

AVR-AgDb: A Plant-Based Antiviral Repository to Minimize the Detrimental Effects of Frequent Viral Outbreaks and the Next Pandemic

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SUMMARY

There is an imperative need to investigate less toxic antiviral phytochemicals than nucleic acid analogs, enzyme inhibitors, or synthetic molecules as antiviral therapeutics. Agricultural crops and their secondary metabolites have been well known for their healing and immunity-boosting properties throughout the globe since human civilization. A recent global pandemic, COVID-19, caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), has become one of the most devastating challenges for humans, compounded by increasing diffusion due to migration, global travel, and urbanization. Even before this, about >650K annual deaths had been due to seasonal viral flu disease alone. Dramatic mutations in viruses and the time needed in vaccine development have made the world realize nutrition-immunity intervention as a pragmatic preventive approach for most human viral diseases. In the telecommunications era, an efficient, user-friendly database for searching antiviral plants and their constituents is a prerequisite. Such a database will also facilitate post-COVID economic resilience in the agricultural system. It may also accelerate the research and development of eco-friendly antiviral molecules from natural resources. It further provides classified antiviral molecules with their specific names and structure, their modes of action, and model organisms studied, along with respective literature references. This information can be accessed or retrieved plant-wise, viral disease-wise and chemical compound class/sub-class-wise using a URL (<https://avragdb.abrl.in/>). It comprehensively comprehends about >350 molecules with antiviral properties from >500 plants of medicinal and agricultural importance. The database could be useful for phytotherapy research and spreading the accountability of plant-based antiviral formulations.

Keywords: Database; Virus; Viral diseases; Plant-based; Antiviral compounds; COVID-19; AVR-AgDb.

1. INTRODUCTION

Viruses are the rapidly evolving, minuscule, deadliest obligate infectious agent that replicates within the living cell of an organism (Adeosun and Loots, 2024). They can infect all life domains including Plantae, Animalia, and Archaea and present almost in all ecosystem (Koonin *et al.* 2006). Viruses have been characterized by an acellular, nonliving structure composed of a protein coat called capsid uncoated by nucleic acid (DNA or RNA) and potential of hijacking host machinery to replicate and survive (Adhikari *et al.* 2021, Trivedi *et al.* 2022). The current scenario indicates that most of the devastating pandemics

that occurred throughout human history in terms of mortality were caused by viruses (Piret and Boivin, 2021). A recent ongoing COVID-19 pandemic caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), had caused more than 641 million infections and 6.63 million deaths, making it one of the most life-threatening pandemics in human history (ArcGIS. Johns Hopkins University, 2022). Such disastrous outbreaks are always very frequent and sudden, with diverse symptoms, and are associated with significant mortality and morbidity. The co-relationship between plants and humans has existed since antiquity, and their legacy continues as they are

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basic providers of energy, nutrition, medicine, and other commodities to sustain across the globe (Raven, 2019, Ali *et al.* 2021, Pastor *et al.* 2021). Besides being staple food providers, plants harboring medicinal properties and are considered medicinal plants (Perez, 2003, Ali *et al.* 2021). Nature harbors a plethora of plants that have medicinal properties. Though several plants species possess broad-spectrum antiviral properties, a huge diversity of unexplored medicinal plants has also been shown to reduce a myriad of viral infections (Perez, 2003, Mukhtar *et al.* 2008, Patel *et al.* 2021, Bachar *et al.* 2021, Adhikari *et al.* 2021). Notably, plant-derived active compounds inhibit the spread of highly contagious and often emerging SARS-CoV-2 variants (Al-Beltagi *et al.* 2021, Khuntia *et al.* 2022, Trivedi *et al.* 2022). Moreover, nutritional deficiency has been associated with an impaired immune response allowing virus infestation, but plant-based antivirals, which act as preventive measure exert their effect by boosting the immunity of the host and demonstrating powerful immunomodulation (Singh *et al.* 2021, Patel *et al.* 2021, Alhazmi *et al.* 2021).

Viral outbreaks are frequent and can spread to the point pandemics and tackling viral diseases is technically difficult to cure because they lack the fundamental feature of a living system that can be targeted or modulated by the application of antibiotics, medicine, and other therapeutics (Rolland, 2020). Although targeted pharmaceutical interventions are promising candidate approaches for virus management, however, the spreading speed of the virus is occasionally uncontrolled over incubation time (Rolland, 2020, Adamson *et al.* 2021). In other aspects, it is a time-consuming approach that is not feasible to control viruses with contagious spread, which is frequent in the case of viruses (Sabbaghi *et al.* 2019, Rolland, 2020). The primary defense against any viral infection is counterbalanced by a different layer of the immune system. Plants and derivative products are potent immunomodulators and stimulators that neutralize virus effectiveness (Sultan *et al.* 2014). In addition to immune stimulation, plants and their derivative products inhibit the growth of viral particles in vivo and in vitro, and are considered a potential alternative solution to manage viral diseases up to the greatest extent possible (Amoros *et al.* 1987, Kurokawa *et al.* 1999, Mukhtar *et al.* 2008, Yang *et al.* 2012, Ben-

Shabat *et al.* 2020). The tremendous flora on earth makes it difficult to identify suitable antivirals for immediate action against a specific virus. Information in the form of research articles, literature reviews, and conference papers is not easily accessible to laymen or intended users. In the era of telecommunication, the database could be an asset to expand and retrieve information using electronic gazettes. Although, antiviral peptide database has been developed covering over 60 important viruses (Qureshi *et al.* 2014), to provide speedy progress on antiviral vaccines and drugs (Coulibaly, 2021), development of multiple databases for the calamitous SARS-COVID-19 (Aher and Sarkar, 2021), and a recently developed curated database of plant-derived antiviral phytochemicals, integrating information relevant to major diseases such as cancer (Ullah *et al.* 2023), and another more recently developed novel and comprehensive antiviral biodiversity-derived medicinal plant with natural product information is presented (Quadros de Azevedo *et al.* 2024), however, the comprehensive repertoire of regional medicinal and aromatic plant and antiviral product derivatives database is still unreachable. It is therefore necessary to develop a comprehensive up-to-date information system with user-friendly access for devastating viral disease management. To implement the aforesaid idea, we have developed a database called “AVR-AgDb,” a collective repository of the plant-based anti-viral drugs that entails their origin, efficacy, and usage for viral disease management in economic and sustainable ways. It will be a remarkable archive to mitigate deleterious virus invasions in eco-friendly and efficient ways to improve life and prolong survival.

2. MATERIALS AND METHODS

2.1 Data acquisition

A pertinent holistic concomitant literature survey was performed by “PubMed”, “Scopus”, “Web of Science” and “Google scholar” with the keywords “Plants derived antiviral molecules” or related words viz. alkaloids, polyphenols, lignin, etc. All the scientifically significant contribution to plant-based antiviral molecule has been taken into consideration with well-described methodology and results. Gathered literature on sixteen major viral diseases with the highest mortality and morbidity and their causative agents has been aligned and

tabulated in the form of a virtual cascade. These are HIV (Human immunodeficiency virus) (Douek *et al.* 2009), Severe acute respiratory syndrome coronavirus 2 (Hu *et al.* 2021), Herpes simplex virus (Whitley and Roizman, 2001), Hepatitis virus (Quer *et al.* 2017), Influenza and parainfluenza virus (Liu *et al.* 2020), Respiratory syncytial virus (Griffiths *et al.* 2017), Vesicular stomatitis virus (Gangal *et al.* 2020), Measles virus (Griffin *et al.* 2012), Coxsackieviruses (Baboonian *et al.* 1997), Poliovirus (Racaniello, 2006), Japanese encephalitis virus (Endy and Nisalak, 2002), Rhinovirus (Denyer *et al.* (1994), Vaccinia virus (Cryer *et al.* 2017), Dengue virus (Phumesin *et al.* (2023), Zika virus (Sharma *et al.* 2017) and Astrovirus (Kudi and Myint, 1999). Further, search accelerate on a repertoire of plant metabolites with specific antiviral action on virus pathogenesis. For example. Lignans, a huge class of compounds consisting of two phenyl propane units exhibit antiviral effects against a wide array of viruses (Xu *et al.* 2021). Polyphenols restrict viral invasion by innumerable modes of action (Kamboj *et al.* 2012). An important class of natural compounds is alkaloids which provide broad-spectrum antiviral resistance using diverse acting modes (Abookleesh *et al.* 2022). An essential phyto-compound terpenoid activity has been evaluated in the long past against acute respiratory syndrome-associated coronavirus (SARS-CoV) using a cell-based assay (Wen *et al.* 2007). Other major classes viz. Cyclotides are potent antiviral (Ireland *et al.* 2008), post-translationally modified peptides (RiPPs) (Fu *et al.* 2021), Lectins (Ahmed *et al.* 2022), Antimicrobial peptides of plants origin (Mammari *et al.* 2021), Lipid transfer proteins (LTPs) (Maximiano and Franco, 2021) and many more classes of known bioactive compounds harboring antiviral properties (Ghildiyal *et al.* 2020, Thomas *et al.* 2021). All-inclusive has taken together, we acquire an exhaustive literate survey on plant-based potential antiviral compounds and their derivatives, further cataloged them as a database for user-friendly accession and retrieval.

2.2 Database Development and Architecture

A web resources “AVR-AgDb” has been developed with three-tier architecture, namely, a client tier, middle tier, and database tier (**Fig. 1**) (Yang *et al.* 2008, Malgwi *et al.* 2018). XAMPP framework was used to design and deploy the web page technology described (Walia and Gill, 2014, Goyal and Gill, 2021). Briefly, the website

framework was made using HTML, followed by design using CSS and dynamic JavaScript with a Linux platform for the operating system (Al-Hawari *et al.* 2017) combined with HTTP apache server to facilitate functioning using multi-processing modules (Do *et al.* 2008). Further, using PHP programming language assisted MySQL has been deployed for the relational database management system (Walia and Gill, 2014, Iquebal *et al.* 2017, Malgwi *et al.* 2018). It comprised the MySQL backend enforces primary key, foreign key, unique, and NOT NULL constraints to maintain consistency and prevent redundancy. The PHP frontend performs input validation and sanitization to ensure accurate data entry. Secure data exchange is achieved using prepared statements and parameterized queries, while transaction management ensures atomic and consistent database operations (Iquebal *et al.* 2017). The whole architecture comprised a webpage with the title “AVR-AgDb: A database for antiviral agricultural crop produce and phytochemical” with four icons namely “Home”, “Virus wise search”, “Plantwise search”, and “Team”. Icon “Home” comprised basic information about viruses and the defensive role of the plant-derived bioactive compound against the deadliest virus. Another icon displayed on the webpage is “Virus-wise search.” It represents an option to choose a virus, clicking on assigned icons reflects sixteen different kinds of viruses and one can choose a single virus at a time which further redirects another page with full details of concerning viruses. These parameters include the common scientific name of plants, common name, virus types, potential bioactive compound, plant part used or extract types, assessed model organism to check efficiency and efficacy, their mode of action on cellular protein and other mechanism, and related reference for further understandings. Beside others, icon for plant scientific name, active compounds and references link can be further redirect to extend the further evaluation and reading upon user interest. Interestingly, it will take user through details of each parameter viz. plant’s morphology, their biochemical composition and medicinal properties for a specific disease and pathogens. Likewise, icon active compounds can redirect to the largest repository of freely accessible chemical information “PubChem”, which further could be used for *in silico* studies on various novel antiviral formulation development by predicting

their affinity for enzyme and target protein through docking and simulation and other bioinformatics tools and techniques. Moreover, references can be further redirected for cross-reading and validation of the functionality of active biomolecule, synergistic effects of other biomolecule and experimental authenticity. Overall, the developed database could be accessed in easily operated ways with top to bottom retrieval of the plant-based antiviral compound for their downstream use and further research.

2.3 Database Statistics

It catalogs antiviral molecules derived from >500 plants along with their activities against sixteen catastrophic human viral diseases. Similarly, It contains about >350 molecules of antiviral properties with different biochemical and molecular compositions. These are putative of the approximate target of diverse viral types of machinery. It contains about 33 selected compounds for Human immunodeficiency virus (HIV), 108 searches for bioactive molecules for the Herpes simplex virus (HSV), 31 references for the Influenza and Para-influenza virus (IV and PIV), 9 molecules for the Respiratory syncytial virus (RSV), and 15 plant derivatives of antiviral properties for Vesicular stomatitis virus (VSV), 13 antiviral plants for Hepatitis virus (HV), 17 phyto-virals compounds for Measles virus (MV), 30 plants derivatives for (CSKV) Cocksackieviruses, 27 for Poliovirus (PV), 17 for Japanese encephalitis virus (JEV), 24 for Rhinovirus (RV), 11 for Vaccinia virus (VV), 12 for Dengue virus (DV), 39 for Zika virus (ZV), 6 for Astrovirus (AV) and about 126 phyto-compounds for Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). Overall, it contains a comprehensive module for different antiviral molecules for most life-threatening virus and their related belongings. Similarly, about >500 easy access concerned references have been provided to recheck or reconfirm and further reading and evaluation. Furthermore, there are two modes of data retrieval and accesses available to make it an easily operated web system to find active antiviral biomolecules of interest against a particular viral disease. The overall statistics of the antiviral database comprises about >500 medicinal and aromatic crops, their global presence, the bioactive ingredient with antiviral properties, mode of action, and their efficacy on used plant part or extract type on the tested model organism or specific cell lines. These

statistics could be a prerequisite for future plant-based antiviral formulation and derived medicinal use for the sudden viral outbreak and subsequent infestation.

3. RESULTS

3.1 Database Background and Configuration

We have developed an antiviral database “AVR-AgDb” by compiled information retrieved from holistic literature search on antiviral medicinal plants, their ingredients, with few of them with agricultural importance. A gathered exhaustive table has been utilized to put together all authentic to generate a database which could be accessed and retrieved by using link (<https://avragdb.abrl.in/>). By clicking on the mentioned link, it will redirect to database home page where it features a title along with five main icons namely “Home”, “Virus wise search”, “Plant wise search”, “Compound wise search” and “Team”. Icon “Home” reflects basic information about cataclysmic viruses and their causative disease, discussed virus on database and utility of developed database for managing viral disease efficiently. Icon “Virus wise search” open a window upon clicking reflecting name for discussed virus on databases. A further click on particular virus name fetch information about antiviral behavior of respective plants for concerned virus in a series of Plant name, Common Name, Virus, Active compounds, Plant part and extract type, Model organism/Cells/ Assay, Mode of action and References. Clicking on icon “Plant name”, “Active compounds” and reference further redirect the webpage for further information.

3.2 Database Utilization and Retrieval

The developed database has been deployed in user-friendly ways. The user can fetch the data from the database and execute the query fired by the user in three ways. The intended user can search “Viruses wise search” “Plant-wise search” and “Compound wise search” using search option. One can choose a particular virus from the dropdown menu and click ‘Submit’. It will fetch data from the server. In addition, users can click on a particular plant name to know more by redirecting to the concerned “Wikipedia” webpage. Users can also click for active compounds reported in particular studies which allow user to redirect the “PubChem” page further analysis and evaluation. It will enlighten the chemistry of concerned antiviral

compound and open a window to screen more additive and efficient molecules with potent effects via chemical synthesis and modification. For further access reference, links are also provided. Furthermore, the user can click on “Plantwise” to get an alphabetically arranged letter with numerals representing number of studied plants whose name starts with similar alphabetical order, which upon clicking on the intended letter retrieves another page containing information on the antiviral plant for the questioned letter. It will be allowed the user to access all the plants whose names started from the same letter all along with complete information on particular queries viz. plant common name, virus categories, active ingredients, used plant part, prepared extract type, screened model system, acting mode on viral machinery and concerned reference for further explanation and troubleshoot. “Compound wise search” delineate number of compounds which starts with given alphabetical acronyms with numerals representing the number of compound name started with similar alphabet. Any clarification on the proper functioning and possible update of database-related issues could be rectified by clicking on the icon “About” which will facilitate the affiliated person’s profile and contact details.

4. DISCUSSION

Applications of “AVR-AgDb” have been described by three interesting case studies, viz., farmers (local level), agricultural export (global level), and researchers’ benefit, taking the example of the COVID-19 outbreak. Case study 1 reports that if farmers are advised with prudent policy, then in post COVID world, farmers can have better return. This is the case in India where there is tenfold price difference has been seen if a farmer changes the crop from rice to Lavender, an essential oil crop that is known for its antibacterial and antiviral properties (Fidanka, 2021, Abou Baker *et al.* 2021). Essentials oils (EO) are extremely volatile mixtures of mainly mono- and sesquiterpenoids, phenylpropanoids, etc., which can easily reach both the upper and lower parts respiratory tract via inhalation (Cavanagh and Wilkinson, 2002, Abou Baker *et al.* 2021). It has antimicrobial and anti-inflammatory potency in the effective treatment of respiratory tract infections (RTIs) (Cavanagh and Wilkinson, 2002, Pandur *et al.* 2021). Essential oil plays a preventive role in the treatment of

RTIs most effectively by its volatile nature by reaching the intended site of treatment. As per WHO estimates, lower RTIs and chronic obstructive pulmonary disease (COPD) remain the top major killers during the past decade causing 5% of deaths worldwide (3.1 million people) (Horvath and Acs, 2015). Apart from the farmer’s profitability case, if the environmental cost in terms of water foot printing of rice (2000–3000 liter/kg) is compared with the lavender plant it’s drastically very low. This demonstrates that there is a need for a paradigm shift in crop selection in the tune of the post-COVID world for faster economic resilience as well as a new opportunity with better income and environmental sustainability as well. Therefore, “AVR-AgDb” can be an easily accessible and cataloged atlas for the farmers which can direct and accelerate the advantage of medicinal plant propagation over staple crop in post COVID world.

Case study 2 reports how the viral outbreak has dramatically impacted the global market for agricultural and horticultural crops with medicinal values. Their consumption has been elevated by about 30% as observed in the case of the demand for garlic and turmeric in many countries (Budhwar *et al.* 2020, Hamulka *et al.* 2021). A similar trend has been seen in many other crops having antiviral activities in various parts of the world (Budhwar *et al.* 2020). This was well predicted in the FAO report, “Future Trend of Crops” that there will be high demand for anti-viral crop and their produce in the next few decades reflects a paradigm shift in crop production (Salmeron-Manzano *et al.* 2020, Mukherjee *et al.* 2021).

Case study 3 describes how this “AVR-AgDb” can be used for in silico evaluation of antiviral molecules before in vitro or in vivo assay is performed by taking the example of targeted viral protein and enzyme molecule from PDB (<http://www.rcsb.org/pdb/>). The antiviral phytochemical compound from “AVR-AgDb” can be obtained from Drug bank and PubChem in .sdf format. To evaluate bioactivity via oral administration and in silico analysis of absorption, distribution, metabolism, and excretion (ADME) for its drug-like properties can be calculated using Lipinski’s rule of five using SWISSADME prediction (<http://www.swissadme.ch/>) (Lipinski, 2004). The active site can be predicted by structural analysis of the binding pocket using CASTp 3.0 software (

uic.edu/castp/). As a representative example of the in silico workflow, resveratrol derived from Peppervine was docked against the SARS-CoV-2 main protease (Mpro) and the molecular docking analysis yielded a binding affinity score of [e.g., -7.8 kcal/mol], indicating a favorable interaction with the active site residues. Key interactions included hydrogen bonding with residues such as His41 and Cys145, which are critical for protease activity strengthen the practical applicability of the database for rapid screening and prioritization of antiviral compounds. Furthermore, the ligand-binding pocket located in the catalytic site can be obtained manually and then verified by a modified priori docking approach (Sellers and Hurley, 2016). The determination of the amino acids in the active site can be used to analyze the grid box and docking evaluation results. A molecular docking study can be done to get insight into the most preferred binding mode of the selected natural antiviral compound into the binding active site of the enzyme of animal virus (Cherrak *et al.* 2020, Gupta *et al.* 2021). The ligand binding affinity with the active site of the enzyme can be confirmed by energy score (S, Kcal/mol) (Yuce *et al.* 2021). Molecular docking can be performed using the crystal structure of a viral targeted protein using Autodock 4.2 (Rizvi *et al.* 2013, Khaerunnisa *et al.* 2020). The results obtained from the docking simulation can be visualized with the Pymol version 1.7.4.5 Edu. (Gad *et al.* 2021). Structural conformations of proteins can be improved by MDS (Hospital *et al.* 2015). The structural flexibility of the selected natural compounds can be analyzed by CABS-flex 2.0 server (Kuriata *et al.* 2018, Badaczewska-Dawid *et al.* 2020). Toxicity analysis of selected antiviral compounds can be done in the virtual lab of the ProTox-II web server which integrates several parameters like molecular similarity, fragment propensities, and most frequent features (Banerjee *et al.* 2018). Similarity with FDA-approved drug compounds can be searched with SWISS similarity (<http://www.swiss similarity.ch>) for the best binding energy among the selected natural compounds.

4.1 Significance Of AVR-AgDb design

In the era of technical development, databases exist as a single unit of multi-functioning. It refers to the collection of data (files and records) which can be stored and manipulated using integrated software and its management systems (Fig. 2) (Yang *et al.* 2008,

Qureshi *et al.* 2014). It can reduce the amount of time to retrieve data on intended medicinal plants and crops to analyses the collective quality and consistent data in multiple ways (Qureshi *et al.* 2014, Aher and Sarkar, 2021). To our best knowledge, though, surplus literature exists, there is no such database that has been developed on the plant-based antiviral molecule, their cataloging, and management for threatening virus families. It can provide updated and improved data sharing to the farmers and users. It also broadens the existence of diverse antiviral molecules, their origin, and dispersal, and their usage as preventive and post infections measures on a local and global scale. It may allow us to find an antiviral molecule with regional importance and availability on a socioeconomic scale. Notably, it will assist herd immunity upon consumption by a community, especially in developing countries where a tremendous population is densely packed. In addition to benefit, certain limit also exists to running the database in a well-planned manner and often suffer failure in internet connectivity which in turn cause a severe negative impact on the operation.

5. CONCLUSION

Our proposed “AVR-AgDb” database can be a research-accelerating tool before conducting in vitro and in vivo viral assays. It can be used for designing in silico viral protein and phytochemical simulation dynamics studies to select the most potent molecule saving time and cost with the rapid evaluation of a large number of antiviral molecules. Since the database contains >500 authenticated references, thus any new molecule can readily be searched for quick literature validation. This database may help in developing nutritional guidelines in the post-COVID era where a paradigm shift is expected to have a balanced diet with locally and regionally available antiviral agricultural produce based on standard guidelines, making the best use of available anti-viral agricultural produce. This single point source database for antiviral bioactive molecules will be of multifarious use in the endeavor to reduce the economic burden for small, medium, and large economies and also for better innate immunity of the human population for the future threat of unforeseen viral outbreak at endemic or pandemic level. Further featuring other classes of viruses and regular updation will allow it more robust and popular database among

phytochemical societies and researchers across the world.

5.1 Data Availability

The authors confirm that the data supporting the findings of this study are available within the article or its supplementary materials.

5.2 Abbreviations

SARS-CoV-2: Severe acute respiratory syndrome coronavirus 2, AVR-AgDb: Antiviral agricultural based database, URL: Uniform resource locator, HIV: Human immunodeficiency virus, HSV: Herpes simplex virus, IV and PIV: Influenza and para-influenza virus, RSV: Respiratory syncytial virus, VSV: Vesicular stomatitis virus, HV: Hepatitis virus, MV: Measles virus, CSKV: Cocksackieviruses, PV: Poliovirus, JEV: Japanese encephalitis virus, RV: Rhinovirus, VV: Vaccinia virus, DV: Dengue virus, ZV: Zika virus, AV: Astrovirus, RiPPs: post-translationally modified peptides, LTPs: lipid transfer proteins, HTML: Hypertext markup language, CCS: Cascading style sheets, XAMPP: X-operating system, Apache, Mysql, Php, Perl, EO: Essentials oils, RTIs: Respiratory tract infections, WHO: World health organization, COPD: Chronic obstructive pulmonary disease, FAO: Food and agriculture organization, PDB: Protein data bank, ACE: Acetylcholinesterase, ADME: absorption, distribution, metabolism and excretion, CASTp 3.0: Computed atlas of surface topography of proteins, MDS: Multi-dimensional scaling, CABS-flex 2.0: Classical simulations of protein flexibility, ProTox-II: Prediction of TOXicity of chemicals

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AUTHOR CONTRIBUTIONS

SJ, MAI and DK conceived theme of the study. TC, SKD, SJ and MAI collected and curated all information; BS and UBA designed and developed the database; TC,

SJ and MAI drafted the manuscript; MAI, AR and DK reviewed and edited the manuscript; all authors read and approved the final manuscript and contributed to the article and approved the submitted version.

CONFLICT OF INTEREST

The authors declare that they have no competing interests.

Ethical approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Author Contributions

SJ, MAI and DK conceived theme of the study. TC, SKD, SJ and MAI collected and curated all information; TC, SJ and MAI drafted the manuscript; MAI, AR and DK reviewed and edited the manuscript; all authors read and approved the final manuscript and contributed to the article and approved the submitted version.

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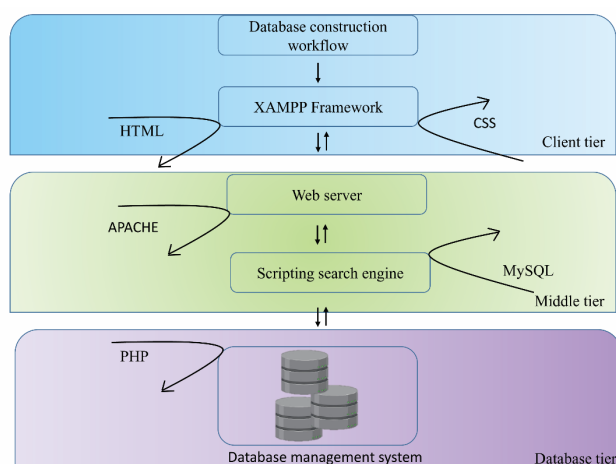


Fig. 1 A web resource, AVR-AgDb: A plant-based antiviral repository was created using the three-tier architecture viz. client, middle, and database tier to contain all the collective and compiled results on plant-based antiviral molecules, their characteristic features. XAMPP framework was used to design and deploy the webpage. The website framework was made using HTML, designing was done by using CSS, and was made dynamic using JavaScript, while software Apache was used as the web server, the website was supported by the MySQL database in the backend, and PHP was used as the server-side language and for database connectivity.

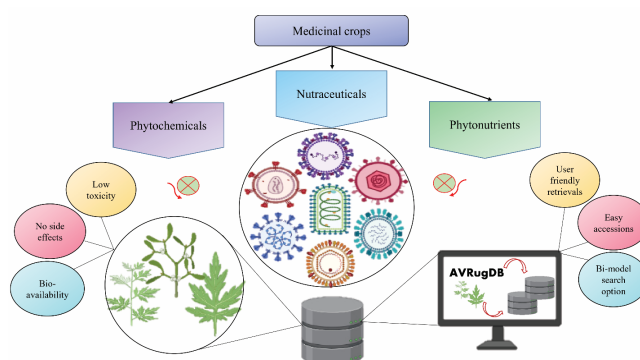


Fig. 2. The cartoon diagram summarizes that medicinal agricultural crops produce three kinds of phyto-compounds. These are phytonutrients, nutraceuticals, and phytochemicals. These plants' derivative antiviral compounds are used as preventive antiviral measures or utilized post-viral infection. These compounds act directly on the virus life cycle or boost host immunity in multifarious ways. A centrally developed database collectively provides user-friendly access to known antiviral molecules, their mode of action, and other necessary related information with a single click. Bi-model search option makes it more effortless to find plant-based antiviral molecules for the sixteen deadliest viruses. The virus and database figures have been fetched from BioRender (<https://biorender.com/>).