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Review Article

Reviewing Efficiency of Traditional Medicinal Approaches Against Covid-19

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This study aimed to study the different variants of corona viruses, their mutation and associated Naturopathic system for treatments available for patient along with their effectiveness. Social and economic sectors witnessed upheaval and disruption with arrival of SARS Coronavirus and its following variants leading to high transmission and in turn high infection rate. Pattern of appearance of variants is based on evolution mechanisms, alterations, recombinant methods which have been explained in this review, explaining journey of virus from early arrival of Wuhan strain to rise of succeeding variants such as concerning, variants of interest and those under monitoring that allowed virus to spread faster leading to high infection and mortality rates. So, we justify the contribution of Traditional healthcare systems, such as AYUSH, which provide countless formulations with detailed mechanisms. Polyherbal formulations such as Ayush kwath, Ayush-64, along with Samshamani Vati, serve as strong immune regulators. Traditional Chinese medicine, Traditional Tibetan methods, Siddha formulations, along with naturopathic treatments including naturally occurring preparations and their phytoconstituents, are also effective against various phases of life cycle of virus. Traditional herbal remedies not just enhance immunity but also interfere with virus entry and replication procedure, which in turn serve as a wide-ranging defence mechanism, and a powerful approach helping to maintain immune strength.

Keywords: *SARS Coronavirus 2; Variants; Evolution; AYUSH; TTM; Siddha System*

Introduction

Severe acute respiratory viruses have led to a widespread disturbance and they are well familiar for their prompt effects leading to quick onset of disease, arrival of signs in a small period and their long-term consequences, which have a notable and arduous impact all over the world. According to global cumulative data by the WHO (World Health Organisation), in the 28 days from 22 December 2025 to 18 January 2026, 68 countries across three WHO regions reported new COVID-19 cases. During these 28 days, a total of 39,424 new cases were reported, which is a decrease compared to the 65,087 new cases reported from 89 countries in the previous 28-day period (World Health Organization, n.d). China witnessed the first case of arrival of the virus in the Guangdong Province around November 2002 (Vijayanand et al., 2004). Rumours of the presence of a similar virus arose around 31 December 2019 in Wuhan, China, and genomic study of this new virus exposed 72% likeness in sequences showing a familial relation and close link with SARS-CoV (2002-2003), thus it was regarded as SARS-CoV-2 (Rathore & Ghosh, 2020). Classification system thus placed them in genus Beta coronavirus and sub-genus Sarbecovirus (Rathore & Ghosh, 2020). Emergence of alternatives and its progression over time became universal fear. Evolving pattern is justified based on changes mainly in proteins present in spike and by selection pressure idea as well. Varied methods are used for the diagnosis of this virus, but still various unique and new variants were observed due to difference in proteins present on the surface of the virus, which decreases the reliability of previous methods. As progression of virus occurs and arrival of new variants continue vaccines and allopathic systems effectiveness may decline over time but in spite of that traditional systems remain unaffected by these patterns and continue to show their efficient roles. Traditional and time-tested approaches are being chosen such as Ayurveda, Siddha formulations, TCM, TTM to tackle this virus. Also, there is need molecular and genetic engineering studies to upregulate the genes responsible for production of secondary metabolites in plants (Kumar et al., 2024). These remedies are favoured for their specific roles, like their immune-regulating ability, capability to overcome viral infections, their antipyretic role, and other significant properties. The medicinal plants diversity and are used for various pharmacological activities are reviewed and known to have anticancer, anti-inflammatory, antiviral (Sharma et al., 2024c). The review discusses different case-based approaches across various areas used to tackle the virus and also aims to bring suitable evidence justifying the judicious role of ethnomedicine for future pandemic preparedness.

Methodology

The systematic search across electronic databases and search involving grey literature sources initially identified a total of 580 records. After removal of 195 duplicates, 385 records remained for title and abstract screening. Following the application of inclusion and exclusion criteria, 125 reports were sought for full-text retrieval. A final synthesis of 67 studies was conducted, comprising peer-reviewed virological analyses, clinical case reports, and ethnopharmacological reviews. Systematic search process was adopted which aims at assessing the efficacy of traditional medicinal systems against SARS Coronavirus 2. A methodology for synthesis was adopted which permits for the synthesis of already present information from a wide range of peer reviewed literature, clinical studies, ethnobotanical records, and pharmacological studies. This approach is particularly used to address the three main objectives: To review the available literature regarding COVID involving Morphology, Evolution and emergence of variants, and potential factors impacting severity of SARS infection and to evaluate the efficient role of traditional medicinal systems against SARS virus through case studies.

Types of Research

The research process uses a methodology based on qualitative systematic review. The research process is descriptive based and analytical in nature. It involves:

collection and critical assessment of published studies and peer-reviewed studies, review articles and grey literatures.

Evaluation and judgement of findings across traditional medicinal systems including Ayurveda, Traditional Chinese Medicine, Unani Siddha and African Medicinal Systems.

Sources of Data

The primary data source is existing available literature. Following databases and repositories were systematically searched:

Electronic Databases such as PubMed/MEDLINE**,** Google scholar, ScienceDirect and grey literature sources such as WHO technical reports and guidelines on COVID-19 https://data.who.int/dashboards/covid19/summary **,** Ministry of Ayush [Internet]. [cited 2026 Apr 23]. Available from: https://ayush.gov.in/#!/aboutus

Data collection

Selection and search process:

A structured search query was conducted using keywords and Boolean operators to capture the intersection of viral evolution and mechanism of traditional medicinal systems.

Keywords and Boolean operators: SARS-CoV-2, Variants, Evolution, AYUSH, SIDDHA, Traditional Chinese Medicine.

Boolean Search Combinations:

The search involves Boolean search combinations such as AND, OR, NOT to combine terms:

(COVID-19 OR SARS coronavirus 2 OR Coronavirus) AND (traditional medicine OR herbal medicine OR TCM OR Ayurveda); (COVID-19 OR SARS-CoV-2) AND (spike protein OR viral variants); (traditional medicine OR herbal medicine) AND (immunomodulation OR antiviral) AND (clinical trial OR efficiency); (coronavirus OR COVID-19) AND (variant evolution OR emergence OR morphology).

Eligibility criteria:

To ensure methodological rigour and relevance, specific inclusion and exclusion criteria were applied during the literature screening process. Peer reviewed articles published in English between 2000 to 2025 and ongoing 2026 were given priority for COVID-19 studies. Studies focussing on SARS Coronavirus, SARS Coronavirus 2 and some related to MERS Coronavirus structural and morphological properties; Studies reporting Evolutionary genetics, phylogenetics and receptor binding characters of COVID-19 were included.

Exclusion criteria:

Studies not related to COVID-19 and other coronaviruses; Articles not published in peer-reviewed journals (unless classified as significant grey literature) were not given priority.

SARS Coronavirus 2 Progress, Arrival, Circulation of Mutants

Progress of the SARS virus is described in view of two main key factors: first, the case of acute infections, and second, progression at level of host population (Ramesh et al., 2021). In acute infections, once the virus enter body, it multiplies rapidly and reaches peak level in a few days, such as 3 days in case of SARS Coronavirus 2, except omicron variant (Ramesh et al., 2021). Spread of virus is influenced by an important phenomenon called transmission bottleneck, in which few virus particles successfully establish a new infection, in a similar way one or two virions establish SARS virus in host, and only a few manage to breach the host's defences thus the iSNVs are transferred from one person to another on a rare basis, making it difficult to measure the benefit of the mutations (Markov et al., 2023) (Sharma et al., 2024e). Progress at host population level, justifies consensus sequences are primary target, that is, a version of the viral genome created by taking the most common variant at each position. Evolutionary pattern among the variants show, alpha variant appeared at the end of 2020 and soon replaced other variants, and South Africa and Botswana observed onset of omicron in November 2021 (Mohapatra et al., 2022). These variants were regarded as variants of concern and arose in different regions and have common mutations, justifying the concept of convergent evolution (Markov et al., 2023) (Alhamlan & Al-Qahtani, 2025). The evolution pattern is also explained involving concept of selection pressure justifying that the evolution is a type of humoral immune response (Case et al., 2026). Annual nucleotide evolutionary rate of 0.0004 to 0.002 is seen (Tao et al., 2021). RNA viruses, the typical mutation rate is around 10 substitutions per site each year. Although coronavirus is an RNA virus, its mutation speed is slow. This reduced mutation rate results from coronaviruses possessing a checking enzyme, nsp-14ExoN, which rectifies errors (Flores-Vega et al., 2022) Recombination plays key role in the progress of SARS Coronavirus 2, such that one central mutation event in XBB variants, is formed from recombination between omicron BA.2 subvariants (Holmes, 2024).

Table 1. Mutations are mainly responsible for the emergence of different variants

Mutation region	Some key mutations	Function
A mutation in the spike glycoprotein	D614G	The mutation favors cell entry by the ACE2 receptor, leading to a high infection rate
	H69/v70	Deletion impacting communication with receptors
	N501Y	Lead to a high transmission rate by enhancing ACE2 binding
	P681H	Enhance the entry of the virus and infection rate
Nucleocapsid protein mutation	Nucleocapsid phosphoprotein mutations	The alteration leads to mild to severe symptoms of COVID, with most changes clustered between amino acid positions 194–204
Mutation in the open reading frame (ORF)	Q57H, A99V, G252V, G196, and V13l	Mediates viral entry and replication

SARS Coronavirus 2 emerged and began to spread at a rapid rate. With continuous spreading many alterations began to arise due to change in proteins of spike leading to emergence of new variants. Concerning variants termed as variant of concern and others like variants of interest were identified by WHO (Cantón et al., 2021). Variant with genetic alterations is known as variant of interest (Houge et al., 2021). These changes affect their ability to spread, tendency to bind to receptors, degree of disease they can cause, and detection capabilities. These changes also help the virus to avoid the immune system. Variants of concern have high infection rates, spread quickly, and are more infectious than others (Cantón et al., 2021).

Epidemiological Classification: Variants of Concern

Variant Alpha (B.1.1.7)

Reports of arrival observed in United Kingdom around September 2020 and spread out rapidly with significant cases reported in Europe, North America and various other regions around mid-year of 2021. Transmission rate, was 50% higher as compared to other variants due to mutations, among which 17 are non-synonymous, 6 are synonymous mutations, and 3 are deletions (Alhamlan & Al-Qahtani, 2025) (Ramesh et al., 2021). It has nine key variations in the spike proteins like deletions at locations 69–70 and 114, changes like N501Y and P68H1 impacts joining to ACE2 receptor, change in replicating ability observed due to mutation in ORF1ab and ORF8 outside the spike proteins, resulting in high infection cases, high frequency hospitalisation and even higher death rates as well (Alhamlan & Al-Qahtani, 2025).

Variant Beta (B.1.351)

List of concerning variants observed a new addition on 18 December 2020 after its initial discovery in South Africa in 2020 (Alhamlan & Al-Qahtani, 2025). The variant displayed multiple mutations, such as K417N, N501Y, and E484K, which have been known to occur in the beta variant and alterations such as N501Y, toughen the joining affinity of virus and host cell; E484K, avoid antibodies from previous infections; and K417N, which also helps in immune escape (Flores-Vega et al., 2022).

Gamma Variant (P.1)

Discovered in Manaus, Amazonas, Brazil, in December 2020, and was reported to the WHO in January 2021 (Alhamlan & Al-Qahtani, 2025). Emerged as a result of the changes in the RBD domain region of spike protein like N501Y, toughen the joining affinity of virus and host cell, E484K, allow pathogen to remain unnoticed by immune system, K417T alters the reduces vaccine efficacy (non-mRNA vaccines) and increases susceptibility to reinfection (Cantón et al., 2021) (Ramesh et al., 2021).

Delta Variant (B.1.617.2)

Worldwide domination began will reports of arrival of variant in India in October 2020 and was reported to the World Health Organisation in May 2021 (Alhamlan & Al-Qahtani, 2025). Cases of transmission were found among both vaccinated and unvaccinated individuals and have a transmission rate of 60% higher than that of the Alpha, with fever, respiratory problems, and headaches as common symptoms (Flores-Vega et al., 2022). Mutations such as 19R, 156 del, R158G, P681R, T478K, and D614G in spike protein, L452R in RBD domain, were found which increase transmission rate; thus, attacks of the delta variant were recognised more than the alpha variant (Chavda et al., 2022).

Variant Omicron (B.1.1.529)

Addition in list of Concerning variants was done on November 24, 2021 when South Africa and Botswana reported omicron arrival (Alhamlan & Al-Qahtani, 2025). This variant is unique and is thought to arrive independently of other variants. Apart from the B.1.1.529 lineage, others, such as BA.1, BA.2, and BA.3, were also described, among which BA.2 outcompeted BA.1, thus positioning itself as the most important lineage during 2019 pandemic (Kung et al., 2025). BA.1 was most widespread of the three lineages, whereas BA.2 was isolated mainly in Denmark, Nepal, and the Philippines, BA.3 has been less common (Flores-Vega et al., 2022).

Table 2. Variants of Concern of SARS: distribution, key mutations and function associated with that mutation.

Variant (Lineage) of VOCs	Spike Protein Mutations (RBD/Other)	Function linked to mutation	References
Variant Alpha (B.1.1.7)	N501Y (RBD), P681H1, Delta69-70, Delta114 (Deletions)	N501Y toughen the joining affinity of virus and host cell. Delta69-70 impact spike proteins, influencing cell infection and immune escape.	(Alhamlan & Al-Qahtani, 2025) (Ramesh et al., 2021)
Beta (B.1.351)	RBD alterations like N501Y, K417N, E484K.	Joining affinity of virus and host cell is tightened by N501Y.	(Flores-Vega et al., 2022)

		Pathogen to remain unnoticed by immune system by E484K and K417N.	
Gamma (P.1)	N501Y, E484K, K417T (all RBD); D614G, H655Y, T1027I, V1176F (Other)	N501Y toughen the joining affinity of virus and host cell. E484 allow pathogen to remain unnoticed by immune system. K417T change in ACE2 attaching, vaccine efficacy decreased.	(Cantón et al., 2021) (Ramesh et al., 2021)
Delta (B.1.617.2)	L452R, T478K (RBD); P681R close to furin cleavage site.	L452R toughen the joining affinity of virus and host cell. T478K allow pathogen to remain unnoticed by immune system. P681R spike protein cleavage, cell fusion enhancement and increased host cell fusion.	(Flores-Vega et al., 2022)
Omicron (B.1.1.529)	Proteins in spike show 35 mutations and RBD has 15.	Allow pathogen to remain unnoticed by immune system.	(Kung et al., 2025)

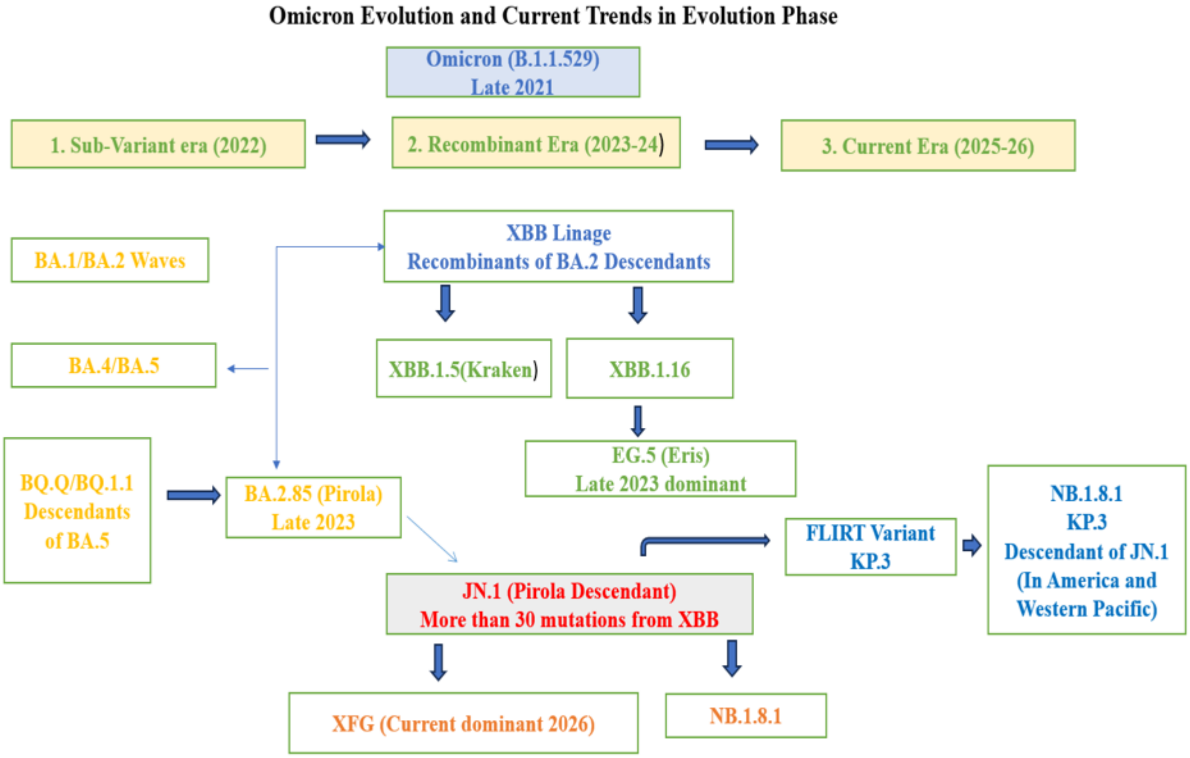

Figure 1. Omicron Evolving Outline and Circulating trend in present variations

Variants of Interest of SARS

B.1.427 and B.1.429, the Epsilon Variant

Variant of interest observed new arrival by the WHO (World Health Organisation) after its initial discovery in California, USA, in May 2020. It was present in trace amounts and occupied a prominent place in the California pandemic between November and December 2020, then proceeded to be the most prevalent variant from January to March 2021 and exhibit mutations in the RBD domain such as L452R, which help in joining the receptor present on cell surface to proteins of virus. (Zaputra & Utama, Mar - Apr 2024).

Variant B.1.526 Iota

Reported in New York, USA, in November 2020, and WHO declared it a variant of interest on March 24, 2021. It has multiple polymorphisms in spike proteins, often reported among two lines: B.1.526 line with alteration in the RBD domain, B.1.526 line with S477N alteration that support joining of protein of virus to ACE2 receptor and in September 2021, WHO deleted this variant from its list of variants of interest since it had started declining rapidly in the middle of that year (Flores-Vega et al., 2022) (Dubey et al., 2021).

Variant of Eta (B.1.525)

By March 2021, the variant had been reported in about 23 countries worldwide after its first discovery in Nigeria and the UK in December 2020 (Janik et al., 2021). It is undergoing some of the major changes, such as the E484K alteration in the RBD, sometimes referred to as the "escape mutation," a genetic change in the pathogen that somehow allows it to escape the host immune response, such as neutralisation by antibodies, ΔH69/ΔV70 deletion, disrupts the spike proteins of virus (Focosi et al., 2021).

Kappa Variant (B.1.617.1)

This strain had its first discovery in India in December 2020, and thereafter, it spread rapidly to infect 41 countries by the end of May 2021. Variant shows multiple important mutations in the spike protein, such as L452R in the RBD domain, which support joining to ACE2 receptor, T95I disappear from pseudo types and is thought to assist virus evasion of the immune response, D614G in the proteins of spike increases the tendency of virus to cause infection (Ren et al., 2022).

Table 3. Variants of Interest of SARS: their distribution, key mutation and associated function

Variant (Lineage) of VOIs	Key Spike Protein Mutations (RBD/Other)	Function linked to mutation	References
Epsilon (B.1.427/9)	L452R (RBD); W152C (NTD); S13I (N-terminal)	L452R toughen the joining affinity of virus and host cell. W152C reduced neutralization by antibodies.	(Zaputra & Utama, Mar - Apr 2024)
Iota (B.1.526)	E484K (RBD); S477N (RBD)	E484K allow pathogen to remain unnoticed by immune system. S477N toughen the joining affinity of virus and host cell.	(Flores-Vega et al., 2022) (Dubey et al., 2021)
Eta (B.1.525)	E484K (RBD); Q677H (near furin cleavage site); DeltaH69 DeltaV70 (Deletion)	E484K is linked to the escape mutation. Q677H changes the efficiency of spike cleavage, viral entry, and cell infection. ΔH69/ΔV70 toughen the joining affinity of virus and host cell. and cell infection enhancement.	(Focosi et al., 2021)
Kappa (B.1.617.1)	L452R (RBD); P681R (near furin cleavage site); T95I; D614G	L452R toughen the joining affinity of virus and host cell. P681R virus entry and infection rate increase. T95I allow pathogen to remain unnoticed by immune system.	(Ren et al., 2022)

Traditional Medicinal Approaches Justifying their Efficient Role Through Case Based Approaches

Due to changing climatic shifts there is a great impact on diversity of flora around the globe and the distribution of secondary metabolites in their plant parts (Sharma et al., 2020a). Medicinal plants are the primary source of natural products which possesses healing properties (Sharma et al., 2020b; Kaushal et al., 2020). Medicinal plants were used over the last many centuries for medicinal purposes (Sharma et al., 2020c) and the indigenous knowledge about the uses known as folklore system were passed from ancestors to future generation (Sharma et al., 2020d). Himalayan regions were known for hub of the diversity of these medicinal herbs used in folklore uses (Sharma et al., 2021a) and also some medicinal plants were reviewed to have potential to heal from viral SARS infection (Sharma et al., 2021b). Natural products from various herbal plants have that potential to emerge as potent source for drug like candidate and development (Sharma et al., 2022a). The traditional knowledge also helped in developing the new drig like candidates for the management of diseases (Sharma et al., 2022b). The landuse and climate change severly effect and need to conserve the diversity is needed as discussed (Sharma et al., 2022c).

1. Herbal interventions involving AYUSH Formulations

Ethnobotanical knowledge from tribal and local peoples were the sole option of treatment in earlier days and where the modern health care was not available (Sharma et al., 2024a; Sharma et al., 2022b). The herbal plants and other natural wild fruits and vegetables were used as functional food and nutraceuticals (Sharma et al., 2024b; Sharma et al., 2024d). Traditional knowledge involves a large number of possible approaches that are widely used to tackle the SARS virus. It involves a wide range of approaches, like the use of herbal formulations involved in Traditional Chinese medicine, ayurvedic medicinal practices, etc., which are considered effective to overcome the virus.AYUSH (ayurveda, yoga, naturopathy, siddha and homoeopathy) is a system launched by the Ministry of AYUSH; are widely used as an ethnomedicine system and shows great efficiency towards the SARS virus. The AYUSH Ministry has adopted several methods to overcome the potential impact of the SARS virus and employs natural products derived from plants, animals, minerals and their formulations to tackle this virus and has also launches AYUSH Sanjivani mobile application for providing data regarding accepting AYUSH decisions (Kotecha, 2021). Among its multiple AYUSH formulations, notable Ayurvedic ones include: AYUSH 64, which is a combination of 4 different constituents, that helps to provide relief from symptoms of COVID (Panda et al., 2022). Similar to that, Ayush kwath, a typical Ayurvedic kada, is made by mixing several botanicals and boosts immunity. It is advisable to take it once or twice daily. *Ocimum sanctum, Cinnamomum zeylanicum, Piper nigrum, and Zingiber officinale* are the main herbs used in the formulation and are available in powder and tablet forms (Gautam et al., 2022). Sanshamani Vati, or often referred to as Guduchi Ghan Vati, is directed as a 500mg tablet with warm water. The most important ingredient in Sanshamani Vati is *Tinospora cordifolia*. Some other AYUSH formulations include Yashtimadhu, Agasthya Hareetaki, and Anuthiala, which are also found to be very effective against the SARS virus (Sruthi D et al., 2023) (Sharma et al., 2024e).

(a) **Ayush kwath:** Ayush kwath has different components which are used in various proportions and their specific parts are utilized, extracting of phytoconstituents is done which help to maintain overall health and wellbeing providing protection against SARS virus (Gautam et al., 2022).

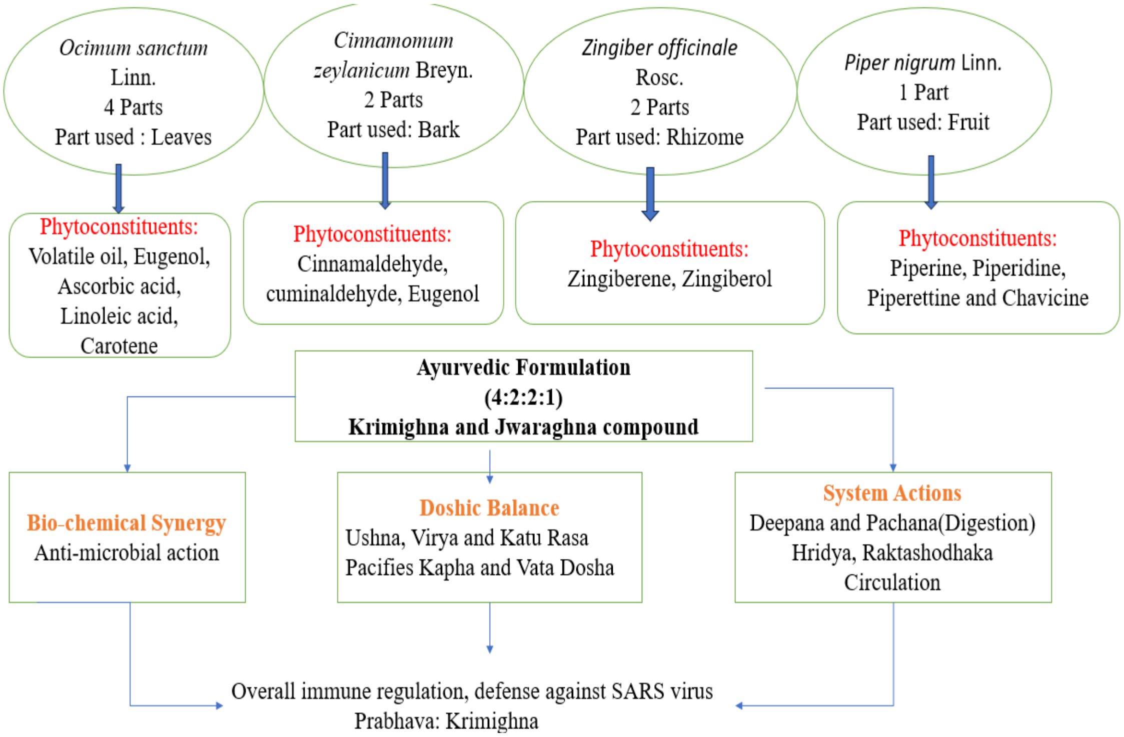

Figure 2. Ayush kwath role against SARS Virus (Gautam et al., 2022) (Sharma et al., 2022)

(b) **Ayush 64 constituents-** Ayush 64 is known for its potential impact to control COVID-19 symptoms, and its constituents are known for maintaining digestion and metabolism which remove undigested matter from body and Kiratatikta plant inhibit inflammatory response and has antioxidant activities (Panda et al., 2022)(Sharma et al., 2024e).

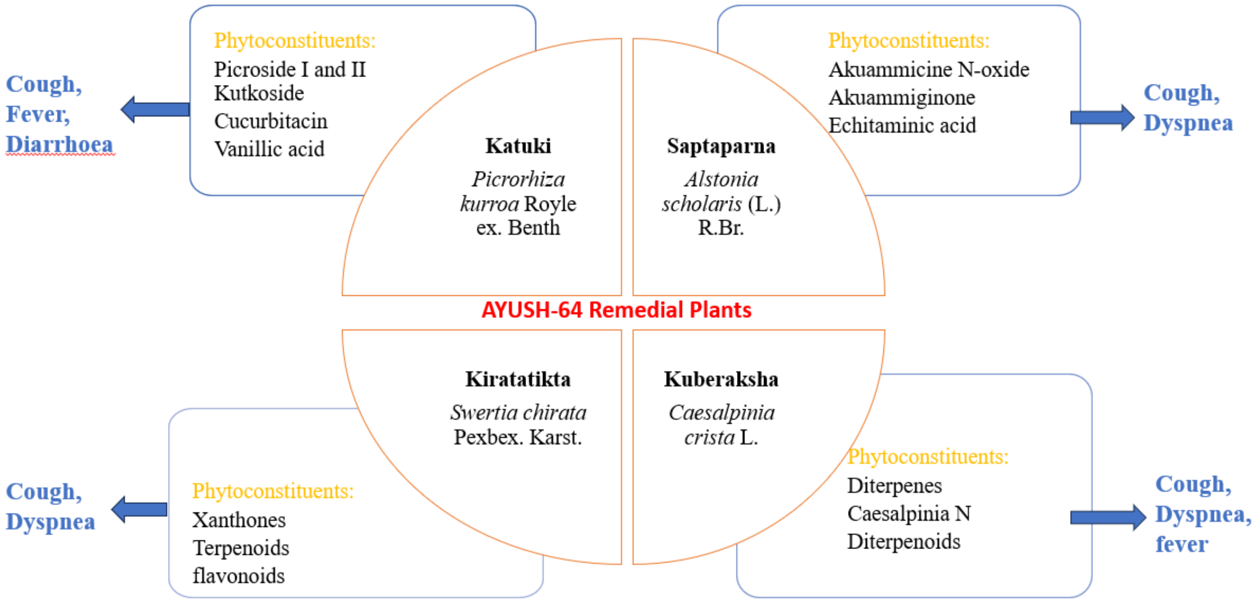

Figure 3. Ayush-64 role against COVID-19. (Panda et al., 2022)

(b) **Samshamani Vati** also named as Guduchi Ghan Vati is decoction present in concentrated form. It is a secondary preparation obtained from the main Kwatha Kalpana and is well recognized for COVID-19 signs. Dhanwantari Nighantu classified Guduchi into two types as *Tinospora cordifolia (Wild.) Miers and Tinospora cordifolia (Lour). Merr.* (Kar et al., A single-arm pilot study to analyse the hepatic safety of Samshamani Vati / Guduchi Ghana Vati (*Tinospora cordifolia* (Willd.) Miers) for the prevention of COVID-19., 2024).

Table 4. Samshamani Vati and its role in COVID

Formulation Name	Key Components (Main Herbs)	Traditional Ayurvedic Function	Modern Use for COVID-19	References
Samshamani Vati / Guduchi Ghan Vati	**Guduchi/Giloy** (*Tinospora cordifolia*) extract (Ghana)	Aqueous extract of *Tinospora* is used as an immunomodulator, Antipyretic (Jwaraghna), and has antiviral activity as well.	Useful in the treatment of all varieties of fevers and boosts the immune system during and after infections.	(Sruthi D et al., 2023)

2. Traditional Chinese Medicine (TCM)

The TCM originated around 1600-1046 BC, traced back to the Shang dynasty and includes the concept of Shangdi, which describes that illness arises from the invasion of evil spirits or the displeasure of ancestors. TCM is based on a system of five elements, which are: wood, water, earth, metal, and fire, each linked to different organs of the body and includes various herbal medicine formulations, which are known for their potent role against the SARS virus and were much preferred to be used during the 2019 pandemic (Gaur, 2024).The TCM system uses various herbal formulations such as *Yin Qiao San* and *Shuang Huang Lia* for upper respiratory infections, *Ma Xin Gan Shi Tang* used against SARS Coronavirus 2, similarly, for treating coronavirus infected patients TCM based Injections are used, along with other TCM herbal medicines, such as *Lianhua Qingwen* and *Quinfei Paidu* decoction are recognised for alleviating fever, cough, and other COVID-19 symptoms (Gaur, 2024). These formulations are identified for their active role against SARS Coronavirus 2 and stop entry of the virus in cells by disrupting binding to the spike protein. TCM formulations are generally administered orally or as decoction, granules, teas, tablets or in form of capsules (Capodice & Chubak, 2021).

Traditional Chinese Formulation and their Use Against SARS

TCM Formulation	Herbal components	Use against SARS
Yin Qiao San	*Lonicera japonica, Forsythia suspensa, Mentha haplocalyx, Arctium arvensis, Platycodon grandifloras, Glycine max, Lopthatherum uralensis, Shizonepta tenuifolia.*	Infections of upper respiratory passage are improved and immune system functioning of upper respiratory pathway is improved.
Yu Ping Fang San	*Astragalus membranaceus, Saposhnikovia divaricate, Atractylodes macrocephala.*	Enhancement of immunity and protection against virus.
Sang Ju Yin	*Morus alba, Chrysanthemum, Mentha haplocalyx, Platycodon grandifloras, Phragmites australis, Glycyrrhiza uralensis.*	Enhancement of immunity and protection against virus.
Lian Hua Qing Wen Capsule	*Forsythia suspensa, Lonicera japonica, Ephedra sinica, Prunus sibirica, Glycyrrhiza uralensis, Mentha haplocalyx.*	Clears heat in lungs and protect against virus.
Shuang Luang Lian	*Lonicera japonica, Scutellaria baicalensis, Forsythia suspensa.*	Clears heat in lungs and protect against virus.
Ma Xin Jan Shi Tang	*Ephedra sinica, Prunus armeniaca, Glycyrrhiza radix, Gypsum fibrosum.*	Protection against virus.

Figure 4. (Yang et al., Traditional Chinese medicine in the treatment of patients infected with 2019-new coronavirus (SARS-CoV-2): A review and perspective, 2020)

3. Siddha formulations

AYUSH Ministry recommends Siddha formulations because they help fight COVID and the symptoms that follow. Among the Siddha formulations, *Kabasura kudineer* is a blend of phytoconstituents of fifteen herbs, which bind to SARS-CoV-2 virus and stop replication of virus and is used to treat fever that comes with some breathing problems by acting against viruses and bacteria and is known to reduce inflammation (Khapre et al., 2023). Another formulation, Nilavembu kudineer, comprises nine main herbs, which include *Andrographis paniculata* and has been proven beneficial in alleviating cough and sore throat symptoms when used with other formulations like Kabasura kudineer (Sruthi D et al., 2023).

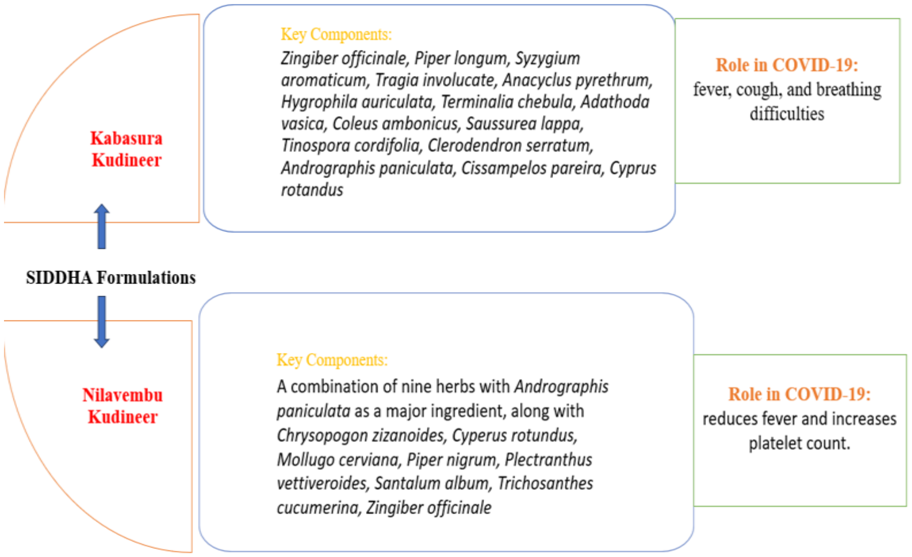

Figure 5. Siddha Formulations and their role against SARS Coronavirus (Sruthi D et al., 2023).

4. Traditional Tibetan approaches:

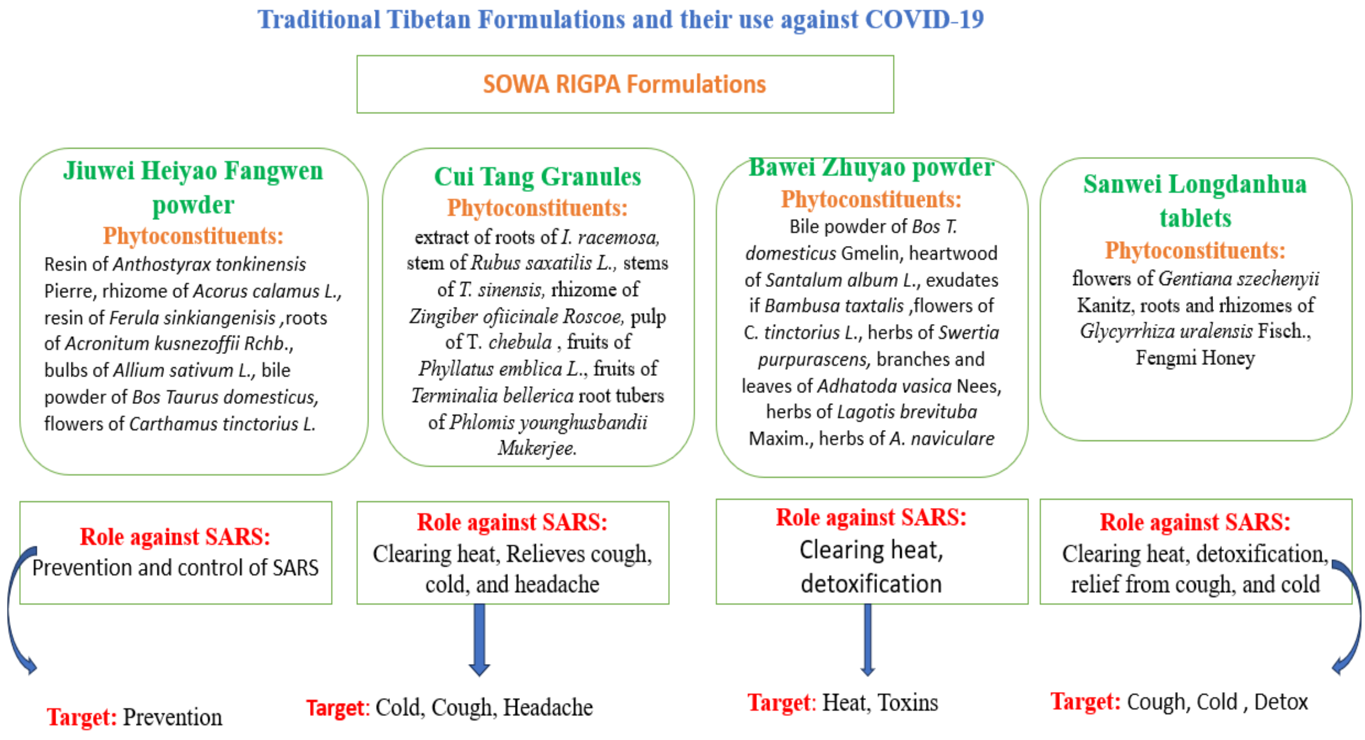

Figure 6. Traditional Tibetan formulations against SARS (Zhang et al., 2023).

5. Naturopathic approaches for COVID-19

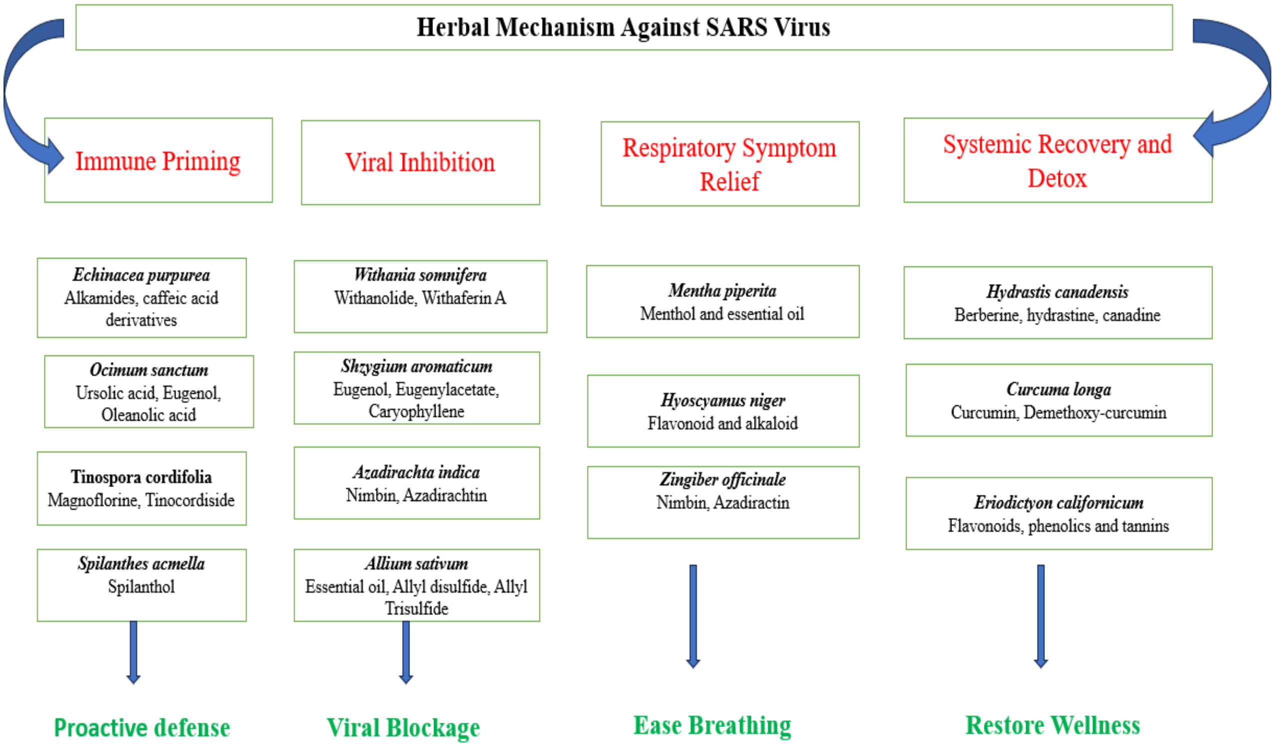

Figure 7. Herbal medicines recommended for COVID patients (Barber et al., 2021) (Kushwaha et al., 2024)

Naturopathy, also termed as nature care, incorporates the use of natural methods to heal the body, enhance immunity, overall well-being and detoxification of individuals suffering from COVID and involves nature-based methods such as hydrotherapy, fasting, dietary therapies, and many more (Juhi et al., 2025). Hot Foot baths, steam inhalation, were some hydrotherapy techniques that help to improve the circulation process in the body, while fasting therapies were also opted favouring autophagy (Raghavan, 2025). Naturopathic approach also justifies the use of vitamins such as Vitamin C, Vitamin D, minerals such as zinc, many probiotics and herbal remedies (Vishwakarma et al., 2022). Herbal medicines are used, prepared by extracting certain phytoconstituents from plant parts and provide immune support (Barber et al., 2021).

Table 5. Potential Vitamins and Minerals for COVID-19 (Barber et al., 2021)

Ingredient	**Potential**
Magnesium chloride	Improve functioning of Vitamin D due to Magnesium; constrains calcium entry in immunocompetent cells; can hinder calcium influx.
Ascorbic acid/Vitamin C	Cytokine storm components are blocked by Vitamin C and decrease ventilation in Intensive Care Unit (ICU) patients.
Methylcobalamin/Vitamin	Leukocyte making and increase macrophage role by Vitamin B12.
Zinc sulphate	Organ damage by hypoxia is reduced by zinc.

The evaluation of traditional medicinal systems through documented case studies demonstrated effective management of mild to moderate COVID-19 cases. Case studies from India, China and others as well revealed consistent patterns: traditional medicines showed effectiveness in early-stage disease management, particularly in reducing extreme respiratory complications and reduce hospitalization duration.

Table 6. Case based clinical evidence justifying efficient role of Ayush kwath

AYUSH Formulation	**Problem observed**	**Clinical features observed**	**Treatment provided**	**Result observed**	**References**
Ayush Kwath	26-year-old computer operator tested positive at COVID center.	Fever, a sore throat, fatigue, and body aches for the last two days and there was no traceable history of contact with a COVID-positive individual.	*Ayush kwath,* 20-30ml in lukewarm water, 60 minutes before meals, *Sanshamani Vati,* 500mg with lukewarm water, three times daily after meals. Dietetic approvals involved bed rest, isolation, warm fluids etc.	Better feeling in patients within the first two days, with relief from common symptoms like fever, loss of appetite, sore throat, and body aches. By the fourth to fifth day, most symptoms had subsided. By the sixth day, few patients regained sense of smell and taste.	(M. Sharma et al., 2021)

Table 7. Case based clinical evidence justifying efficient role of Siddha Formulations

Formulation	**Problem observed**	**Clinical features observed**	**Treatment provided**	**Result observed**	**References**
Siddha formulations **Nilavembu kudineer**	RT-PCR detect COVID-19 in a 39-year-old woman.	Loss of appetite, gastric issues, a bitter taste, mild skin rashes, and frequent loose stools. Pain in all joints and body heaviness by the second day. On the third day, she experienced a progressive loss of smell, followed by a mild sore throat and dry cough.	Joint treatment of Siddha medicine and normal biomedicine, along with nutritional guidance and usual confinement. Nilavembu Kudineer directed two times day-to-day at a quantity of 60 ml, after the beginning of joined treatment.	Patient showed improvement to gradual fading of symptoms without any reported adverse effects. Enhancement in overall well-being was observed, and after 14 days of integrative therapy, another test was done, leading to a negative report.	(Kudineer et al., 2022)
Kabasura Kudineer	COVID test found positive in	Fever, fatigue, and body aches.	60 ml of the decoction was given daily after food to adults,15 ml to	RT-PCR was done for six direct positive contact cases,	(Maideen & Mohamed, 2021)

	certain individuals.		children, for a period of 14 days. This was done while the patients were in a quarantine facility.	and a negative result was observed.	

Table 8. Case based clinical evidence justifying efficient role of Naturopathic approaches

Formulation	Problem observed	Clinical features observed	Treatment provided	Result observed	References
Naturopathy Approach in Prevention of SARS	COVID was found in about 30 individuals.	Majority of complaints among patients were tiredness (90%), myalgias (80%), dry cough (63%), and fever (60%).	Nutrient intravenous therapy for patients who are moderately ill. Echinacea, Elecampane, and Osha, ingredients of the herbal tincture, were credited with immunomodulation and antiviral activity. IV nutrient therapy administered high doses of Magnesium, Vitamin C, Vitamin B12, and Zinc.	No side effects or adverse events associated with the treatments were recorded. Improvement in overall health status was observed	(Barber et al., 2021)

Evidence Interpretation

The review displays possible influence of traditional medicinal systems against COVID-19. Traditional approaches such as Traditional Chinese Medicine have robust evidence, with studies presenting that it helps in reducing symptoms, clears the virus, stops the disease from getting worse, and improves life quality for long COVID. Herbal medicines such as Lianhua Qingwen and Qingfei Paidu decoction are used for mild to moderate COVID as a part of wide range treatment strategy. Ayurvedic medicine reveals promising role such as the AYUSH-64 gives best data, and large studies on prevention offer useful information, even though they have some minor flaws (Sharma et al., 2024e).

Extended COVID-19 Opportunity

Traditional Medicine might help to manage long COVID which is a good chance to combine it with regular healthcare. Long COVID has no approved drugs, involves many health issues and needs ongoing care. This fits well with traditional medicine based holistic approaches. Many studies have shown that Traditional approaches can help with fatigue, overthinking problems and life quality in long COVID. These are most problematic symptoms to treat (Sharma et al., 2024e).

Fairness and Opportunity Framework

Traditional Medicines are usually much cheaper and easier to get than patented COVID-19 drugs in low to middle income countries. Molnupiravir and Paxlovid, are best COVID drugs but were too expensive and hard to find for most COVID patients in places where resources were limited. In this situation. Local traditional medicines that are safe and work well are preferred most and is important for their fair role. The WHO Global Traditional Medicine Strategy 2025-2034`s approach emphasis on universal access to safe, effective and people centred traditional medicines acknowledges this equity dimensional explicitly. Combining Traditional Medicines into national health systems in low to middle income countries, supported by quality regulation and generation of evidence, could considerably improve COVID-19 for future pandemic responses (Sharma et al., 2024e).

Strength and Limitations:

The review tracks macro-evolutionary trajectory of SARS Coronavirus 2 from original Wuhan strain through recombinant era to modern 2026 linages. The paper balances distinct traditional medical philosophies by comparing various multi-target approaches. While the genomic tracking data for new variants is updated through 2026, large scale randomized controlled trails verifying traditional formula efficiency against new recombinant sub-variants fairly constrained.

Future Directions:

COVID-19 virus continuously evolves producing new variants so future research should focus on prioritizing high throughout molecular docking and dynamic stimulations of traditional phytoconstituents against modified spike protein domains of modern 2026 linages. Additionally herbal formulations are made from various constituents whose strength can change depending on conditions where and when those plants were grown. So, future research should focus on creating a chemical blueprint so that every batch made anywhere works same.

Conclusion

The rise of COVID-19 and related signs contributed to a global pandemic, in turn providing a direction towards the development of harmless and operative health care tactics and action methods to slow down the rate of spread of the virus and related death cases. The process of vaccine development also made progress, but over time, the virus began to evolve, several mutations were reported, and a variance in their ability to infect humans was also reported. As the evolution of virus occurs and appearance of new variants continue vaccines and allopathic systems efficiency may decline over time but instead of that traditional systems remain unaffected by these patterns and continue to show their efficient roles. Traditional Chinese Medicine, Traditional Tibetan approaches, Ayurvedic, Siddha systems and their key formulations, such as have shown their potent role in reducing COVID-19 symptoms. These traditional approaches enhance immune response, lower the inflammation process and are efficient during the post-acute phase. Traditional approaches not just attack virus but also helps to improve response of immune system by enhancing the activity of natural killer cells. Thus, the capability to tackle virus depend on the integration of all these systems rather than solely depending on allopathic systems or a single approach.

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The author declares no conflict of interest. The manuscript has not been submitted for publication in another journal.

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Not applicable

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