

Exploring Medication Patterns and Mechanisms of Medicinal-and-Edible Homologous Traditional Chinese Medicine (TCM) in Obesity Treatment: A Data Mining Study

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Abstract:

This study systematically investigates the medication patterns and mechanisms of medicinal-and-edible homologous Traditional Chinese Medicine (TCM) in obesity treatment through integrated data mining and network pharmacology. By analyzing 454 TCM patent formulations from the China National Intellectual Property Administration, we identified herb utilization patterns dominated by sweet-warm and bitter-cold properties with spleen-liver meridian tropism. Core herbs (Poria cocos, Lotus leaf, Hawthorn, and Tangerine peel) were determined via frequency statistics, association rules, and cluster analysis. Network pharmacology revealed 38 active components (including quercetin, kaempferol, and naringenin) interacting with 227 targets, notably AKT1, PPARG, and BCL2, primarily regulating lipid metabolism, PI3K-Akt signaling, and AGE-RAGE pathways. Molecular docking confirmed strong binding affinities between core components and targets. The anti-obesity mechanisms involve synergistic effects of fortifying the spleen, regulating qi, and resolving dampness through multi-component, multi-target interactions. These findings provide a scientific foundation for developing TCM-derived dietary therapies against obesity, while highlighting the need for further experimental validation of predicted targets and pathway dynamics.

Keywords:

Medicinal-and-Edible Homologous, Obesity, Data Mining, Network Pharmacology, Molecular Docking

1. Introduction

With the transformation of modern lifestyles, obesity—a chronic metabolic disorder resulting from complex interactions between genetic and environmental factors [1]—has emerged as a critical public health challenge [2]. Obesity is not merely characterized by abnormal fat accumulation, but also serves as a precursor to multiple

health complications, including type 2 diabetes, cardiovascular diseases, osteoarthritis, and various cancers (e.g., breast, colorectal, and endometrial cancers) [3,4,5], profoundly jeopardizing human health. Additionally, obesity is frequently accompanied by psychological disorders such as anxiety and depression [6].

Confronting this pressing issue, conventional therapies—including dietary control, exercise interventions, pharmacological treatments, and bariatric surgery—have demonstrated limited efficacy due to substantial interindividual variability and unsustainable weight-loss outcomes [7]. Consequently, there is an urgent need to explore more comprehensive, mechanism-driven, and long-term therapeutic strategies for obesity management.

The holistic theory of TCM and its principle of pattern differentiation-based treatment offer unique advantages in addressing obesity [8]. TCM dietary therapy, which integrates the concept of medicinal-and-edible homologous herbs with modern health paradigms, aims to resolve obesity by regulating qi and blood and restoring yin-yang balance, rather than focusing solely on weight reduction. Against this backdrop, the rational utilization of 102 medicinal-and-edible homologous herbs officially recognized by the National Health Commission has become pivotal in TCM-based obesity interventions. These herbs exhibit dual attributes as both medicines and foods, with mild properties, minimal adverse effects, and multi-target mechanisms [9], thereby providing novel insights for obesity treatment.

However, current research lacks systematic and in-depth exploration of the specific mechanisms underlying medicinal-and-edible homologous herbs in obesity management. To address this gap, this study employs data mining to analyze patented TCM formulations for obesity, aiming to elucidate their medication patterns. Furthermore, network pharmacology and molecular docking technologies are integrated to investigate their potential mechanisms of action.

2. Materials and Methods

2.1. Data Mining Analysis of Obesity

2.1.1. Data Collection and Screening

Using “obesity” as the search keyword and selecting IPC classification “A61—Medical or Veterinary Science; Hygiene”, we retrieved invention patents and published applications related to TCM formulations for obesity treatment from the China National Intellectual Property Administration (<http://epub.cnipa.gov.cn/>), covering all records from the database inception to June 2024.

2.1.2. Inclusion criteria

- ① Patents explicitly stating the use of TCM or TCM extracts for obesity treatment;
- ② Oral administration as the primary delivery method;
- ③ Formulations containing ≥ 2 herbs with fully disclosed compositions.

2.1.3. Exclusion criteria

- ① Topical TCM formulations (including but not limited to patches, enemas, and medicinal baths);

- ② Patents targeting animal obesity;
- ③ Lack of clinical efficacy data;
- ④ Duplicate formulations under different patent claims (only one entry was retained).

2.1.4. Data Standardization and Entry

Standardized herbal names in eligible patent formulations were standardized according to the *Chinese Pharmacopoeia (2020)* and *Chinese Materia Medica Dictionary*. Examples include: Normalizing “Jinwen Dahuang, Jiujun, and Huoshen” to “Rheum palmatum”; normalize “Caojueming” to “Celosia argentea”; normalize “Xianlingpi” to “Epimedium brevicornum”. Herbs not listed in the above references were recorded as per original patent descriptions. To ensure accuracy, two researchers independently entered data into Excel, with a third researcher auditing and consolidating the database.

2.1.5. Data Statistics and Analysis

The dataset was imported into the TCM Inheritance Computing Platform (V3.0) for analysis. Frequency and distribution analyses were performed for all herbs, followed by statistical analysis of their herbal properties, flavors, and meridian tropism. Core herb combinations were screened using association rules based on confidence and support. Cluster analysis was then applied to identify core formula patterns. Finally, core medicinal-and-edible homologous herbs for obesity treatment were identified by integrating: high-frequency herbs, association rules, and cluster groupings.

2.2. Network Pharmacology Investigation

2.2.1. Screening Active Components and Targets

Active components and targets of core medicinal-and-edible homologous herbs were retrieved from the Encyclopedia of Traditional Chinese Medicine (ETCM) (<http://www.tcmip.cn/ETCM/>), filtered by Lipinski's Rule of Five [10]. Additional components and targets were supplemented via the TCM Systems Pharmacology (TCMSP) (<https://old.tcmsp-e.com/tcmsp.php>). Human protein targets were standardized using UniProt Database (<https://www.uniprot.org/>).

2.2.2. Acquisition of Obesity-Related Disease Targets

Using “Obesity” as the keyword, disease targets were retrieved from Genecards (<https://www.genecards.org/>), OMIM (<https://www.omim.org/>), PharmGKB (<https://www.pharmgkb.org/>), TTD (<https://db.idrblab.net/ttd/>), and DrugBank (<https://go.drugbank.com/>). Merged targets were deduplicated.

2.2.3. Construction of “Herbs-Component-Target” Network

Intersection targets between herb-related targets (§1.2.1) and obesity-related targets (§1.2.2) were identified as potential therapeutic targets. These targets and corresponding components were imported into Cytoscape 3.9.1 to construct the network. Network Analyzer calculated degree centrality to identify core components.

2.2.4. PPI Network Construction and Core Target Screening

Potential therapeutic targets were uploaded to STRING Database (<https://cn.string-db.org>) with the species set to “Homo sapiens”. Interactions with confidence scores >0.400 were selected, while isolated nodes were removed. PPI data were analyzed in Cytoscape using CytoNCA plugin. Core targets were screened by topological parameters: Betweenness Centrality, Closeness Centrality, and Degree Centrality.

2.2.5. GO and KEGG Enrichment Analysis

The “clusterProfiler” package in R software performed GO and KEGG enrichment analyses. GO covered three domains: Biological Processes (BP), Cellular Components (CC), and Molecular Functions (MF). Results were visualized via “ggplot2” package.

2.3. Molecular Docking Validation

Core targets and their corresponding core active components identified in §1.2.4 underwent molecular docking to evaluate binding potential. First, the 3D structures of core target were retrieved from the RCSB PDB (<https://www.rcsb.org>), followed by dehydration and ligand separation using PyMOL. Simultaneously, the 3D structures of core active components were downloaded from PubChem (<https://pubchem.ncbi.nlm.nih.gov>) and optimized via Chem3D. Receptor proteins and ligand molecules were processed using AutoDock Tools. To ensure docking accuracy, an appropriate docking box was set based on the structural dimensions of the receptor and ligand for semi-flexible docking. Finally, optimal docking results were selected for interaction pattern analysis. A negative binding energy value indicates spontaneous binding between the receptor protein and ligand molecule, with lower values reflecting greater conformational stability [11].

3. Results

3.1. Data Mining for Obesity Treatment

3.1.1. Frequency Distribution, Herbal Properties, Flavors, and Meridian tropisms

Through systematic search and collation, 454 eligible TCM patent formulations targeting obesity treatment were included. These formulations comprised 382 distinct herbs, among which 90 herbs (medicinal-and-edible homologous category) were used 2,229 times, with a medication rate of 50.2%. Notably, 9 out of the top 15 high-frequency herbs were medicinal-and-edible homologous (Table 1).

Table 1. Frequency distribution on the use of herbs.

No.	Name of TCM	Frequency	Medication rate %	Utilization rate %	No.	Name of TCM	Frequency	Medication rate %	Utilization rate %
-	Medicinal and edible homologous TCM	2229	50.2	-	8	Astragalus membranaceus *	103	2.3	22.7
1	Poria cocos *	170	3.8	37.4	9	Cassia obtusifolia *	102	2.3	22.5
2	Hawthorn *	158	3.6	34.8	10	Coix seed *	94	2.1	20.7
3	Lotus leaf *	154	3.5	33.9	11	Rheum	86	1.9	18.9

						palmatum			
4	Licorice *	129	2.9	28.4	12	Pinellia ternata	77	1.7	17.0
5	Tangerine peel *	121	2.7	26.7	13	Atractylodes lancea	72	1.6	15.9
6	Alisma orientale	117	2.6	25.8	14	Salvia miltiorrhiza	69	1.6	15.2
7	Atractylodes macrocephala	112	2.5	24.7	15	Dioscorea opposita *	56	1.3	12.3

* Indicates that medicinal-and-edible homologous herbs

Analysis of herbal properties, flavors, and meridian tropisms revealed distinct characteristics of anti-obesity herbs:

Herbal Properties: Predominantly warm and cold properties.

Herbal Flavors: Most common flavors were sweet and bitter.

Meridian Tropism: Predominantly targeted the spleen and liver meridians.

3.1.2. Association Rule Analysis of Herbal Formulations

Association rule analysis of obesity TCM prescriptions identified 12 herbal combinations with a frequency ≥ 55 , representing common compatibility patterns in obesity treatment. The top three combinations were: Hawthorn - Lotus leaf, Poria cocos - Tangerine peel, Poria cocos - Lotus leaf (Table 2).

Table 2. Patterns of herbal combinations in treating obesity.

No.	Combination of TCM	Frequency	No.	Combination of TCM	Frequency
1	Hawthorn - Lotus leaf	85	7	Poria cocos - Alisma orientale	64
2	Poria cocos - Tangerine peel	81	8	Poria cocos - Licorice	63
3	Poria cocos - Lotus leaf	72	9	Hawthorn - Cassia obtusifolia	62
4	Lotus leaf - Cassia obtusifolia	68	10	Lotus leaf - Tangerine peel	60
5	Poria cocos - Atractylodes macrocephala	66	11	Hawthorn - Alisma orientale	60
6	Poria cocos - Hawthorn	65	12	Poria cocos - Coix seed	58

3.1.3. Clustering of Anti-Obesity Herbal Formulations

Cluster analysis of 454 obesity patent prescriptions identified 3 core cluster groups, as summarized in Table 3. By integrating high-frequency herbs, association rules, and cluster patterns, the following medicinal-and-edible homologous herbs were selected as core anti-obesity agents: Poria cocos, Lotus leaf, Hawthorn, and Tangerine peel.

Table 3. Core clustering herbal combinations.

Category	Core clustering combinations	Number of clusters	Efficiency
1	Lotus leaf, Poria cocos, Hawthorn, Alisma orientale,	265	Fortify the spleen and regulate qi, Promote diuresis and drain

	Tangerine peel		dampness, Resolve food stagnation
2	Hawthorn, Poria cocos, Astragalus membranaceus, Dioscorea opposite, Lotus leaf	121	Fortify the spleen and boost qi, Promote diuresis and drain dampness, Resolve food stagnation
3	Poria cocos, Licorice, cinnamon, Tangerine peel, Hawthorn	68	Fortify the spleen and warm yang, Regulate qi to resolve food stagnation and dispel accumulation

3.2. Mechanisms of Core Medicinal-and-Edible Homologous Herbs in Anti-obesity

3.2.1. Core Herb Targets and Obesity-Related Targets

Four core medicinal-and-edible homologous herbs—Poria cocos, Lotus leaf, Hawthorn, and Tangerine peel—were analyzed. Initial screening via the ETCM identified 28 active components and 251 targets, supplemented by 13 additional components and 231 targets from the TCMSP, yielding 38 active components and 416 targets after deduplication.

With a Relevance score threshold >1 in GeneCards, 3,733 obesity-related targets were identified. Integration with OMIM, PharmGKB, TTD, and DrugBank databases consolidated 4,044 obesity-related disease targets (Figure 1). Intersection analysis revealed 227 potential therapeutic targets shared between herbs and obesity (Figure 2).

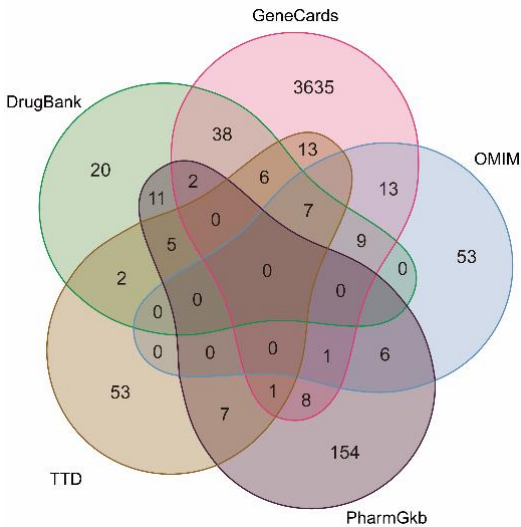


Figure 1. Obesity-related targets.



Figure 2. Common targets of herbs and obesity.

3.2.2. “Herbs-Component-Target” Network

The Cytoscape-constructed network (Figure 3) demonstrated interactions among herbs, components, and targets. Network Analyzer identified degree centrality as a key metric, with higher-degree components occupying central network positions. The top 5 components by degree were: Naringenin, Kaempferol, Isorhamnetin, Hesperetin, and Quercetin. These were defined as core therapeutic components for obesity treatment.

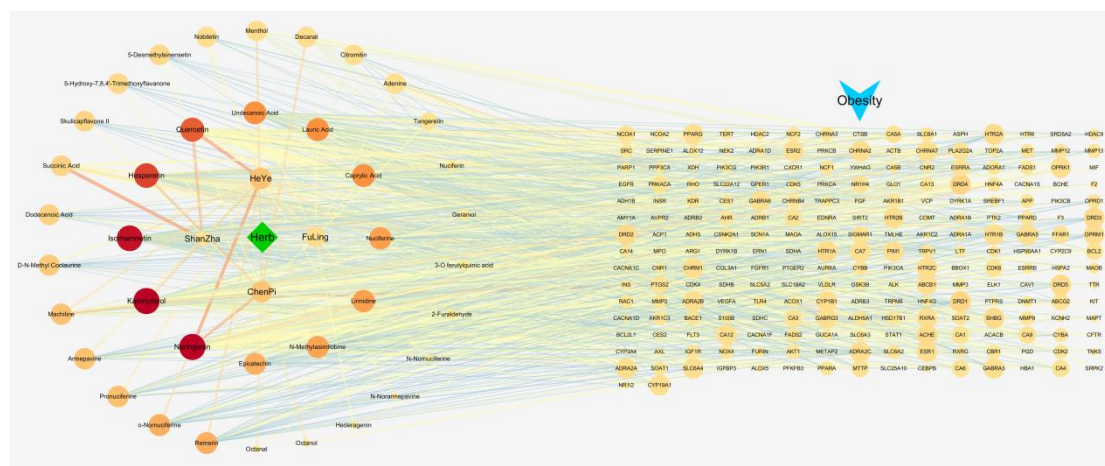


Figure 3. Network diagram of “Herbs-Component-Target”.

3.2.3. PPI Network and Core Target Screening

The PPI network of potential therapeutic targets for medicinal-and-edible homologous herbs comprises 227 nodes and 2,497 edges, where each edge precisely delineates complex inter-target interactions. To identify core nodes, CytoNCA plugin quantified key topological parameters. Nodes underwent two rounds of stringent filtering based on median values of Betweenness Centrality, Closeness Centrality, and Degree Centrality. Further prioritization by Degree Centrality (the most critical metric) pinpointed AKT1, ACTB, ESR1, PPARG, and BCL2 as core therapeutic targets (Figure 4).

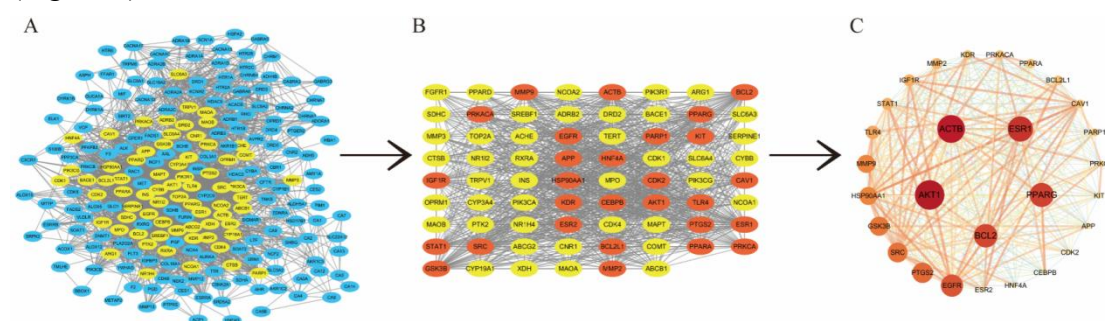


Figure 4. PPI network of potential targets and screening of core targets.

3.2.4. GO and KEGG Enrichment Results

GO functional enrichment yielded 2,492 entries, including 2,109 BP, 141 CC, and 242 MF.

BP: Primarily involved positive regulation of MAPK cascade, regulation of membrane potential, regulation of tube diameter, and blood vessel diameter maintenance.

CC: Enriched in synaptic membrane, postsynaptic membrane, and distal axon.

MF: Associated with G protein-coupled amine receptor activity, neurotransmitter receptor activity, catecholamine binding, and nuclear receptor activity.

Top 6 BP, CC, and MF entries by P-value are shown in Figure 5.

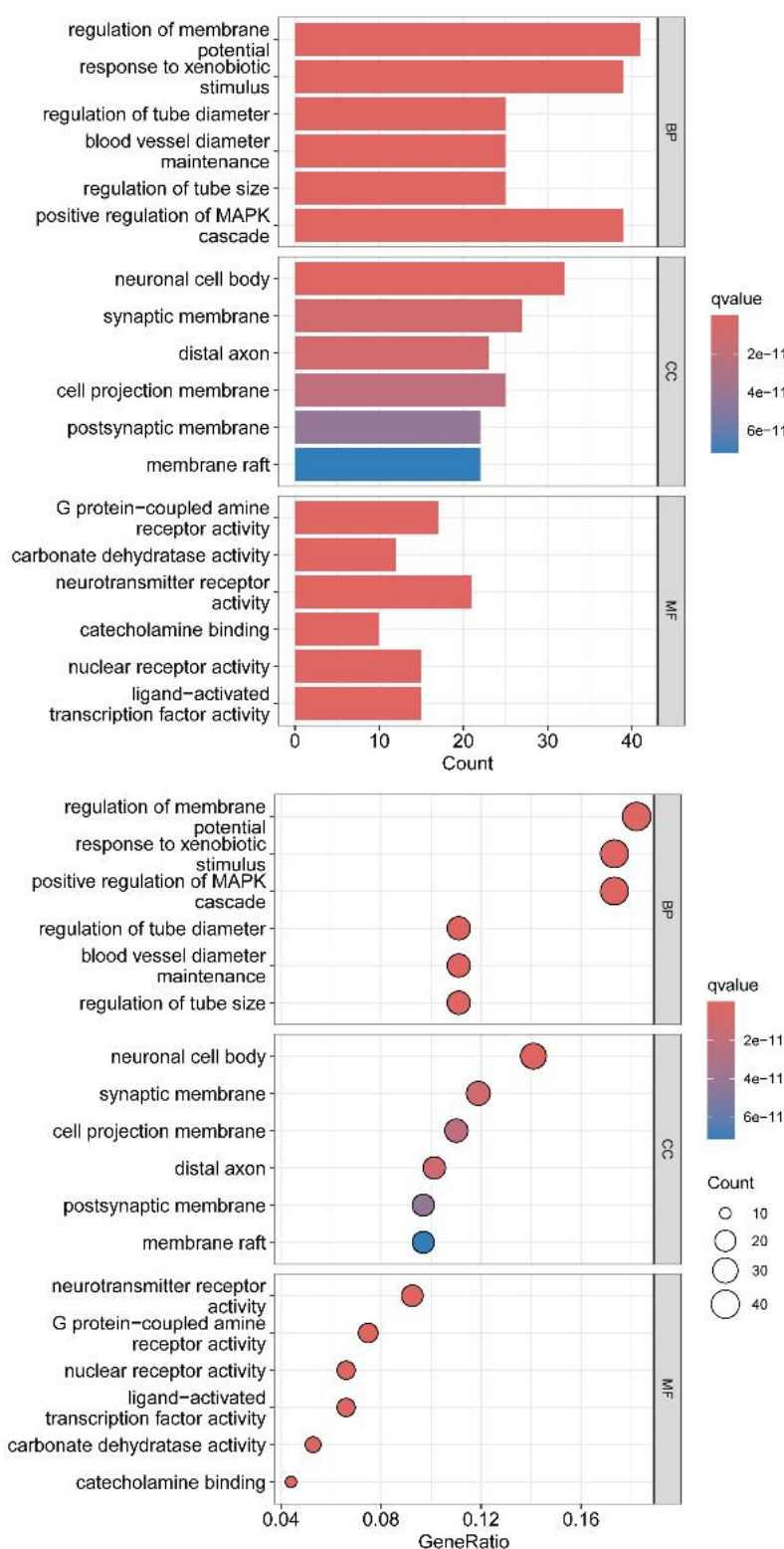


Figure 5. GO enrichment analysis of potential targets in treating obesity.

KEGG pathway analysis identified 173 enriched pathways, with the top 15 displayed in Figure 6. Significantly enriched pathways included: PI3K-Akt signaling pathway, Lipid and atherosclerosis, and AGE-RAGE signaling pathway in diabetic complications.

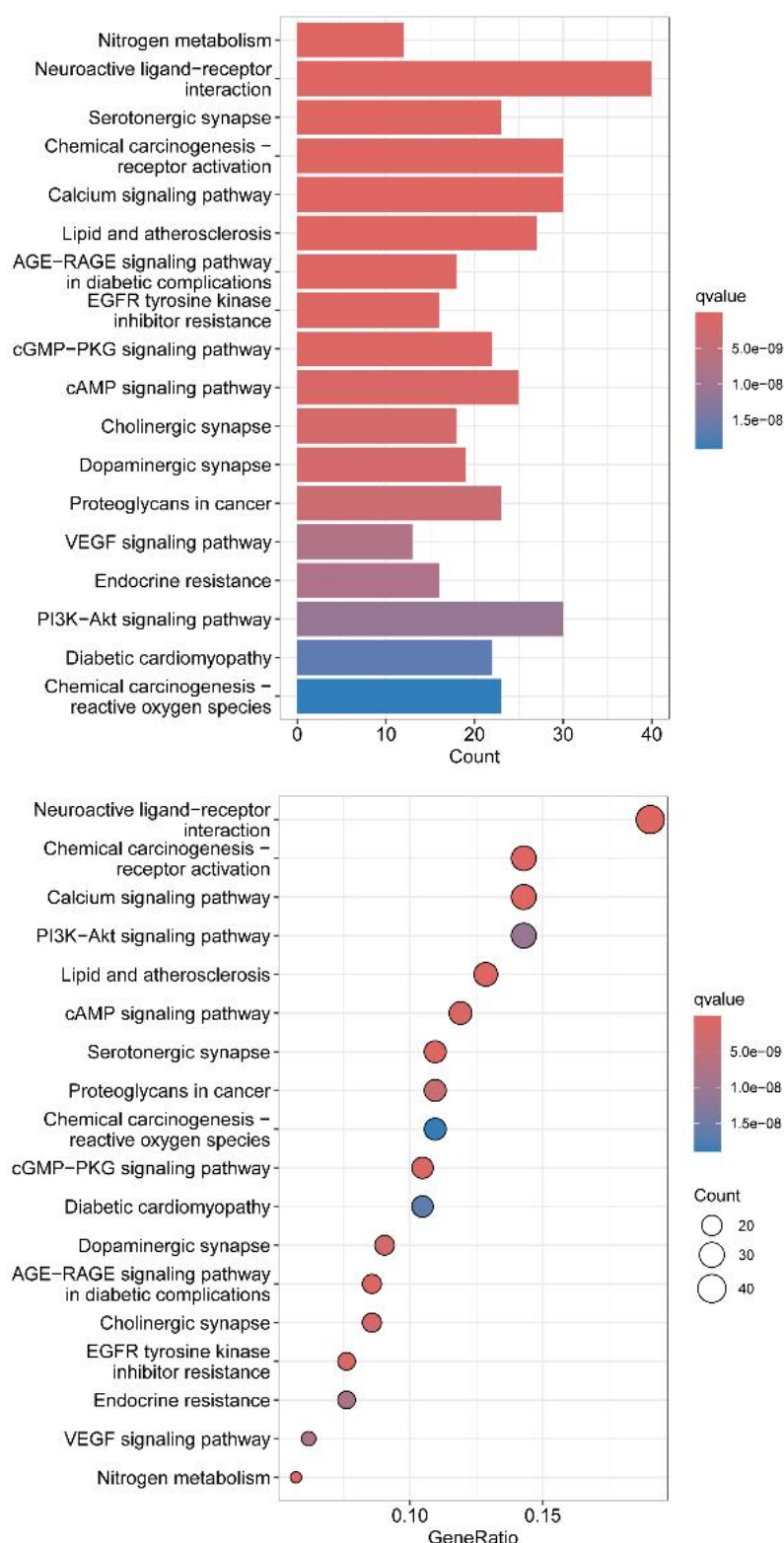


Figure 6. KEGG enrichment analysis of potential targets in treating obesity.

3.3. Binding Mode of Core Targets and Components

Semi-flexible docking between core targets (AKT1, ACTB, ESR1, PPARG, BCL2) and core components (naringenin, kaempferol, isorhamnetin, hesperetin, quercetin) revealed binding energies detailed in Table 4. All small molecules successfully occupied the active sites of target proteins. Binding energies ranged below -10.92

KJ/mol, indicating strong ligand-receptor interactions. Visualization of docking poses is shown in Figure 7.

Table 4. Docking binding energies of core targets and core components.

Core target	PDB ID	Core active component	Binding energy / (KJ·mol ⁻¹)
BCL2	6GLB	Naringenin	-18.54
		Hesperetin	-17.58
		Kaempferol	-18.71
		Quercetin	-24.42
ESR1	3OS8	Naringenin	-17.75
		Hesperetin	-10.96
		Kaempferol	-10.92
		Quercetin	-14.00
AKT1	3O96	Isorhamnetin	-20.04
		Kaempferol	-18.88
		Quercetin	-21.46
PPARG	2P4Y	Naringenin	-21.29
		Hesperetin	-13.54
ACTB	6ICT	Quercetin	-11.08

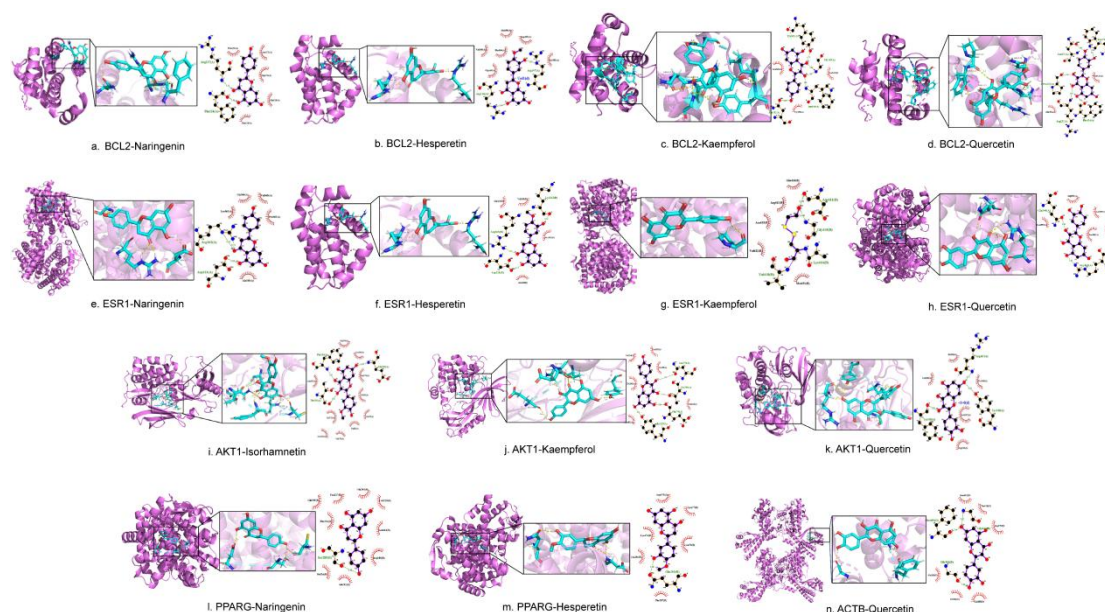


Figure 7. Results of molecular docking.

4. Discussion

Ancient TCM texts, notably *Huangdi Neijing*, classified obesity into three constitutional types: “Zhi Ren”(excess adipose), “Gao Ren”(excess dampness), and “Rou Ren”(excess muscle), highlighting the heterogeneity of obesity phenotypes. *Suwen* further emphasized the link between dietary habits and obesity pathogenesis. While traditional therapies—decoctions, herbal teas, acupuncture, and tuina—demonstrate efficacy, weight regain remains a challenge post-treatment. Thus, sustainable interventions are imperative. Medicinal-and-edible homologous TCM, with their high safety profiles and nutritional benefits, offer promising alternatives.

Data mining of anti-obesity patent formulations identified high-frequency herbs: Sweet-warm herbs for tonifying deficiency (e.g., *Atractylodes macrocephala*, *Licorice*, *Astragalus membranaceus*), Bitter-cold herbs for clearing

heat (e.g., *Alisma orientale*), Dampness-resolving herbs (e.g., *Poria cocos*, *Alisma orientale*), and Lipid-modulating herbs (e.g., Hawthorn, Lotus leaf, Tangerine peel, *Cassia obtusifolia*, Coix seed) [12,13,14]. Obesity, characterized by “deficiency in origin and excess in manifestation”, arises from food stagnation, qi-blood stasis, and phlegm-dampness accumulation [15]. Our findings align with TCM principles: sweet-warm herbs address root deficiency, bitter-cold herbs clear pathogenic excess, and dampness-resolving herbs synergistically target symptoms.

Association rules highlighted core herb pairs: Hawthorn - Lotus leaf, *Poria cocos* - Tangerine peel, and *Poria cocos* - Lotus leaf. Cluster analysis further revealed Lotus leaf, *Poria cocos*, Hawthorn, *Alisma orientale*, Tangerine peel that synergistically fortify the spleen, resolve food stagnation, drain dampness, and regulate qi, particularly effective for spleen deficiency-dampness stagnation pattern obesity—the most prevalent clinical subtype. Despite the efficacy of *Atractylodes macrocephala* and *Alisma orientale*, their exclusion from the medicinal-and-edible homologous list led to the selection of *Poria cocos*, Lotus leaf, Hawthorn, and Tangerine peel as core herbs, prioritized for network pharmacology investigation.

Through network pharmacology, core anti-obesity components were identified: quercetin, kaempferol, isorhamnetin, hesperetin, and naringenin. These compounds modulate obesity and metabolic disorders via multi-target mechanisms: Quercetin alleviates metabolic syndrome by targeting PPAR α/γ to regulate gluconeogenesis, reduce hepatic lipid accumulation, and mitigate obesity-induced oxidative stress [16,17]. Kaempferol suppresses adipogenesis by downregulating *Cebpa* expression in mature adipocytes and modulates lipid/glucose metabolism and gut microbiota [18,19]. Isorhamnetin (a flavonoid from *Opuntia ficus-indica*) reduces high-fat diet-induced weight gain, enhances insulin secretion, and decreases hepatic/adipose lipid deposition [20]. Naringenin (from Tangerine peel) activates AMPK to enhance energy expenditure and autophagy, ameliorating NAFLD and obesity [21]. Hesperetin inhibits pancreatic lipase via hydrogen bonds and van der Waals interactions, attenuating lipid absorption [22].

PPI network analysis identified 28 critical targets, with AKT1, ACTB, ESR1, PPARG, and BCL2 as central hubs. AKT1: Mediate insulin signaling in glucose/lipid metabolism and glycogenesis [23]. PPARG: Regulates adipocyte differentiation, lipid metabolism, and systemic insulin resistance [24]. ESR1: Modulates glucose transport in adipose/muscle tissues [25]. BCL2: Governs apoptosis in β -cells and adipocytes, influencing insulin secretion and adipogenesis [26].

Enriched pathways included MAPK cascade, membrane potential regulation, and vascular diameter control. Key KEGG pathways included Lipid and atherosclerosis, PI3K-Akt signaling, and AGE-RAGE in diabetic complications. Notably, AGE-RAGE pathway inhibition mitigates obesity-driven insulin resistance and inflammation [27]. PI3K-Akt signaling suppression reduces adipocyte lipid accumulation and enhances insulin sensitivity [28].

Obesity-induced chronic inflammation involves adipose tissue macrophages releasing pro-inflammatory cytokines, which exacerbate endothelial dysfunction [29,30]. Modulating lipid-metabolizing enzymes/receptors (e.g., via quercetin's inhibition of MAPK and pro-inflammatory cytokines) restores lipid balance and vascular homeostasis [31]. Molecular docking confirmed stable binding

conformations between core targets (AKT1, ACTB, ESR1, PPARG, BCL2) and components, robustly supporting their anti-obesity efficacy.

This study has several limitations. First, the data mining sample was predominantly sourced from patent literature, which may introduce selection bias. Second, network pharmacology predictions require validation through in vitro and in vivo experiments. Third, while molecular docking demonstrated plausible binding, functional assays are needed to confirm pharmacological efficacy. To further elucidate their therapeutic potential and advance novel anti-obesity drug development, future research should focus on two critical aspects: exploring dynamic regulatory interactions between core targets and signaling pathways, and validating these network pharmacology predictions through mechanistic experiments, thereby confirming the functional significance of these molecular interactions in metabolic regulation.

5. Conclusions

In summary, this study systematically revealed the medication patterns and multi-component, multi-target, multi-pathway mechanisms of medicinal-and-edible homologous herbs in obesity treatment.

Conflicts of Interest

The authors declare that there is no conflict of interest regarding the publication of this article.

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References

- [1] Poorolajal, J.; Sahraei F.; Mohamdadi, Y. et al. Behavioral factors influencing childhood obesity: a systematic review and meta-analysis. *Obes Res Clin Pract*, 2020,14(2), 109-118.
- [2] Tam, C.S.; Lecoultre, V.; Ravussin, E. Brown adipose tissue: mechanisms and potential therapeutic targets. *Circulation*, 2012, 125(22), 2782-91.
- [3] Piché, M.E.; Tchernof, A.; Després, J.P. Obesity phenotypes, diabetes, and cardiovascular diseases. *Circ Res*, 2020, 126(11), 1477-1500.
- [4] Lauby-Secretan, B.; Scoccianti, C.; Loomis, D. et al. Body fatness and cancer--viewpoint of the IARC working group. *N Engl J Med*, 2016, 375(8), 794-8.
- [5] Iyengar, N.M.; Gucalp, A.; Dannenberg, A.J. et al. Obesity and cancer mechanisms: tumor microenvironment and inflammation. *J Clin Oncol*, 2016, 34(35), 4270-4276.
- [6] Tang, X.J.; Hu, M.X.; Bi, J. et al. Study on the correlation between the severity of obesity combined with gastroesophageal reflux disease patients and their anxiety,depression and nutritional status. *Chinese Journal of Digestion and Medical Imageology (Electronic Edition)*, 2024, 14(04), 360-364.

- [7] Perdomo, C.M.; Cohen, R.V.; Sumithran, P. et al. Contemporary medical, device, and surgical therapies for obesity in adults. *Lancet*, 2023, 401(10382), 1116-1130.
- [8] Li, L.L.; Hu, X.; Liu, H.X. Efficacy of Cangzhu Mahuang decoction on lipid levels and body mass index in patients of dyslipidemia with phlegm and blood stasis block syndrome. *China Medicine*, 2022, 17(04), 609-614.
- [9] Xu, L.J.; Ma, P.; Yue, L.F. et al. Connotation and Practical Significance of Tea Drinks. *Modern Chinese Medicine*, 2021, 23(09), 1518-1524.
- [10] Lipinski, C.A, Lombardo, F.; Dominy, B.W. et al. Experimental and computational approaches to estimate solubility and permeability in drug discovery and development settings. *Adv Drug Deliv Rev*, 2001, 46(1-3), 3-26.
- [11] Xia, Q.; Liu, M.; Li, H. et al. Network pharmacology strategy to investigate the pharmacological mechanism of HuangQiXiXin decoction on cough variant asthma and evidence-Based medicine approach validation. *Evid Based Complement Alternat Med*, 2020, 2020, 3829092.
- [12] Li, Q.; Li, Y.T.; Xu, H.J.; Et al. Study on the Weight Loss Effect and Mechanism of Turmeric Combined with Hawthorn on C57 Obese Mice. *Science and Technology of Food Industry*, 2024, 45(01), 310-317.
- [13] Wu, R.Y. Therapeutic Efficacy of Oral Carbonized Nelumbo nucifera (Lotus Leaf Ash) in Middle-Aged and Elderly Obese Patients with Secondary Hyperlipidemia. *Chinese Journal of Gerontology*, 2018, 38(08), 1795-1797.
- [14] Ma, L.J.; Li, F.; Li, B. Experimental Study on the Interventional Effects of Cassia obtusifolia on Specific Anthropometric and Physiological Parameters in Obese College Students. *Lishizhen Medicine and Materia Medica Research*, 2009, 20(01), 41-43.
- [15] Lin, T.; Liu, M. Research on Traditional Chinese Medicine Interventions for Simple Obesity. *Journal of Basic Chinese Medicine*, 2021, 27(06), 1036-1040.
- [16] Kábelová, A.; Malínská, H.; Marková, I. et al. Quercetin supplementation alters adipose tissue and hepatic transcriptomes and ameliorates adiposity, dyslipidemia, and glucose intolerance in adult male rats. *Front Nutr*, 2022, 9, 952065.
- [17] Zhao, J.; Sun Y.; Yuan C. et al. Quercetin ameliorates hepatic fat accumulation in high-fat diet-induced obese mice via PPARs. *Food Funct*, 2023, 14(3), 1674-1684.
- [18] Torres-Villarreal D.; Camacho A.; Castro H. et al. Anti-obesity effects of kaempferol by inhibiting adipogenesis and increasing lipolysis in 3T3-L1 cells. *J Physiol Biochem*, 2019, 75(1), 83-88.
- [19] Nejabati, H.R.; Nikzad, S.; Roshangar L. Kaempferol: A dietary flavonol in alleviating obesity. *Curr Pharm Des*, 2023, 29(20), 1547-1556.
- [20] Rodríguez-Rodríguez, C.; Torres, N.; Gutiérrez-Urbe, J.A. et al. The effect of isorhamnetin glycosides extracted from *Opuntia ficus-indica* in a mouse model of diet induced obesity. *Food Funct*, 2015, 6(3), 805-15.
- [21] Yang, Y.; Wu, Y.; Zou, J. et al. Naringenin attenuates non-Alcoholic fatty liver disease by enhancing energy expenditure and regulating autophagy via AMPK. *Front Pharmacol*, 2021, 12, 687095.

- [22]Huang, R. Comparative Analysis of Spectrophotometric Methods for Citrus Flavonoids and Evaluation of Their Antioxidant Efficacy and Pancreatic Lipase Inhibitory Activity. Zhejiang University, 2019.
- [23]Demir S.; Wolff G.; Wieder A. et al. TSC22D4 interacts with Akt1 to regulate glucose metabolism. *Sci Adv*, 2022, 8(42)m eabo5555.
- [24]Zhuang, J.L.; Liu, Y.Y.; Li, Z.Z. et al. Amentoflavone prevents ox-LDL-induced lipid accumulation by suppressing the PPAR γ /CD36 signal pathway. *Toxicol Appl Pharmacol*, 2021, 431, 115733.
- [25]Fatima, L.A.; Campello, R.S.; Barreto-Andrade, J.N. et al. Estradiol stimulates adipogenesis and Slc2a4/GLUT4 expression via ESR1-mediated activation of CEBPA. *Mol Cell Endocrinol*, 2019, 498, 110447.
- [26]Bai, R.; Zhang, T.; Gao, Y. et al. Rab31, a receptor of advanced glycation end products (RAGE) interacting protein, inhibits AGE induced pancreatic β -cell apoptosis through the pAKT/BCL2 pathway. *Endocr J*, 2022, 69(8), 1015-1026.
- [27]Xia, B.; Zhu, R.; Zhang, H. et al. Lycopene improves bone quality and regulates AGE/RAGE/NF- κ B signaling pathway in high-fat diet-induced obese mice. *Oxid Med Cell Longev*, 2022, 2022, 3697067.
- [28]Yin, X.; Xu, Z.; Zhang, Z. et al. Association of PI3K/AKT/mTOR pathway genetic variants with type 2 diabetes mellitus in Chinese. *Diabetes Res Clin Pract*, 2017, 128, 127-135.
- [29]Zang, Y.Q.; Liu, S.Q.; Zhao, R.Q. et al. Research progress of adipokines in regulating cancer metabolism. *Chinese Journal of Clinical Oncology*, 2022, 49(14), 748-752.
- [30]Aota, K.; Yamanoi, T.; Kani, K. et al. Cepharanthine inhibits IFN- γ -Induced CXCL10 by suppressing the JAK2/STAT1 signal pathway in human salivary gland ductal cells. *Inflammation*, 2018, 41(1), 50-58.
- [31]Seo, M.J.; Lee, Y.J.; Hwang, J.H. et al. The inhibitory effects of quercetin on obesity and obesity-induced inflammation by regulation of MAPK signaling. *J Nutr Biochem*, 2015, 26(11), 1308-16.



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