Exploring TCM Syndrome-Medication Patterns in the Diagnosis and Treatment Protocol for COVID-19 Using Text Mining and Network Pharmacology

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Date: 2023-09-04T00:00:00+00:00

Abstract

Objective: To explore the TCM syndrome-medication patterns in the "Diagnosis and Treatment Protocol for COVID-19" based on text mining technology and network pharmacology. Methods: Using the "Diagnosis and Treatment Protocol for COVID-19" (hereinafter referred to as the "Protocol") obtained by searching "COVID-19 Diagnosis and Treatment Protocol" on the official website of the National Health Commission as the data source, information related to symptoms and prescriptions/herbal medicines involved in the document was collected and a corresponding database was established to include relevant information from the Protocol. Text Mining, VOS Viewer, SPSS, and R were used to perform word segmentation, frequency statistics, adjacency list construction, word cloud generation, topic clustering, association rule analysis, and visualization of herbal medicine and symptom texts that met the inclusion criteria. Cytoscape and R were used to construct syndrome-medication relationships based on TCM theory, construct "disease-herb-component-target" relationships, build PPI networks, and perform GO and KEGG enrichment analysis of intersecting targets along with visualization. Results: A total of 13,126 characters of text were extracted, including 8,291 characters related to prescriptions and herbal medicines, and 4,835 characters related to symptoms. From the text, 87 herbal medicines and 137 symptoms were extracted. The top 5 most frequently used herbal medicines were Glycyrrhizae Radix et Rhizoma (licorice), Gypsum Fibrosum (gypsum), Ephedrae Herba (ephedra), Pogostemonis Herba (patchouli), and Armeniacae Semen Amarum (bitter apricot seed). The top 5 most frequent symptoms were greasy tongue coating, pale tongue, fatigue, white tongue coating, and fever. In terms of therapeutic function classification, dampness-transforming herbs were the most common. Regarding medicinal properties, warm nature was predominant. For medicinal flavors, pungent and bitter tastes were most common. The herbs mainly entered the Lung, Spleen, and Stomach meridians. Frequency statistics identified 22 high-frequency herbal medicines (frequency $\geq$ 10) and 33 high-frequency symptoms (frequency $\geq$ 10). Association rule analysis yielded 22 pairs of herbal association rules and 105 sets of herbal medicine association rules. Topic clustering identified 5 clustered formulas and 5 clustered syndromes. A syndrome-medication relationship diagram based on TCM theory was constructed. Through the TCMSP database, 62 active components were screened from high-frequency herbal medicines (top 7 frequency), with 229 targets for active components. Through DrugBank and GeneCards databases, 526 COVID-19 targets were screened, and 42 intersecting targets were obtained via Venn diagram analysis. GO and KEGG enrichment analysis through the DAVID platform identified 339 biological processes, 20 cellular components, 41 molecular functions, and 98 metabolic pathways. Conclusion: The TCM symptom patterns, medication patterns, and syndrome-medication patterns for COVID-19 (hereinafter referred to as novel coronavirus pneumonia) in the Protocol: COVID-19 belongs to the category of cold-dampness epidemic, with etiology of externally contracted pestilential toxins, pathogenesis of dampness-toxin invasion, and disease location concentrated in the Lung. Pungent, bitter, and warm-natured herbal medicines are commonly used to treat COVID-19. Symptoms mostly belong to interior patterns and excess patterns, while herbal medicines mostly belong to the categories of "treating interior" and "purging excess," demonstrating high compatibility between syndromes and medications.

Full Text

Preamble

Exploring TCM Syndrome-Medication Patterns in the "Diagnosis and Treatment Protocol for COVID-19" Through Text Mining and Network Pharmacology

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Abstract

Objective: To explore Traditional Chinese Medicine (TCM) syndrome-medication patterns in the "Diagnosis and Treatment Protocol for COVID-19" using text mining technology and network pharmacology. **Methods:** We searched the official website of the National Health Commission for "Diagnosis and Treatment Protocol for COVID-19" (hereinafter referred to as the "Protocol") and collected information on symptoms and herbal formulas mentioned in the documents to establish a corresponding database. Texts meeting inclusion criteria for herbs and symptoms were analyzed using Text Mining, VOS Viewer, SPSS, and R for word segmentation, frequency statistics, adjacency table generation, word cloud visualization, topic clustering, association rule analysis, and visualization. Cytoscape and R were employed to construct syndrome-herb relationships based on TCM theory, "disease-herb-component-target" networks, PPI networks, and to perform GO and KEGG enrichment analyses of intersecting targets with visualization. **Results:** A total of 13,126 characters were extracted, including 8,291 characters related to formulas and herbs and 4,835 characters related to symptoms. From these texts, 87 herbs and 137 symptoms were identified. The top five most frequently used herbs were Licorice, Gypsum, Ephedra, Huoxiang (Agastache), and Almond, while the top five symptoms were greasy tongue coating, pale tongue, fatigue, white tongue coating, and fever. Herb efficacy classification showed dampness-transforming herbs as the most common, with warm properties predominating, flavors primarily pungent and bitter, and primary meridian affiliations to the lung, spleen, and stomach. Frequency analysis identified 22 high-frequency herbs (frequency $ $10) and 33 high-frequency symptoms (frequency $ $10). Association rule analysis yielded 22 herb-pair association rules and 105 herbal association rules. Topic clustering revealed five clustered formulas and five clustered syndromes. A syndrome-herb relationship diagram based on TCM theory was constructed. Through the TCMSP database, 62 active components from high-frequency herbs (top 7) and 229 active component targets were screened. DrugBank and GeneCards databases identified 526 COVID-19 targets, with 42 intersecting targets identified via Venn diagram. GO and KEGG enrichment analysis via the DAVID platform revealed 339 biological processes, 20 cellular components, 41 molecular functions, and 98 metabolic pathways. **Conclusion:** The TCM symptom patterns, medication patterns, and syndrome-herb patterns for COVID-19 in the "Protocol" indicate that COVID-19 belongs to the category of cold-damp epidemic disease, caused by external contraction of pestilential toxins with dampness-toxin invasion as the pathogenesis, primarily affecting the lung. Pungent, bitter, and warm herbs are commonly used, with symptoms mostly belonging to interior and excess patterns, and herbs primarily having "interior-treating" and "excess-purging" properties, demonstrating high matching between symptoms and herbs.

Keywords: Text mining technology; Network pharmacology; "Diagnosis and Treatment Protocol for COVID-19"; COVID-19; Syndrome-herb patterns

Introduction

Coronavirus disease 2019 (COVID-19) is an acute respiratory infectious disease caused by SARS-CoV-2, with infected patients primarily presenting with dry throat, sore throat, cough, and fever [1]. Research indicates that COVID-19 infection may cause significant long-term damage across multiple organ systems, with some patients experiencing symptoms lasting over two years since the early pandemic [2]. TCM epidemic theory has developed over centuries, making the utilization of Chinese medicine for COVID-19 prevention and treatment particularly significant. COVID-19 falls under the category of TCM epidemic diseases, yet possesses unique characteristics compared to historical epidemic diseases in terms of seasonal and geographic occurrence, transmission patterns, symptom onset speed, and treatment efficacy [3]. Since the outbreak, the medical community has accumulated extensive experience in epidemic prevention and patient treatment, achieving clearer understanding of COVID-19's pathogenesis and pathological features, with the advantages of TCM gradually becoming evident [4]. Consequently, national authorities have issued multiple versions of the "Diagnosis and Treatment Protocol for COVID-19," incorporating TCM diagnosis and treatment as an essential component [5]. This study employs text mining technology and network pharmacology to conduct statistical analysis of TCM clinical treatment methods for COVID-19, extracting effective information from the "Protocol" to derive TCM syndrome-herb patterns and summarize clinical experience, thereby facilitating systematic, standardized, and orderly approaches to TCM clinical issues in COVID-19 patients.

Methods

1.1 Data Sources

Documents were retrieved from the official website of the National Health Commission of the People's Republic of China (nhc.gov.cn) using "Diagnosis and Treatment Protocol for COVID-19" as the search term from January 1, 2020, to February 1, 2023, yielding eight relevant documents.

1.2 Text Data Processing

1.2.1 Inclusion Criteria

- Text content related to formulas, herbs, and symptoms for COVID-19 in the "Protocol"
- Complete formulas and clearly defined symptoms

1.2.2 Exclusion Criteria

- Text content unrelated to COVID-19 formulas, herbs, and symptoms
- Incomplete formulas or unclear symptoms
- For texts with identical or similar meanings, only one representative entry was retained

1.2.3 Text Extraction and Entry Eight usable documents were screened, extracting 13,126 characters total, including 8,291 characters related to formulas and herbs and 4,835 characters related to symptoms. After keyword extraction, data for 87 herbs and 137 symptoms were entered.

1.2.4 Text Standardization References including *Chinese Materia Medica* [6], *Formulas of Chinese Medicine* [7], and *TCM Diagnostics* [8] published by China Press of Traditional Chinese Medicine in 2016 were used to standardize herb names, properties, meridian affiliations, efficacy classifications, and symptom terminology (e.g., “Heishunpian” standardized to “Fuzi”).

1.2.5 Text Processing and Analysis

- Text Mining 5.9 [9] was used for word segmentation, frequency statistics, adjacency table generation, and word cloud visualization
- VOS Viewer 1.6.13 was employed for topic clustering
- SPSS Modeler 18.0 was used for association rule analysis based on the Apriori algorithm (support: 20%, confidence: 80%, maximum antecedents: 1, lift $ $1.0) with network diagram generation
- R 4.2.1 was utilized for association rule analysis (maximum antecedents: 2, other parameters unchanged) to generate scatter plots, grouped matrix visualizations, relationship diagrams, and parallel coordinate plots

Results

2.1 Analysis of Individual Herbs for COVID-19 Treatment

A total of 87 herbs were identified with a cumulative frequency of 768 occurrences. Twenty-two herbs had frequency $ $10, accounting for 473 occurrences. The most frequent herbs were Licorice (41 times, 8.67%), Gypsum (37 times, 7.82%), Ephedra (37 times, 7.82%), Huoxiang (36 times, 7.61%), Almond (29 times, 6.13%), and Cangzhu (29 times, 6.13%). See Table 1 .

2.2 Property, Flavor, Meridian, and Efficacy Classification of COVID-19 Herbs

Analysis of the 22 high-frequency herbs (frequency $ $10) revealed 10 meridian affiliations and 5 efficacy categories. The “four properties” frequencies were: warm (234 times, 49.47%), cold (78 times, 16.49%), neutral (64 times, 13.53%), slightly warm (58 times, 12.26%), and slightly cold (39 times, 8.25%). See Figure 1 [Figure 1: see original paper]. The “five flavors” frequencies were: pungent (304 times, 44.57%), bitter (239 times, 35.04%), sweet (139 times, 20.38%), sour (0 times, 0%), and salty (0 times, 0%). See Figure 2 [Figure 2: see original paper]. Meridian frequencies were: lung (357 times, 27.96%), stomach (268 times, 20.99%), spleen (268 times, 20.99%), large intestine (99 times, 7.75%), heart (76 times, 5.95%), liver (56 times, 4.39%), kidney (37 times, 2.90%), bladder (70 times, 5.48%), small intestine (23 times, 1.80%), and gallbladder (23 times, 1.80%). See Figure 3 [Figure 3: see original paper]. Efficacy frequencies were: dampness-transforming herbs (92 times, 24.60%), heat-clearing herbs (86 times, 22.99%), deficiency-tonifying herbs (68 times, 18.18%), exterior-releasing herbs (80 times, 21.39%), and cough-relieving/asthma-alleviating herbs (48 times, 12.84%). See Figure 4 [Figure 4: see original paper].

2.3 Topic Clustering and Word Cloud Analysis of COVID-19 Herbs

High-frequency herbs (frequency $ $10) were analyzed using Text Mining 5.9 for topic clustering and word cloud visualization. See Figures 5 [Figure 5: see original paper] and 6 [Figure 6: see original paper].

Topic clustering yielded five formula clusters: Cluster 1: Huoxiang, Chenpi, Baizhu, Fuling, Banxia; Cluster 2: Gancao, Chishao; Cluster 3: Shigao, Xingren, Tinglizi; Cluster 4: Mahuang, Shengjiang; Cluster 5: Cangzhu, Caoguo, Houpo, Binglang.

The word cloud intuitively displayed the frequency distribution of herbs with frequency $ $10.

2.4 Association Rule Analysis of High-Frequency COVID-19 Herbs

Association rule analysis of herbs with frequency $ $10 identified the top 10 support-ranked combinations, yielding 10 core herb pairs. See Table 2 . SPSS Modeler 18.0 generated an association rule network diagram (Figure 7 [Figure 7: see original paper]), while R 4.2.1 produced various visualizations (Figures 8 [Figure 8: see original paper]-11 [Figure 11: see original paper]).

The top 10 herb combinations by support were: Caoguo-Cangzhu, Shigao-Xingren, Mahuang-Xingren, Mahuang-Cangzhu, Shigao-Tinglizi, Houpo-Caoguo, Cangzhu-Caoguo, Mahuang-Caoguo, Huoxiang-Fuling, and Huoxiang-Chenpi.

The association rule network diagram (Figure 7) showed the strongest links as Chaihu-Huangqin and Huangqi-Banxia, with link counts representing association rules and link strength indicating lift magnitude.

R analysis generated 105 association rules, visualized in a scatter plot (Figure 8) with support on the x-axis, confidence on the y-axis, and point color representing lift. Grouped matrix visualization (Figure 9) showed most rules had support $ $0.26, confidence $ $0.8, and lift $ 2.0, *indicatingstrongassociations.Therelationshipdiagram*(*Figure*10)*identifiedherbswithhighsupport*(0.4
Shigao, *Mahuang*, *andXingren*; *andhighlift*(2.4) : *Cangzhu*, *Caoguo*, *Shigao*, *andMahuang.Theparallelcoor*
concentrated in seven herbs: Houpo, Caoguo, Cangzhu, Mahuang, Huoxiang, Shigao, and Xingren.

2.5 Symptom Frequency Analysis for COVID-19 Treatment

A total of 137 symptoms were identified with 1,096 cumulative occurrences. Thirty-three symptoms had frequency $ $10, accounting for 609 occurrences. The most frequent symptoms were greasy tongue coating (43 times, 6.90%), pale tongue (32 times, 5.14%), fatigue (31 times, 4.98%), white tongue coating (31 times, 4.98%), and fever (28 times, 4.49%). See Table 3 .

2.6 Topic Clustering and Word Cloud Analysis of High-Frequency COVID-19 Symptoms

High-frequency symptoms (frequency $ $10) were analyzed using Text Mining 5.9. See Figures 12 [Figure 12: see original paper] and 13 [Figure 13: see original paper].

Topic clustering yielded five syndrome clusters: Cluster 1: Nausea, poor appetite, shortness of breath, weak defecation, epigastric fullness; Cluster 2: Lassitude, epigastric oppression, loose stools, chest tightness, scant sputum, dry cough, low-grade fever, dry mouth; Cluster 3: Poor appetite, fatigue, gastrointestinal discomfort; Cluster 4: Fever, dry throat, nausea, body aches, cough, shortness of breath, dyspnea; Cluster 5: Scant sputum, constipation, abdominal distension, yellow sputum.

The word cloud intuitively displayed symptom frequencies.

Network Pharmacology Mechanism Study

3.1 Construction of Syndrome-Herb Relationships Based on TCM Theory

Symptom and TCM-related texts from the Protocol for mild, moderate, severe, and critical COVID-19 cases were processed to extract high-frequency symptoms (frequency $ $10) and herbs (frequency $ $10). After excluding tongue and pulse manifestations, 18 symptoms and 22 herbs were selected. High-frequency symptoms were classified by interior/exterior, cold/heat, and deficiency/excess patterns according to the Protocol and *TCM Diagnostics*. High-frequency herbs were categorized by four properties, target locations, and tonifying/purging properties according to *Chinese Materia Medica* and *Formulas of Chinese Medicine*. Based on *Suwen: Sanbu Jiuhou Lun* ("Treat excess by purging, treat deficiency by tonifying") and *Suwen: Zhi Zhen Yao Da Lun* ("Treat cold with heat, treat heat with cold; tonify the weak, purge the strong"), syndrome-herb relationships were constructed using Cytoscape. See Figure 14 [Figure 14: see original paper].

3.2 Mechanism Study of High-Frequency Herbs in the Protocol

3.2.1 Screening of Active Components and Targets The TCMSP database was searched for active components and targets of high-frequency herbs (top 7). Gypsum, being a mineral drug without target information, was excluded. Sixty-two active components were identified (11 shared), with 229 active component targets (666 shared component-target interactions). See Table 4 .

3.2.2 COVID-19 Target Screening DrugBank database yielded 26 targets; GeneCards database initially provided 6,050 targets, from which the top 500 by relevance score were selected, totaling 526 COVID-19 targets.

3.2.3 Intersection of Herb and COVID-19 Targets Venn diagram analysis of herb targets and COVID-19 targets identified 42 intersecting targets. See Figure 15 [Figure 15: see original paper].

3.2.4 Construction of "Disease-Herb-Component-Target" Network and PPI Network Cytoscape 3.7.2 constructed the "disease-herb-component-target" network for high-frequency herbs (top 7). See Figure 16 [Figure 16: see original paper]. Core targets (degree $ $30) included quercetin, wogonin, stigmasterol, vestitol, shinpterocarpin, and l-SPD.

The String platform analyzed 42 intersecting targets (high confidence $ $0.7), yielding 37 targets after removing isolated nodes. The PPI network (Figure 17 [Figure 17: see original paper]) identified top-scoring targets: TNF, IL6, IL1B, IL10, ICAM1, CXCL8, VEGFA, CCL2, and RELA.

3.2.5 GO and KEGG Enrichment Analysis DAVID platform analysis of 42 intersecting targets revealed 339 biological processes, 20 cellular components, 41 molecular functions, and 98 metabolic pathways. Visualizations were generated using R 4.2.1 (Figures 18 [Figure 18: see original paper] and 19 [Figure 19: see original paper]). Key biological processes included lipopolysaccharide-mediated signaling, positive regulation of pri-miRNA transcription, smooth muscle cell proliferation, and angiogenesis. Cellular components comprised platelet alpha granule lumen, secretory granules, membrane rafts, and cell surface. Molecular functions included CXCR chemokine receptor binding, transcription coactivator binding, and cytokine activity. KEGG pathways were concentrated in AGE-RAGE signaling in diabetic complications, Chagas disease, fluid shear stress and atherosclerosis, rheumatoid arthritis, and influenza A.

Discussion

4.1 Medication Patterns for COVID-19

Statistical analysis of formula and herb texts revealed that "warm," "pungent," and "bitter" are the primary property and flavor characteristics. Warm herbs dispel wind-cold, warm the middle, and tonify yang, aligning with the principle "treat cold with heat" and Academician Tong Xiaolin's classification of COVID-19 as "cold-damp epidemic" [12]. Pungent herbs disperse and move qi-blood to dissipate pestilential toxins, while bitter herbs clear heat, dry dampness, and purge fire. Combined pungent-bitter usage regulates qi movement, corresponding to COVID-19's progression to the spleen-stomach with impaired qi ascent/descent [13]. Commonly used categories include heat-clearing, dampness-transforming, and exterior-releasing herbs, targeting damp-pestilence obstruction in spleen-lung. Meridian analysis showed predominant lung, stomach, and spleen affiliation, with lung being most common, confirming COVID-19's primary location in the lung with close spleen-stomach relationships.

Association rule analysis identified 22 herb-pair and 105 herbal association rules. Top herb pairs included Caoguo-Cangzhu, Shigao-Xingren, Mahuang-Xingren, and Mahuang-Cangzhu. Caoguo-Cangzhu combines aromatic dampness-transforming effects. Mahuang-Cangzhu appears in Xu Gongyan's Cangma Pill for lung diseases with phlegm-dampness, matching COVID-19 pathogenesis [15]. Mahuang-Xingren and Shigao-Xingren are key pairs from Mahuang Tang and Maxing Shigan Tang, respectively. The strongest network links were Chaihu-Huangqin and Huangqi-Banxia. Most association rules showed support $ $0.26, confidence $ $0.8, and lift $ $2.0, indicating strong, reliable associations.

Topic clustering yielded five formula clusters. Cluster 1 (Huoxiang, Chenpi, Baizhu, Fuling, Banxia) resembles Liujunzi Tang, effective for spleen-stomach qi deficiency with phlegm-dampness [16]. Cluster 2 (Gancao, Chishao) includes Chishao for COVID-19-related coagulation dysfunction [17] and Gancao with antiviral effects against respiratory viruses [18], forming the classic Shaoyao Gancao Tang. Cluster 3 (Shigao, Xingren, Tinglizi) comprises Qingfei Xiaoyan Wan, clinically effective for viral pneumonia [19]. Cluster 4 (Mahuang, Shengjiang) enhances exterior-releasing effects, with Mahuang showing multi-target mechanisms for pneumonia [20-21] and Shengjiang containing 18 targets for COVID-19 [22]. Cluster 5 (Cangzhu, Caoguo, Houpo, Binglang) includes components of Dayuan Yin, important in COVID-19 treatment [25].

4.2 Symptom Patterns of COVID-19

Symptom analysis identified "greasy tongue coating," "pale tongue," "fatigue," "white tongue coating," and "fever" as the most frequent symptoms. Greasy coating reflects prominent dampness-phlegm pathology, a key pathogenic factor [26-27]. Pale tongue, fatigue, and white coating indicate qi deficiency and impaired qi movement, core pathologies in recovery phase [28] and risk factors for infection [29]. Fever, an initial symptom, manifests as damp-heat invading the lung in mild cases and damp-heat accumulating in the lung in severe cases [30].

Topic clustering identified five syndrome clusters: Cluster 1 (nausea, poor appetite, shortness of breath, weak defecation, epigastric fullness) matches damp-heat accumulating in spleen; Cluster 2 (lassitude, epigastric oppression, loose stools, chest tightness, scant sputum, dry cough, low-grade fever, dry mouth) matches damp-heat accumulating in lung; Cluster 3 (poor appetite, fatigue, gastrointestinal discomfort) matches spleen deficiency with dampness; Cluster 4 (fever, dry throat, nausea, body aches, cough, shortness of breath, dyspnea) matches damp-toxin stagnating in lung; Cluster 5 (scant sputum, constipation, abdominal distension, yellow sputum) matches damp-heat stagnating in spleen-lung.

4.3 Syndrome-Herb Patterns Based on TCM Theory

This study extracted 18 symptoms and 22 herbs (frequency $ $10), classifying symptoms by pattern and herbs by property, target location, and tonifying/purging effects. The syndrome-herb network showed symptoms predominantly belonging to excess and interior patterns, with herbs primarily having interior-treating and excess-purging properties, demonstrating high matching and validating TCM diagnostic and therapeutic theory.

Notably, the same symptom may have different pathogenic natures across patterns (e.g., fever as heat pattern in pestilential toxin fettering exterior but cold pattern in cold-dampness stagnating lung), requiring systematic syndrome differentiation to avoid erroneous treatment.

4.4 Network Pharmacology Mechanisms

Network pharmacology analysis of high-frequency herbs (top 7) identified 62 active components, 229 component targets, 526 COVID-19 targets, 42 intersecting targets, 339 biological processes, 20 cellular components, 41 molecular functions, and 98 metabolic pathways.

Key active components included quercetin, wogonin, stigmasterol, vestitol, shinpterocarpin, and l-SPD. Flavonoids like quercetin, wogonin, and l-SPD exhibit anti-inflammatory, antioxidant, and immunomodulatory effects, enhancing myocardial contractility via cardiac dopamine D1 receptors [33-34]. Quercetin also modulates immune cell functions and inhibits inflammatory pathways [35]. Vestitol and shinpterocarpin from Gancao show anti-inflammatory effects and neuraminidase inhibition, respectively, potentially inhibiting viral release and spread [36-39].

Key PPI network targets included TNF, IL6, IL1B, IL10, ICAM1, CXCL8, VEGFA, CCL2, and RELA. TNF plays a central role in COVID-19 inflammation by activating immune cells and pro-inflammatory cytokines [40-41].

GO and KEGG enrichment revealed pathways in lipopolysaccharide signaling, pri-miRNA transcription, smooth muscle cell proliferation, AGE-RAGE signaling, fluid shear stress, and atherosclerosis, representing effective routes for controlling inflammatory cytokines [42-43].

Conclusion

TCM has accumulated extensive experience in COVID-19 etiology, pathogenesis, and treatment, demonstrating unique advantages. Clinical trials show significant efficacy, with possible positive correlation between cure rates and TCM participation [44]. Pathogenesis centers on dampness as the core factor with “dampness-toxin” as the main mechanism, readily transforming into heat [45]. Early-stage treatment focuses on resolving dampness, detoxifying, and ventilating lung qi; mid-stage on ventilating lung, detoxifying, and unblocking bowels; severe-stage on opening orifices and preventing collapse; and recovery-stage on tonifying deficiency and dispelling residual pathogens [46-48].

This systematic statistical analysis of formulas and symptoms from the National Health Commission’s “Protocol” using text mining and network pharmacology provides new insights for TCM clinical practice and drug development for COVID-19.

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Note: Figure translations are in progress. See original paper for figures.