

Research Progress on the Chemical Constituents, Pharmacological Activity and Related Signaling Pathways of Coptis Chinensis Franch

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Abstract. *Coptis chinensis* Franch. is a representative herb in traditional Chinese medicine. Its core active components are isoquinoline alkaloids, with berberine being the most abundant, along with palmatine, jatrorrhizine, coptisine, and others. *Coptis chinensis* Franch. exhibits various pharmacological activities, including antibacterial and anti-endotoxin effects, antiviral activity, hypoglycemic action, and anticancer properties. Berberine, one of its key components, functions through multiple targets by modulating pathways such as the AMPK/PI3K-Akt signaling pathway, the AMPK/mTOR autophagy regulation pathway, and the TLR4/MyD88 inflammatory signaling pathway.

Keywords: *Coptis chinensis* Franch., berberine, alkaloid, signaling pathways

1. Introduction

Coptis chinensis Franch., as a classic traditional Chinese medicine, possesses the functions of clearing heat, drying dampness, purging fire, and detoxifying. Its modern pharmacological value is increasingly gaining widespread attention. This article systematically reviews the research progress on the chemical constituents, multiple pharmacological activities, and related molecular signaling pathways of *Coptis chinensis* Franch., aiming to provide a theoretical basis for its further development and clinical application. Studies on chemical constituents have shown that *Coptis chinensis* Franch. is rich in isoquinoline alkaloids [1], with berberine being the most abundant, along with other active components such as palmatine and coptisine, which collectively form the material basis for its efficacy [2]. Furthermore, components such as flavonoids, lignans, and organic acids also play synergistic roles [3]. In terms of pharmacological activities, *Coptis chinensis* Franch. exhibits broad-spectrum and significant biological activities. Research has confirmed that it possesses potent antibacterial [4-6] and antiviral [7-9] effects, can effectively improve insulin resistance and lower blood glucose [10-12], and also demonstrates anti-tumor effects by inhibiting cell proliferation [13] and inducing apoptosis [14], among other mechanisms [15,16]. Research on the mechanisms of action further reveals that berberine, the core active component of *Coptis chinensis* Franch., primarily functions by modulating several key signaling pathways. These include the AMPK/PI3K-Akt pathway involved in regulating energy metabolism [11,17], the AMPK/mTOR

pathway regulating autophagy and cell growth [18-20], and the TLR4/MyD88/NF- κ B pathway that inhibits inflammatory responses [21,22].

2. Chemical composition

Coptis chinensis Franch. contains various compounds, including alkaloids, flavonoids, lignans, and organic acids, among which alkaloids are the primary active constituents [1].

2.1. Alkaloids

Alkaloids are the primary active constituents in *Coptis chinensis* Franch., mainly comprising isoquinoline alkaloids, with berberine being the most abundant [23]. Li Feng conducted a study on the extraction and isolation of the main chemical components from the rhizomes of ten varieties of *Coptis chinensis* Franch. (Weilian) from Emeishan City. The six major protoberberine-type alkaloids in *Coptis chinensis* Franch. were quantified in the following descending order: berberine (1) > coptisine (2) $\geq$ palmatine (3) > epiberberine (4) > columbamine (5) $\geq$ jatrorrhizine (6). Their approximate ratios were 5.4~8.3 : 1.4~2.5: 1.3~2.4: 1: 0.4~0.8: 0.4~0.7 [24]. The 2015 edition of the Chinese Pharmacopoeia specifies coptisine, berberine, epiberberine, and palmatine as indicative components for *Coptis chinensis* Franch. [2]. The berberine content varies across different parts of the plant: rhizomes contain 5% ~ 8%, fibrous roots contain up to 5%, and leaves contain 1.4% ~ 2.9% [25]. Differences in berberine content are also observed among different varieties of *Coptis chinensis* Franch.: *Coptis chinensis* Franch. (Weilian) contains 5.56% ~ 7.25%, *Coptis deltoidea* C. Y. Cheng et Hsiao (Yalian) contains 5.20% ~ 5.32%, and *Coptis teeta* Wall. (Yunlian) contains 6.83% ~ 7.69% [26]. The structures of compounds 1~6 are shown in Figure 1.

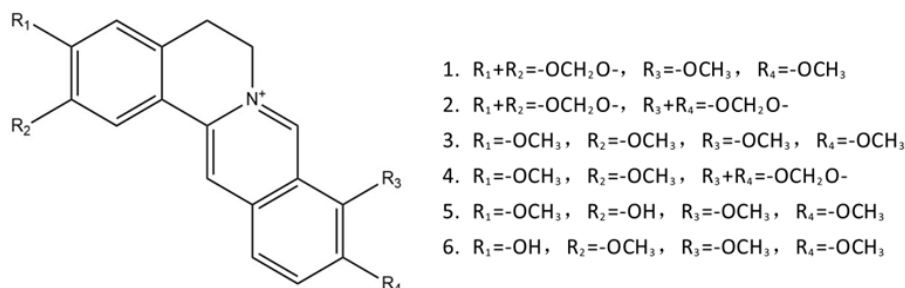


Figure 1. Structures of the six protoberberine-type alkaloids in *Coptis chinensis* Franch.

2.2. Flavonoids

Flavonoids are a class of compounds in nature characterized by the 2-phenylchromone structure. They typically exist in plants as glycosides conjugated with sugars, while a small portion occur in the form of aglycones. *Coptis chinensis* Franch. contains a wide variety of flavonoid compounds, such as rhamnetin, wogonin, 3,5,7-trihydroxy-6,8-dimethoxyflavone, coptis saponin I, 2',4,4'-trihydroxy-6'-methoxydihydrochalcone, evodioside XII, 7,4'-dihydroxy-5-methoxyflavanone, 6,8-dimethyl-3,5,7-trihydroxyphenone-coptis saponin II, among others [2].

2.3. Lignans

Lignans are natural compounds formed by the polymerization of two phenylpropanoid derivatives. Chen Liang et al. [27] isolated 13 compounds from a 90% ethanol extract of *Coptis chinensis*

Franch., seven of which were lignans. These include erythro-guaiacylglycerol-8-O-4'-(coniferyl alcohol) ether (7), threo-guaiacylglycerol-8-O-4'-(coniferyl alcohol) ether (8), (±)-pinoresinol (9), (±)-medioresinol (10), (±)-lariciresinol (11), (±)-5'-methoxylariciresinol (12), and (±)-isolariciresinol (13). Among these, compounds 7, 8, 10, and 12 were isolated from the *Coptis* genus for the first time.

2.4. Organic acids

The acidic compounds in *Coptis chinensis* Franch. are mostly small molecules containing acidic groups such as hydroxyl and carboxyl groups, and they often form glycosides with glucose. *Coptis chinensis* Franch. contains a variety of organic acids, such as scopolin, protocatechuic acid, ferulic acid, chlorogenic acid, catechol, lactic acid, vanillic acid, and gentisic acid, among others [3]. Meng Fancheng et al. [28] isolated 12 compounds from the ethanol extract of dried rhizomes of *Coptis teeta* Wall. (Yunnan Huanglian), six of which were organic acids. These include ferulic acid (14), Z-octadecyl caffeate (15), protocatechuic acid (16), methyl-3,4-dihydroxyphenyl lactate (17), 3,4-dihydroxyphenethyl alcohol (18), and 3,5-dihydroxyphenethyl alcohol-3-O-β-D-glucopyranoside (19). All these compounds were isolated from *Coptis teeta* Wall. for the first time, with compounds 16 and 19 being the first reported from the *Coptis* genus. Li Xuegai et al. [29] isolated nine organic acid compounds from the aqueous extract of *Coptis chinensis* Franch., including 5-O-feruloyl D-quinic acid (20), 4-O-feruloyl D-quinic acid (21), 3-methoxy-4-hydroxybenzoic acid (22), ferulic acid (23), vanillic acid-4-O-β-D-glucopyranoside (24), 3-(3',4'-dihydroxyphenyl)-(2R)-lactic acid-4'-O-β-D-glucopyranoside (25), 3-(4'-hydroxyphenyl)-(2R)-lactic acid (26), 3-(3',4'-dihydroxyphenyl)-(2R)-lactic acid (27), and 3-(3',4'-dihydroxyphenyl)-(2R)-lactic acid methyl ester (28). The structures of compounds 14–19 are shown in Figure 2.

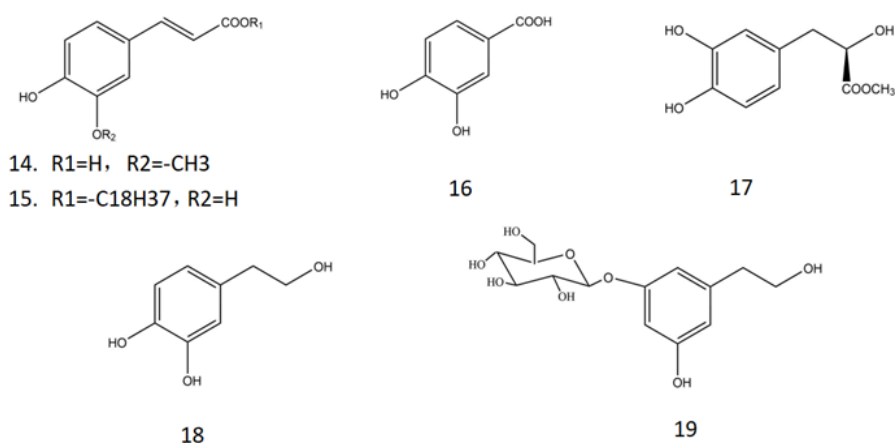


Figure 2. Structures of the six organic acids in *Coptis chinensis* Franch.

3. Pharmacological activities

3.1. Antibacterial effects

Berberine and other active components in *Coptis chinensis* Franch. exhibit broad-spectrum antimicrobial activity, demonstrating significant inhibitory effects against Gram-positive bacteria, Gram-negative bacteria, and fungi [3]. Huang Yanfei et al. [4] determined that the minimum inhibitory concentration (MIC) of the aqueous extract of *Coptis chinensis* Franch. against *Shigella dysenteriae* was 5 mg/mL, and found that the antibacterial effect strengthened with increasing

concentration and prolonged exposure time. Li Qiaoru et al. [5] used in vitro screening to evaluate the antimicrobial activity of aqueous and ethanol extracts of *Coptis chinensis* Franch., Daqingcao, Donglingcao and 17 other Chinese herbal medicines against *Staphylococcus aureus*, *Neisseria gonorrhoeae*, and *Candida albicans*. The study found that the aqueous and ethanol extract of *Coptis chinensis* Franch. show strong antibacterial activity against *Staphylococcus aureus* and significant inhibitory effect on *Candida albicans*, while their antibacterial activity against *Neisseria gonorrhoeae* is weak, with a MIC greater than 1:32. Yang Xingtang et al. [6] conducted a susceptibility test of berberine against *Helicobacter pylori* and found a correlation between the diameter of the inhibition zone and the concentration of berberine within a certain range. In the 250 µg berberine group, the inhibition zone diameter reached 19.78 mm, with an effectiveness rate of 88.5%, comparable to that of clarithromycin and amoxicillin. The 100 µg berberine group showed a similar effectiveness rate to antibiotics, but the inhibition zone diameter was significantly smaller. The 25 µg and 50 µg berberine groups exhibited significantly lower efficacy compared to the antibiotic group.

3.2. Antiviral effects

Coptis chinensis Franch. exhibits inhibitory effects against multiple viruses, such as herpes simplex virus, influenza virus, and cytomegalovirus. Zhang Yan et al. [7] discovered through in vitro experiments that berberine hydrochloride significantly inhibited the cytopathic effect (CPE) induced by HSV-1 in a dose-dependent manner. In the berberine hydrochloride treatment group, the expression level of gD mRNA was significantly reduced 16 hours after viral infection. Berberine hydrochloride also markedly suppressed the expression of viral proteins ICP27 and ICP8, with a stronger and dose-dependent inhibition observed for ICP27 expression. Chen Xiaoming et al. [8] found in their study that berberine inhibits influenza virus-induced endothelial cell cytoskeletal remodeling and reduces endothelial cell permeability by stabilizing the cytoskeleton and decreasing stress fiber formation. Yang Liumeng et al. [9] systematically compared the anti-HIV-1 activity and cytotoxicity of berberine, palmatine, and their 13-hexyl derivatives (13-hexylberberine and 13-hexylpalmatine). The results showed that berberine and palmatine strongly inhibited HIV-1 reverse transcriptase (RT), with EC₅₀ values of 63.1 µg/mL and 44.52 µg/mL, respectively. In contrast, the hexyl derivatives completely lost their RT inhibitory activity. However, 13-hexylberberine and 13-hexylpalmatine demonstrated significantly stronger anti-HIV-1 activity, with EC₅₀ values of 0.16 µg/mL and 0.08 µg/mL, respectively.

3.3. Hypoglycemic effects

Coptis chinensis Franch. can improve insulin resistance and reduce blood glucose levels through multiple pathways. Berberine primarily exerts its hypoglycemic effects by stimulating glycolysis independently of the AMPK signaling pathway, enhancing the expression of insulin receptor substrate-1 and PI3K proteins, and modulating the LKB1/AMPK/TORC2 signaling pathway, among other mechanisms [23]. Jiang Miao [10] established a type 2 diabetes insulin resistance (IR) rat model and found that the herbal pair of *Coptis chinensis* Franch. and ginseng effectively suppressed weight gain in these rats, significantly reduced fasting blood glucose (FBG) and fasting insulin (FINS) levels, and demonstrated IR-improving effects comparable to pioglitazone. This treatment effectively alleviated hyperglycemia and hyperinsulinemia in type 2 diabetic IR rats and improved the insulin sensitivity index. Huang Xiufang et al. [30] developed an IR rat model using high-fat, high-sugar, and high-salt feed to investigate the effects of Huanglian Jiedu Decoction (HLJD) on inflammatory factors (IL-6, TNF-α) and oxidative stress markers (SOD, MDA). Compared to the

model group, all HLJD groups showed significant reductions in fasting plasma glucose (FPG) and FINS, along with a notable increase in the insulin sensitivity index (ISI). The high- and medium-dose HLJD groups exhibited superior effects to the metformin group. Additionally, all HLJD dose groups demonstrated significantly decreased levels of IL-6, TNF- α , and MDA, and a marked increase in SOD activity. Chen Guang et al. [31] conducted in vivo experiments using a type 2 diabetes mellitus (T2DM) rat model and discovered that berberine significantly inhibited weight gain in the model rats, markedly lowered fasting blood glucose levels, promoted the increased expression of PI3K p85 and GLUT4 proteins, and alleviated insulin resistance in target tissues. Qin Xiaojun et al. [12] established a diabetic rat model with cerebral ischemia-reperfusion injury to explore the impact of *Coptis chinensis* Franch. on the expression of apoptosis-related proteins Bax and Bcl-2. The results indicated that *Coptis chinensis* Franch. downregulated the pro-apoptotic protein Bax and upregulated the anti-apoptotic protein Bcl-2. Furthermore, a high dose of *Coptis chinensis* Franch. significantly improved neurological deficits and reduced blood glucose levels.

3.4. Antitumor effects

Active components in *Coptis chinensis* Franch., such as berberine, have been found to exert antitumor effects by inhibiting tumor cell proliferation, migration, and adhesion, as well as promoting apoptosis [13]. The mechanisms by which berberine inhibits tumor cell proliferation primarily include: arresting the cell cycle, inhibiting the activity of related proteins and enzymes, modulating signaling pathways, inducing changes in mitochondrial membrane potential, reducing IL-6 levels, and blocking potassium ion channels. Huang Linqing et al. [15] demonstrated through in vivo and in vitro antitumor experiments that berberine significantly inhibits S-180 cells both in vitro and in vivo. Bao Jianzhong et al. [14] found that berberine can inhibit the proliferation and differentiation of human colon cancer cells, with the inhibitory effect positively correlating with drug concentration and exposure time. Berberine promotes apoptosis through mechanisms related to the Bcl-2 protein family and the Caspase cascade reaction. Furthermore, multiple studies have indicated that berberine from *Coptis chinensis* Franch. exhibits inhibitory and cytotoxic effects on various tumor cells, including gastric cancer, osteosarcoma, prostate cancer, bladder cancer, mouse S-180 tumor cells, HL-60, MGC-803, HepG2, NT2/D1, and YES-2 cells, among others [16].

4. Related signaling pathways

The pharmacological effects of *Coptis chinensis* Franch. and its active components are closely associated with the modulation of multiple key signaling pathways. These pathways are extensively involved in core biological processes such as energy metabolism, autophagy, and inflammatory responses. The following sections will review critical pathways including AMPK/PI3K-Akt, AMPK/mTOR, and TLR4/MyD88, elucidating the multi-target mechanisms of *Coptis chinensis* Franch. and its role in improving insulin resistance, thereby providing a basis for further exploration of its pharmacological value, as summarized in Table 1.

Table 1. Signaling pathways related to *Coptis chinensis* Franch.

Signaling Pathway	Status and Function in Type 2 Diabetes	Core Mechanisms	Key Molecules and Processes
AMPK/PI3K-Akt Glucose Metabolism Signaling Pathway [32,33]	Status: PI3K-Akt is inhibited; AMPK activity is reduced. Function: Coordinately regulates cellular glucose uptake and utilization.	Inflammatory factors and lipid accumulation activate kinases that inhibit IRS-1, thereby blocking insulin signaling.	AMPK Pathway: Increased AMP/ATP ratio → AMPK → TBC1D1/AS160 → GLUT4 translocation PI3K-Akt Pathway: Insulin receptor → IRS → PI3K → Akt → Promotes GLUT4 translocation and glycogen synthesis
AMPK/mTOR OR Autophagy Regulatory Pathway[34, 17,20]	Status: mTORC1 activity is overactivated; autophagy level is suppressed. Function: AMPK and mTOR act antagonistically to coordinately regulate cell growth and catabolism.	Nutrient excess leads to overactivation of mTORC1, which suppresses autophagy, resulting in the accumulation of damaged mitochondria and misfolded proteins, thereby promoting insulin resistance. AMPK directly inhibits mTORC1 while simultaneously activating autophagy, thereby improving cellular function.	Energy insufficiency → AMPK → inhibits mTORC1 + activates ULK1 → initiates autophagy Sufficient nutrition → Akt → mTORC1 → promotes anabolic processes and suppresses autophagy
TLR4/MyD88 Inflammatory Signaling Pathway [21,35]	Status: The pathway is chronically activated. Function: Serves as a core pathway in innate immunity and links nutrient excess to insulin resistance.	Free fatty acids, endotoxins, and other ligands activate the TLR4 receptor, leading to the production of inflammatory factors, disruption of insulin signaling, and ultimately triggering the development of type 2 diabetes.	Ligand → TLR4 → MyD88 → IKK → NF-κB nuclear translocation → inflammatory gene transcription
Gut Hormones/ Gut-Pancreas Axis Signaling Pathway [36]	Status: Insufficient secretion or accelerated degradation of GLP-1. Function: Postprandial intestinal hormone secretion promotes insulin release and suppresses glucagon secretion in a glucose concentration-dependent manner.	GLP-1 activates GLP-1R on β cells, promotes insulin gene transcription and secretion via the cAMP-PKA pathway, while also inhibiting beta-cell apoptosis, delaying gastric emptying, and suppressing appetite.	Food intake → L cells in the intestine secrete GLP-1 → binds to GLP-1R on beta cells → Gs protein → adenylate cyclase → increased cAMP → PKA → promotes insulin secretion and cell proliferation
Endoplasmic Reticulum Stress Unfolded Protein Response (UPR) [37,38]	Status: Chronic, unresolved endoplasmic reticulum stress. Function: The UPR is an adaptive cellular response to alleviate the accumulation of misfolded proteins in the endoplasmic reticulum.	Under endoplasmic reticulum stress from unfolded/misfolded protein accumulation, UPR is activated. IRE1, PERK, ATF6 alleviate stress by reducing protein synthesis and enhancing folding capacity.	IRE1α: Splices XBP1 or activates JNK. PERK: Phosphorylates eIF2α while activating ATF4/CHOP. ATF6: Transcriptionally regulates molecular chaperones.

4.1. AMPK/PI3K-Akt glucose metabolism signaling pathway

AMPK is a heterotrimeric protein composed of a catalytic α subunit and regulatory β and γ subunits. Its activity is tightly regulated by the intracellular AMP/ATP ratio. Under cellular energy deficiency, elevated AMP stimulates interactions with regulatory proteins, promoting AMPK phosphorylation at Thr172 by tumor suppressor LKB1 to activate it [40]. Activated AMPK then phosphorylates downstream targets to regulate metabolism and restore cellular energy homeostasis. Additionally, the AMPK pathway can be activated through cascade reactions involving calcium/calmodulin-dependent protein kinase β (CaMKK β) and liver kinase B1 (LKB1), among others [39].

When cellular energy supply is insufficient, AMP stimulates interactions with axial proteins, leading to the phosphorylation of AMPK at the Thr172 site by the tumor suppressor liver kinase B1 (LKB1), thereby activating it [40].

When insulin molecules bind to the extracellular domain of the α subunit of the insulin receptor (InsR), the insulin binding induces a conformational change in the α subunit. This brings the intracellular domains of the two β subunits closer together, stabilizing the receptor's dimeric state. The proximity of the β subunit intracellular domains allows the kinase domain of one β subunit to phosphorylate key tyrosine residues on the intracellular domain of the other β subunit. IRS proteins are recruited and anchored near the activated InsR, and tyrosine residues (Tyr) on the IRS proteins are phosphorylated by the InsR kinase domain. The phosphorylated IRS proteins act as a platform to recruit and activate two major signaling pathways: the PI3K-Akt pathway and the Ras-MAPK pathway. The PI3K-Akt pathway is the core pathway for insulin signal transduction. PI3K is recruited to the receptor, and the p85 regulatory subunit of PI3K specifically binds to certain phosphorylated tyrosine residues on the IRS protein, leading to PI3K activation. The activated catalytic subunit of PI3K then converts phosphatidylinositol 4,5-bisphosphate (PIP₂) into phosphatidylinositol (3,4,5)-trisphosphate (PIP₃) [41]. PIP₃ acts as a second messenger, binding to the PH domain of Akt and recruiting Akt to the inner surface of the plasma membrane. The kinases PDK1 and mTORC2 phosphorylate Akt at Thr308 and Ser473, respectively. The activated Akt then dissociates from the plasma membrane and enters the cytoplasm and nucleus, where it phosphorylates numerous downstream substrates.

Under energy stress conditions, activated AMPK negatively regulates the insulin/PI3K-Akt signaling pathway by phosphorylating specific sites on IRS or activating phosphatases to dephosphorylate IRS, thereby reducing unnecessary anabolic processes. Under energy-sufficient conditions, Akt phosphorylates AMPK α at Ser485/491, which inhibits LKB1-mediated phosphorylation at Thr172, consequently suppressing catabolic activity. As shown in Figure 3.

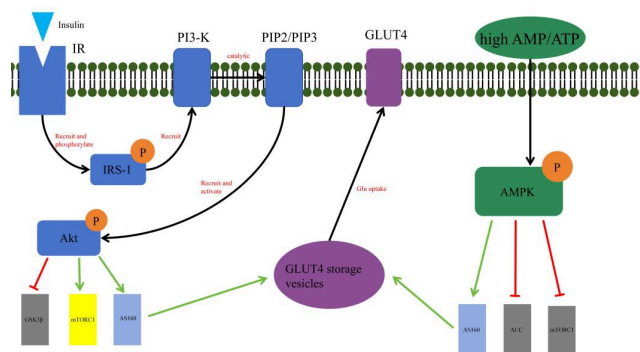


Figure 3. Schematic diagram of the AMPK/PI3k-Akt glucose metabolism signaling pathway

4.2. AMPK/mTOR autophagy regulatory pathway

The mammalian target of rapamycin (mTOR) is a serine/threonine protein kinase composed of two structurally and functionally distinct complexes, mTORC1 and mTORC2. These complexes regulate the expression and activity of transcription factors such as HIF-1 α and the myelocytomatosis oncogene (MYC) to promote glycolysis, glutaminolysis, and the pentose phosphate pathway [42].

Under energy stress conditions, AMPK is activated and strongly inhibits mTORC1 activity, thereby blocking metabolic pathways such as glucose utilization and protein synthesis, which restricts the proliferation of tumor cells. Conversely, when this pathway is impaired and mTOR remains persistently activated, it not only weakens the positive regulation of tumor suppressors like p16 but also relieves the inhibition of various pro-oncogenic factors such as HIF-1 α and β -catenin. This ultimately exacerbates metabolic abnormalities, inflammatory responses, and tumor microenvironment dysregulation, creating favorable conditions for the development of malignancies such as liver cancer [18]. Liu Yang et al. [19] demonstrated through in vitro experiments that, compared to the control group, the expression levels of AMPK and mTOR genes were significantly increased in the berberine-treated group. Additionally, berberine inhibited the proliferation and metabolism of EC9706 cells, indicating that berberine exerts its antitumor effects by modulating the AMPK/mTOR pathway.

4.3. TLR4/MyD88 inflammatory signaling pathway

Toll-like receptors (TLRs) are a class of type I transmembrane protein receptors comprising thirteen members (TLR1-TLR13) [43]. Among them, TLR1, 2, 4, 5, 6, and 10 are involved in recognizing cell surface molecules and are expressed on the cell membrane, whereas TLR3, 7, 8, and 9 recognize nucleic acids and are localized intracellularly within endosomes [44]. TLR4, a key member of the TLR family, specifically recognizes lipopolysaccharide (LPS) from pathogens and stimulates immune-inflammatory responses by activating adaptive immune-related genes.

MyD88 is an adapter protein containing a TIR domain and serves as a downstream signaling factor in the TLR signaling pathway [44]. The MyD88-dependent signaling pathway is commonly present in most TLR family members, though signal transduction in some TLRs does not entirely rely on MyD88. Thus, TLR signaling can be categorized into MyD88-dependent and MyD88-independent pathways. In the MyD88-dependent pathway, signaling is specifically activated by TLR4. The activated TIR domain associates with MyD88, leading to the recruitment of IRAK4 to the TLR-MyD88 complex. Once activated, IRAK4 phosphorylates and recruits IRAK1 and IRAK2, thereby initiating downstream signaling cascades [45]. Ji Lingyun et al. [21] pretreated cells with serum containing Scutellaria-Coptis drug pair at different concentrations, followed by induction of pyroptosis with LPS + ATP. Their findings revealed that the Scutellaria-Coptis drug pair inhibits macrophage pyroptosis by suppressing the TLR4/MyD88/NF- κ B signaling pathway and downregulating NLRP3 inflammasome activation. Similarly, Zhang Hongjie et al. [22] established a neuroinflammation model using LPS and demonstrated that the Scutellaria-Coptis drug pair reduces the release of pro-inflammatory cytokines by inhibiting the activation of the TLR4/MyD88/NF- κ B signaling pathway in microglia.

5. Conclusion

This article systematically reviews the research progress on the chemical constituents, pharmacological activities, and related molecular signaling pathways of *Coptis chinensis* Franch.

Studies have shown that as a classic traditional Chinese medicine, the modern pharmacological value of *Coptis chinensis* Franch. is primarily reflected in the multi-component, multi-target synergistic mechanisms centered on isoquinoline alkaloids. In terms of chemical composition, *Coptis chinensis* Franch. contains not only various alkaloids such as berberine, palmatine, and coptisine but also active components including flavonoids, lignans, and organic acids, which collectively form the material basis for its efficacy. In pharmacological activities, *Coptis chinensis* Franch. demonstrates broad therapeutic potential. Its antibacterial effects are mainly achieved by disrupting bacterial cell membrane permeability and inhibiting key enzyme activities. Its antiviral activity is reflected in inhibiting viral replication and protein expression. The hypoglycemic effect is closely related to improving insulin resistance and regulating glucose metabolism, while its antitumor activity operates through multiple mechanisms such as inducing apoptosis and inhibiting proliferation. Furthermore, multiple studies have found that berberine, the core active component of *Coptis chinensis* Franch., exerts its effects by regulating several key signaling pathways. Among them, the AMPK/PI3K-Akt pathway plays a central role in regulating energy metabolism and insulin sensitivity; the AMPK/mTOR pathway is involved in the regulation of autophagy and cell growth; and the TLR4/MyD88 pathway plays an important role in suppressing inflammatory responses. The crosstalk between these pathways further illustrates the complexity of the mechanisms of action of *Coptis chinensis* Franch.

However, several issues in current research remain to be addressed. Most mechanistic studies are still at the preclinical stage, lacking high-quality clinical research data. The understanding of the synergistic mechanisms among various active components is insufficient, and the bioavailability of berberine needs further improvement. Future research should focus on conducting well-designed clinical trials, delving deeper into the synergistic mechanisms of multiple components, and developing novel drug delivery systems to enhance bioavailability, thereby providing important insights and resources for innovative drug development.

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