectively eliminate odors primarily utilize plant extracts as active components. These extracts are characterized by their abundant availability, natural origin, and environmental friendliness, which has led to their growing application in daily life[30]. Numerous studies have demonstrated that natural Chinese herbal medicines possess inhibitory effects on the unpleasant odor of saliva[31-32]. Both Angelicae Sinensis Radix extract and Sophorae Flavescentis Radix extract exhibit notable efficacy in the removal of ammonia gas. As botanical raw materials or components of formulations, they possess significant potential for applications in deodorization and odor elimination[33]. Certain volatile oil components derived from plants possess distinctive herbal aromas that can partially mask specific odors. Borneolum Syntheticum and the volatile oils extracted from Ramulus Cinnamomi and Angelicae Dahuricae Radix possess a fragrant aroma[34-35]. The volatile components present in the TCM formulation, including Angelicae Sinensis Radix, Ramulus Cinnamomi, Angelica Dahurica, Sophorae Flavescentis Radix, and Borneolum Syntheticum, contribute to masking unpleasant odors.

Modern medical research suggests that the production of body odor is primarily associated with the metabolic byproducts of the microbial flora present on the skin surface. Most deodorants employ antibacterial agents and aromatic compounds to mask these odors, but direct application to sensitive skin areas can lead to adverse reactions, including irritation[36]. Plants, as rich sources of chemical diversity, contain relatively mild antibacterial components, and the various compounds within plant extracts often dem-

onstrate highly effective synergistic interactions[37]. It has been reported that the aqueous extract of Cnidii Fructus, when combined with benzalkonium bromide, exhibits a significant synergistic bactericidal effect against *S. aureus*, *E. coli*, *Aspergillus niger*, and *C. albicans*[38]. Similarly, the aqueous extract of Sophorae Flavescentis Radix demonstrates a synergistic bactericidal effect in conjunction with benzalkonium bromide[39]. Compounds isolated from the root of Stemonae Radix have shown potent antibacterial activity against *C. albicans*[40]. Network pharmacology studies indicate that snow lotus exerts antibacterial effects through bioactive compounds such as quercetin, apigenin, and luteolin[41]. Active components derived from medicinal plants including *S. involucrata*, Fructus Cnidii, Stemonae Radix, and Sophorae Flavescentis Radix contribute to the inhibition and eradication of pathogenic bacteria present on the body surface and in secretions, thereby reducing the production of metabolic substances associated with odor generation.

In addition to possessing a material basis related to flavor masking and antibacterial properties, network pharmacological analysis indicates that Sophorae Flavescentis Radix, Herba Leonuri, and *E. fortunei* are the principal TCMs responsible for the anti-inflammatory effects within this formulation. This preparation may target molecules such as ALB, IL6, TNF, IL-1β, and IFNG through bioactive compounds including quercetin, apigenin, and genistein, thereby modulating cellular responses to bacteria-derived molecules and mitigating chronic inflammation. Moreover, in response to potential tissue and cellular damage induced by inflammation, this TCM formulation may interact with the estrogen receptor ESR1 to exert estrogen-like effects. This interaction could contribute to the reduction of inflammatory factor levels and the enhancement of the physical barrier function of vaginal epithelial cells. Given its capacity to mask odors, inhibit bacterial growth, and mitigate inflammation, the TCM formulation may also regulate malodorous secretions resulting from inflammatory responses. The application and advancement of the anti-inflammatory properties of medicinal plants in the management of body odor present significant research opportunities.

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cal metric to define extraction/concentration specifications. Subsequent single-factor studies targeting granule performance indicators, formation rate, hygroscopicity, flowability, and solubility, optimized the granulation protocol. Scale-up validation via three pilot batches (45.6 kg input each) confirmed the scientific robustness and operational viability of the integrated manufacturing methodology.

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