Molecular Mechanism of Parnassiapalustris in the Treatment of Cervical Cancer Based on Network Pharmacology

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Abstract:

Background: A series of evidence suggests that the chemical constituents such as dichloromethane extracts and ethylacetateextracts from Parnassia palustris can inhibite the proliferation of cervical cancer cells (Hela). But the mechanism of chemical constituents from Parnassia palustris on Cervical Cancer are not Clear, the mechanisms would be reveal based on network pharmacology and molecular docking.

Methods:Main chemical components parnassiapalustris Linn were collected based onliteratrues, and parnassiapalustris'stargets were obtained by Swiss Target Prediction database,SEA search server database and BANTMAN database. Main targets of cervical cancer were obtained from genecards. Common targets betweenparnassiapalustris and cervical cancer were obtained by venndiagram. Cytoscape software and string database were used to construct a network of "parnassiapalustris-components--cervical cancer targets" and protein interaction network(PPI). The Top3 key targets were to dock to extracts from parnassiapalustris, and compounds with the better binding degree were screened for the mechanism of action analysis.

Results:102 targets were obtained related to parnassiapalustris treatment of cervical cancer, the top three protein targets were SRC, EGRF and ESR1. Molecular docking results showed that main active components had good binding activity with their corresponding target proteins, especially, kaempferol-3-rutinoside,

hyperoside,quercetin,Kaempferol and chlorogenic acid and celahin Bhad the best absolute values of the docking scores with all three protein targets.

Conclusions:All results show thatParnassiapalustris has characteristics of multi-component, multi-target and multi-pathway on cervical cance, The main active components for the prevention and treatment of cervical cancer in extract of parnassiapalustris were kaempferol-3-rutinoside,hyperoside, quercetin,kaempferol,chlorogenic acidand celahin B. All conclusions could provide the basis for cervical cancer clinical application. Keywords:Moleculardocking,Parnassiapalustris,Cervicalcancer,Networkpharmacology

I. INTRODUCTION

Cervical cancer (CC) is one of the common gynecologic malignant tumors nowadays. [1],In recent years, cervical cancer is on the rise and is becoming younger, which is one of the biggest malignant tumors threatening women's health and life safety. Western medicine currently mainly adopts chemoradiotherapy and surgery, while tolerance to chemoradiotherapy has become one of the main reasons for cervical cancer treatment failure, cancer metastasis and recurrence[2-3].Parnassiapalustris has the efficacy of clearing heat, suppressing Xieri, and breaking tumor[4-5]_o Modern Mongolian pharmacology believes that Mongolian medicines with "tumor-breaking" function have anti-neoplastic effects and have significant advantages in cancer treatment. [6]_o In order to investigate the inhibition of cervical cancer Hela proliferation by different extract fractions of parnassiapalustris, Xin Ying's team extracted dichloromethane and ethyl acetate extracts of the parnassiapalustris.[7-8], but further studies are needed to determine what components are at work and the exact mechanism of the anti-tumor effects of these components.

Network pharmacology is a new idea of drug design based on network biology and polypharmacology, which provides a scientific channel for the study of the mechanism of Chinese medicine formulations applied to multiple diseases[9]. The systems biology research idea it uses is highly consistent with the features of multi-component, multi-target, and multi-pathway interactions, and its integrality and the systematicness are in line with the holistic view and evidence-based treatment of TCM study [10-15].

Using a network pharmacology approach this study was screened for targets based on the molecular structural characteristics of the main active ingredients of parnassiapalustris in the literature, predicted targets related to cervical cancer, and systematically analyzed the interaction between the two at specific nodes in the network from a holistic perspective. Thereby, it explored the interconnection of the Mongolian medicine parnassiapalustris with cervical cancer targets. Moreover, the binding activity of parnassiapalustris active ingredients and key targets were analysis by molecular docking technique, which provides a basis for the clinical application and in-depth study of parnassiapalustris in the treatment of cervical cancer.

II. Methods

Network pharmacology analysis

Main chemical components Parnassiapalustris Linn were collected from literatrues, and targets of parnassiapalustris were obtained from Swiss Target Prediction database[16],SEA Search Server database

and BANTMAN database. By searching for the "Cervical Cancer" keyword in the GeneCards database[17], the currently reported genes related to cervical Cancer are obtained, and then the gene with score>10.0 is selected and integrated with the calculated potential targets to finally obtain the potential targets for anti-Cervical Cancer. The interaction relationship between the component-target is introduced into the Cytoscape software to construct the Parnassiapalustris-component-target network map. The interaction relationship between the potential targets for against cervical cancer which can be obtained from the string database, and the PPI network graph visualization was performed in the Cytoscape software, and the top three targets were screened according to the display degree value.

Molecular docking

The interaction target of Parnassiapalustris compound was imported into String software for protein network interaction analysis. Using the top three targets in the enrichment results to dock to the active compounds whose corresponding protein crystal structure can be selected in the PDB database. Finally, according to the score value and the binding free energy, the compound with the best binding degree is screened for the mechanism of action analysis.

III. Results

Chemical composition and targets collection

According to related literature reports [18-20], a total of 11 active compounds of Parnassiapalustris were collected from the literatures. The dichloromethane extract and ethyl acetate extract have an effect on resisting to cervical cancer. There are 5 compounds were isolated from the dichloromethane extract, which are celahin B, mussaenin A, gardendiol, isobonein and 4-epi-alyxialactone, and there are 6 compounds were extracted from ethyl acetate extract, which arequercetin, kaempferol, gallic acid, chlorogenic acid, gold Sitoside and kaempferol-3-O- β -rutinoside (see Tab. 1). A total of 329 compound-related targets were collected through databases such as Swiss Target Prediction and SEA Search Server.

Tab. 1 The compounds of Tarnassiaparustris					
No.	Compound	literature report			
MO	Celahin B	active			
MO	Mussaenin A	active			
MO	Gardendiol	active			
MO	Isoboonein	active			
MO	4-epi-alyxialactone	active			
MO	Quercetin	active			
MO	Kaempferol	active			

Tab. 1 The compounds of Parnassiapalustris

МО	Gallic acid	active
MO	chlorogenic acid	active
МО	Hyperoside	active
MO	Kaempferol-3-Rutin	active

A total of 1128 genes related to cervical cancer were collected in the GeneCards database (Relevance score≥10). The 102 common targets between component and the cervical cancer could be obtained. These 102 common targets are regarded as possible potential targets for the treatment of cervical cancer.Using the Cytoscape software to construct the Parnassiapalustris-component-target network. It can be seen from the network diagram that there is a phenomenon in which multiple components correspond to one target or one component corresponds to multiple targets. Selecting the common targets of the compounds in Parnassiapalustris and cervical cancer to analyze the protein network interaction by the string website, thenimporting the result into the Cytoscape software for the visual display of the PPI network diagram. According to the degree value as shown in Tab.2, the key targets of TOP3 are SRC (PDB: 2BDF), EGFR (PDB: 5Y9T), and ESR1 (PDB: 4XI3).

	8	
Protein	Name	Deg
SRC	SRC Proto-Oncogene, Non-Receptor	26
EGFR	Epidermal Growth Factor Receptor	25
ESR1	Estrogen Receptor 1	23
AKT1	AKT Serine/Threonine Kinase 1	22
PTGS2	Prostaglandin-Endoperoxide Synthase 2	20
BCL2L	BCL2 Like 1	18
MMP2	Matrix Metallopeptidase 2	17
KDR	Kinase Insert Domain Receptor	16
MMP9	Matrix Metallopeptidase 9	16
IGF1R	Insulin Like Growth Factor 1 Receptor	15
PTK2	Protein Tyrosine Kinase 2	15
PIK3R1	Phosphoinositide-3-Kinase Regulatory	14
MET	MET Proto-Oncogene, Receptor Tyrosine	14
IL2	Interleukin 2	13
MMP3	Matrix Metallopeptidase 3	12

Tab.2 Degree value information of the common targets

Molecular docking

The top three protein targets ranked by degree value were respectively docked with 11 compounds, and ranked by scoring value. The results of molecular docking are shown in Tab. 3. The greater the absolute value of the docking score S, it means that the active compound of Parnassiapalustris has better binding ability with the cervical cancer target. It is helpful to treat and prevent cervical cancer by analyzing the protein receptor-ligand interaction.

Ligands	S1 (SRC)	S2 (EGRF)	S3 (ESR1)
Celahin B	-7.6662	-7.5227	-6.4598
Mussaenin A	-4.8505	-4.7130	-5.5007
Gardendiol	-5.4743	-4.9383	-5.3515
Isoboonein	-5.0954	-4.6228	-5.2925
4-epi-alyxialactone	-4.9005	-4.9755	-5.3295
Quercetin	-5.9743	-6.0592	-6.9528
Kaempferol	-5.4588	-6.0151	-6.6828
chlorogenic acid	-6.4615	-6.0898	-7.7817
Hyperoside	-7.7211	-7.0513	-8.9218
Kaempferol-3-Rutinoside	-8.4593	-8.0936	-10.3933

Tab. 3 Molecular docking results of compounds

S1 is the score value of the docking results between the target SRC (PDB: 2BDF) and the ten compounds, S2 is the score value of the docking results between the target EGRF (PDB: 5Y9T) and the ten compounds, and S3 is the score value of the docking results between the target ESR1 (PDB: 4XI3) and the ten compounds.

As shown in Tab.3,the docking scores of parnassiapalustris active ingredient and key target for cervical cancer were less than -4.7 kJ/mol. The docking scores of Kaempferol-3-Rutinoside and key target for cervical cancer were less than -8.0. The docking scores of Hyperoside and key targets for cervical cancer were less than -7.0. The docking scores of Celahin B and key targets were less than -6.4 kJ/mol. The docking scores of cervical cancer were less than -6.0. The docking scores of quercetin and key target for cervical cancer were all less than -5.9. The docking scores of kaempferol and

key target for cervical cancer were all less than -5.4. The experimental data demonstrated the strong binding activity of the active ingredients to the corresponding targets.

The compounds with highest scoreswere selected from the three target proteins of SRC, EGRF, and ESR1 to analyze the receptor-ligand interaction mechanism.

As shown in Fig.1, chlorogenic acid interacts with the target SRC through the active pocket formed by the amino acid residues Asp348, Gly344, Met341, Tyr340, etc.; SRC (PDB: 2BDF) interacts withchlorogenicacid mainly through the amino acid residue Met341.

Hyperoside interacts with the target SRC through the active pocket formed by the amino acid residues Asp348, Glu339, Met341, Leu273, etc.; SRC interacts withhyperoside mainly through the amino acid residue Met341. In addition, hyperoside also forms a pi-H bond with Leu273.

Kaempferol interacts with the target SRC through the active pocket formed by the amino acid residues Asp348, Gly344, Met341, Leu273, etc.; SRC interacts withkaempferol mainly through the formation of pi-H bonds with the amino acid residue Leu273.

Kaempferol-3-Rutinoside interacts with the target SRC through the active pocket formed by the amino acid residues Leu273, Ala293, Met341, Val281, Leu393, etc.; The pi-H bond produces between the amino acid residueLeu273 and kaempferol-3-Rutinoside plays a key role in the interaction.

Quercetin interacts with the target SRC through the active pocket formed by the amino acid residues Leu273, Met341, Ala293, etc. However, no obvious binding site was found between SRC and quercetin.

Celahin B interacts withhe target SRC through amino acid residues Lys295, Ala390, Asp404, etc.

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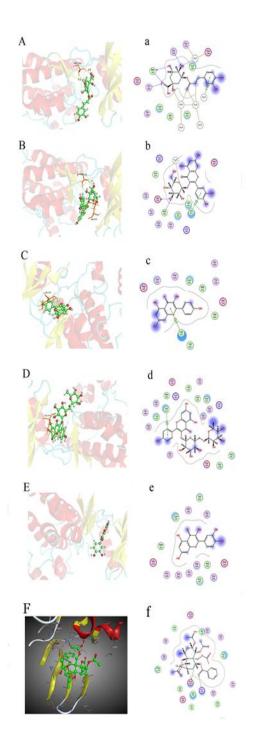


Fig.1The interaction diagram between SRC (PDB: 2BDF) and chlorogenic acid, hyperoside, kaempferol, kaempferol-3-Rutinoside,quercetin andCelahinB (A-F: three-dimensional diagram, a-f: two-dimensional diagram)

As shown in Fig.2, chlorogenic acid interacts with the target ESR1 through the active pocket formed by the amino acid residues Leu387, Met421, Phe404 and Leu391; ESR1 (PDB: 4XI3) interacts withchlorogenicacid mainly through the formation of pi-H bonds with the amino acid residue Leu387.

Hyperoside interacts with the target ESR1 through the active pocket formed by the amino acid residues His524, Leu, 387, Phe404, Leu384, and Met388; ESR1 interacts with hyperoside mainly through the amino acid residue His524. In addition, hyperoside also forms a pi-H bond with Leu387.

Kaempferol interacts with the target ESR1 through the active pocket formed by the amino acid residues Leu346, Gly521, Glu353, His524, Ala350 and Phe404; ESR1 interacts with kaempferol mainly through the amino acid residue His524. In addition, Thesmall molecule also form pi-H bonds with amino acid residues Ala350 and Phe404, respectively.

Kaempferol-3-Rutinoside interacts with the target ESR1 through the active pocket formed by amino acid residues Thr347, Ala350, Trp383, Glu353, etc.; The pi-H bond produces between the amino acid residue Trp383 and kaempferol-3- Rutinoside plays a key role in the interaction.

Quercetin interacts with the target ESR1 through the active pocket formed by the amino acid residues Leu346, Phe404, Glu404 and Gly521. The pi-H bond is formed between Phe404 of the ESR1 targetand quercetin, which generating an interaction.

Celahin B interactshe target ESR1 through the amino acid residue Lys531;

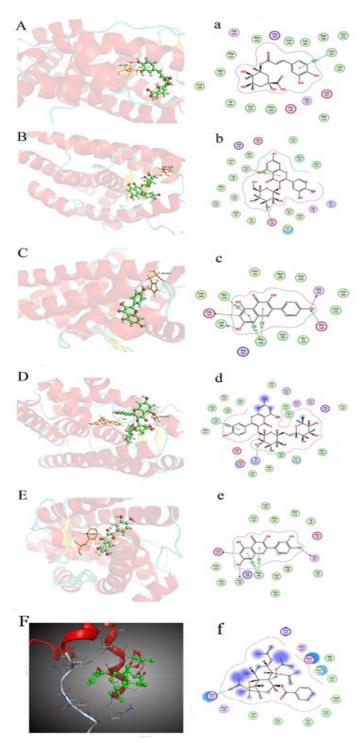


Fig. 2 The interaction diagram between ESR1 (PDB: 4XI3) and chlorogenic acid, hyperoside, kaempferol, kaempferol-3-Rutinoside ,quercetin and Celahin B (A-F: three-dimensional diagram, a-f: two-dimensional diagram)

It can be seen from Fig.3 that chlorogenic acid interacts with the target EGFR through the active pocket formed by the amino acid residues Lys745, Asp855, Thr854 and Met793; EGFR (PDB: 5Y9T) interacts withchlorogenicacid mainly through the amino acid residues Lys745, Asp855 and Thr854.

Hyperoside interacts with the target EGFR through the active pocket formed by amino acid residues Met793, Gly721, Gly796 and Thr854; EGFR interacts withhyperoside mainly through amino acid residues Met793, Gly721 and Gly796.

Kaempferol interacts with the target EGFR through the active pocket formed by the amino acid residues Met790, Met793, Lys745 and Asp855; EGFR interacts withkaempferol mainly through the amino acid residues Met793 and Lys745.

Kaempferol-3-Rutinoside interacts with the target EGFR through the active pocket formed by the amino acid residues Cys797, Met793, Lys745 and Asp800; EGFR interacts with Kaempferol-3-Rutinoside mainly through the amino acid residues Cys797 and Met793.

Quercetin interacts with the target EGFR through an active pocket formed by amino acid residues Met793, Lys745, Asp855 and Glu762. EGFR interacts withquercetin mainly through amino acid residues Met793 and Lys745.

Celahin B interacts with the target EGFR through through the active pocket formed by the amino acid residues Arg841, Asp855, Lys745, Ala743, Met790, Ser720, Val726, Asp800, etc.

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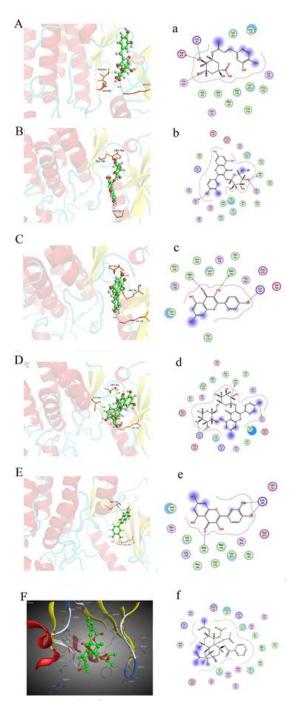


Fig. 3 The interaction diagram between EGRF (PDB: 5Y9T) and chlorogenic acid, hyperoside, kaempferol, kaempferol-3-Rutinoside ,quercetin and Celahin B (A-F: three-dimensional diagram, a-f: two-dimensional diagram)

IV. Discussion

The network pharmacology research of Chinese medicine generally has two purposes: 1. to predict the activity of traditional Chinese medicine or compound based on chemical composition to guide clinical 1807

application and subsequent research; 2. to conduct mechanistic research on traditional Chinese medicine or compound whose efficacy has been proven, and to deeply explore the key nodes and key active compounds. The subject of this paper is Parnassiapalustris, a characteristic Mongolian medicine commonly used by Mongolian folklore for generations. According to the literature, Parnassiapalustris dichloromethane extract has been reported to have an inhibitory effect on cervical cancer Helacells[19],but further studies are needed to determine which active ingredient is responsible for the effect.

Hyperoside can inhibit the growth of cervical cancer hela cells by regulating the expressions of opoptosis-related genes and protains, promoting apopto-sis and reducing antioxidant capacity[21]. Quercetin can significantly inhibit the growth of cervical carcinoma transplant tumor by inducing the phosphorylation of PE R K and eIF2 α proteins, and upregulating the expression of ATF4 and CHOP[22]. Gallicacid regulates the apoptosis of cervical cancerhela cells by regulating P53 signal pathway, regulating the change of Caspase-3level, promoting the increase of ROS level and regulating ADAM17, EGFR, AKT/p-AKT and ERK/p-erksignal pathway[23].

HA-CAliposomescansignificantlyinhibittheeffectofU14cervicalcancernudemicehigherthanthatofCAandCA liposomesowetothemodificationoftheactivetargetligandHA[24].To exert its anti-tumor activity,kaempferol can inhibit the ERK/MAPK pathway and PI3K-AKT pathway, induce apoptosis, and also induce cell cycle arrest and inhibit cancer cell adhesion, migration and invasion [25].Celahin B inhibited the proliferation of human cervical cancer Hela cells in a dose-dependent manner[26].

With the help of web-based pharmacology techniques, A total of 11 active ingredients were screened Parnassiapalustris, 102 main targets for Cervical Cancer from were obtained, Parnassia palustris-components-target network diagram showed that there was a phenomenon in which multiple components correspond to one target or one component corresponds to multiple targets. The top three protein targets (SRC,EGRF and EGRF) ranked by degree valuewere respectively docked with extracts from Parnassiapalustris. The experimental data demonstrated the strong binding activity of the active ingredients to the corresponding targets, The compounds Kaempferol-3-Rutinoside, Hyperoside, Celahin B, Quercetin, Kaempferol, and chlorogenic acid had the highest absolute scores for all three targets, so it can be tentatively judged that these compounds are the main active ingredients of Parnassiapalustris against cervical cancer, which deserve further study.

Combining the results of all these studies, we concluded that Parnassiapalustris has multi-component, multi-target and multi-pathway characteristics against cervical cancer. The compounds Kaempferol-3-Rutinoside, Hyperoside, and Celahin B are the main active components of Parnassiapalustris against cervical cancer. Therefore, Parnassiapalustris is worthy of further investigation as a potential drug for the treatment of cervical cancer. The above conclusions can provide a basis for its clinical application and

study.

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