ISSN PRINT 2319 1775 Online 2320 7876

Research paper UGC CARE Listed (Group -I) Journal Volume 11, S Iss 1,2022

Phyllanthus Species Clustal-W Program For Neighborhood Evolutionary Analysis

Dr Manisha[1]
Associate Professor and Head of Botany Department, Chinmaya Degree College, BHEL, Haridwar, Uttarakhand, manisha26solanki@gmail.com

Bandari Srinivas[2]
Asst Prof of Chemistry, Research Centre, Dept of Chemistry,
SR & BGNR Govt Arts & Science College (Autonomous) Khammam, Khammam-District.
Telangana-507002 , bannubandari@ gmail.com

Dr. Aarti Chouhan[3]
Assistant Professor of Botany
Government Maharani Laxmi Bai Girls PG College, Indore MP India
Affiliation: Devi Ahilya Vishwavidhya, Indore MP India
aarti8090@gmail.com

Dr Arti Gupta[4]
Prof of Chemistry
Affiliation Jiwaji University, Gwalior
artiguptachemistry@gmail.com

ABSTRACT

For efficient use as food and medicine, accurate identification of species of medicinally important plants is valuable. The goal of the study is to identify the critical macro and micro morphological characteristics for diagnostic purposes and to determine the evolutionary connections of two medicinal crops sequence. The two taxa of our species group's sequences, *Phyllanthus amarus* and *Phyllanthus tenellus*, were taken from the national center for Biotechnology's technological home page. Utilizing the neighbours joining strategy, the evolutionary history was deduced. The morpho-anatomical features are regarded as important diagnostic indicators for verification of. It is clear that the genus Phyllanthus tenellus belongs to the phyllanthacae family, which has been studied earlier in current taxonomic schemes.

Keywords: Medicinal plants, Evolutinary analysis, Phylogenetic tree, Hidden markov model

ISSN PRINT 2319 1775 Online 2320 7876

 UGC CARE Listed (Group -I) Journal Volume 11, S Iss 1,2022

INTRODUCTION

The Indian Ayurvedic medical system frequently uses Bhumyaamalaki (*Phyllanthus amarus Schum. & Thonn., Euphorbiaceae*), which is widely distributed throughout tropical and subtropical nations of the world, including India, to treat issues with the stomach, genitourinary system, liver, kidney, and spleen. According to Ayurveda, *P. amarus* is known by the Sanskrit names Bhoomyaamalakee, Taamalakee, and Bhoodhatree. It was said to have Rasa, Guna, Veerya, and Vipaaka qualities. Kaasahara (antitussive), Shwaasahara (antispasmodic, antidyspneic), Kaphapittahara (alleviates Kapha Pitta Dosha), Pipaasaaghna (alleviates Polydipsia), Raktapittahara (alleviates haemorrhage disease), Paanduhara (antianemic), Kaamalaahara (alleviates jaundice) (which cures urinary disorders). Due to *P. amarus*' novel antiviral activity against the hepatitis B virus and other biological activities like kidney and gallbladder stones, colds, flu, tuberculosis, and other viral infections; liver diseases and disorders including hepatitis, jaundice, and liver cancer, the use of *P. amarus* is expanding [1]. It has been discovered to be effective against hepatitis A and works to enhance patients' immune systems while also acting to prevent liver cell damage [2]. In the traditional medical system, *P. amarus* is often prescribed for a number of conditions, including dropsy, diabetes, jaundice, asthma, and bronchial infections [3]. It is used in the Ayurvedic medical system to treat issues with the spleen, liver, kidney, liver, and genitourinary system. It has antibacterial, astringent, stomachic, diuretic, and bitter properties. For gonorrhoea, menorrhagia, and other genital afflictions, the whole plant is utilized. It helps with ulcers, wounds, intermittent fevers, scabies, gastropathy, diarrhoea, and dysentery. It works well as a tonic as well. Several plant species from the Phyllanthus genus have been studied phyto chemically and pharmacologically, and numerous compounds have been extracted and identified.

The two species of *Phyllanthus tenellus Phyllanthus amarus* are included in this review. The protein sequences of *Phyllanthus tenellus* were compared, with numerous alignments in Clustal Omega, construction of a dendogram, and study of the phylogenetic evolutionary relationships between the several taxa.

ISSN PRINT 2319 1775 Online 2320 7876

Research paper UGC CARE Listed (Group -I) Journal Volume 11, S Iss 1,2022

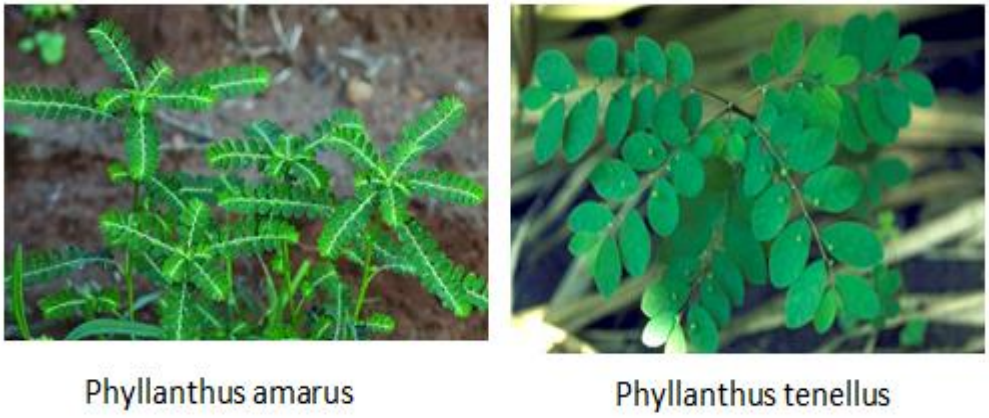

Fig. 1: Phyllanthus species

Methodology

Retrieved the sequence

The protein sequences of the *Phyllanthus amarus Phyllanthus tenellus* species of medicinal plants were obtained from NCBI (National Center for Biotechnology Information).

Omega 2.2 Clustalw (multiple sequence alignment)

It is a brand-new multiple sequence alignment tool that creates alignments between three or more sequences using HMM profile-profile and seeded guide tree approaches. Tools for sequence alignment employ substitute pairs to align two sequences [4].

Basic phylogeny

Typically, the first stages include setting the software input protein sequences, NCBI database. The user may alter the instrument variables by default in the subsequent phases. The tool submission step is always the last step where the user may provide a heading in connection to an email address for email notice and result. Utilizing the submit button will only send the appropriate data from the form to the server, initiating the tool [5].

Input alignment

Input window 2.5

A supported format for phylogeny using an alignment may be entered straight into the input box. Supported alignment formats include Clustal, FASTA, and MSF. Sequences that are partially formatted or out of alignment won't be accepted. A return may be placed at the end of the sequence to help the straightforward Phylogeny tool reorganize the input. Direct access

ISSN PRINT 2319 1775 Online 2320 7876

Research paper UGC CARE Listed (Group -I) Journal Volume 11, S Iss 1,2022

to the data of a word processor might provide unpredictable outcomes in the form of control or hidden letters.

Uploaded files

An uploaded alignment is used in phylogeny. Clustal, FASTA, and MSF are supported alignment file formats. Unaligned or partially structured sequences are often excluded. The basic Phylogeny tool can grasp the input better if a return to the final segment of the sequence is introduced. The yield of control/hidden characters may be directly derived by using the data of a word processor. Direct access to the data of a word processor might provide unpredictable outcomes in the form of control or hidden letters.

Put in Parameters

Tree layout

It is based on this that the Simple Phylogeny tool generates its results.

Table 1: Simple Phylogeny tool results

FORMAT	DESCRIPTION	VALUE
DEFAULT	Tree file in the Newick/PHYLIP format	phylip
CLUSTAL	In addition to the PHYLIP tree, clustal format file	nj
DISTANCE MATRIX	In addition to the PHYLIP tree, a distance matrix file is used.	dist
NEXUS	The PHYLIP tree and a file in the NEXUS format	nexus

Distance correction

This controls the simple Phylogeny's attempt in correcting the substitutions multiple times on same site. That is made to be 'on' for extra divergent sequences and it has the effect of branch lengths stretching. Reliable corrections of distances are disabled for more divergent sequences [6].

ISSN PRINT 2319 1775 Online 2320 7876

Research paper UGC CARE Listed (Group -I) Journal Volume 11, S Iss 1,2022

Leave spaces out

With this option, gaps in the input sequences are often eliminated, enabled columns are forced to take up the optimal locations, and alignments are made to include all of the sequences' information.

System for clustering

The neighbours-joining technique is used in this method to construct trees out of the distance matrix. The quick UPGMA tree construction technique is used [7,8].

Submission

Work Title

It is possible to locate the tool result by providing a name. Almost all graphical representations of results will include the title, which will be related to the outcomes.

Notification through email

Running a tool involves a combination of methods, and once the results are ready, they are given right away to the browser. Time will vary depending on the instrument and its input settings. By checking the box next to "Be alerted by e-mail," it is possible to receive a notice while finishing the task through electronic mail. The email address provided in the appropriate text field may get a message including a link to the findings. For email alerts, email addresses must be current [9, 10].

Phylogenetic tree generated from 10 Phyllanthus sequences shown graphically. *The amarus Phyllanthus in Phyllanthus tenellus,* 100% sequence similarity was shown by the hypothetical root of a straight line, whereas non-sequence similarity was indicated by branch length. Neighbor-joining is used to create dendograms. The findings demonstrate how the many types of therapeutic plants have evolved.

Results

Sequence retrived

ISSN PRINT 2319 1775 Online 2320 7876

Research paper UGC CARE Listed (Group -I) Journal Volume 11, S Iss 1,2022

```
>AWA46134.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large
subunit, partial (chloroplast) [Phyllanthus amarus]
KLTYYTPDYETKDTDILAAFRVTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPV
AGEENQYIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPPAYSKTFQGPPHGIQVERD
KLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLR

>UNJ21533.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large
subunit, partial (chloroplast) [Phyllanthus amarus]
LTYYTPEYETKDTDILAAFRVTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDRDKGQCYHIEPVA
GEETQFIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPPAYTKTFQGPPHGIQVERDK
LNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEAIFKSQAE
TGEIKGHYLNATAGTCEEMIKRAVFARELGVPIVMHDYLTGGFT

>UNA06836.1 maturase K, partial (chloroplast) [Phyllanthus amarus]
LVQTLRYWVKDTSSLHLLRFFLHEYWNWNSLIFPNNFISFFSKSNPRLFLFLYNSHVYEYESIFFFLRKQ
SFHLRSTFFRVLLERIFFYGKIEHFAEVFANDFQAILLLFKDPFMHYVRYQGKSILASKDTPLLIKKWKN
YLVNLCQCHFSVWFQPAKICINPLSKRPLDFLGYLSSLRLNLSVVRSQMLENAFLINNAMKKVDTRIPLF
PLIRSLAKTKFCNAAGHPISQPIWAGSSDSDIINRFVRICRN

>UIE35002.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large
subunit, partial (chloroplast) [Phyllanthus amarus]
KLTYYTPEYETKDTDILAAFRVTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPV
AGEETQFIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPPAYTKTFQGPPHGIQVERD
KLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLR
```

Figure 2: protein sequences for the *Phyllanthus amarus* and *Phyllanthus tenellus* species obtained from NCBI

Sequence submission

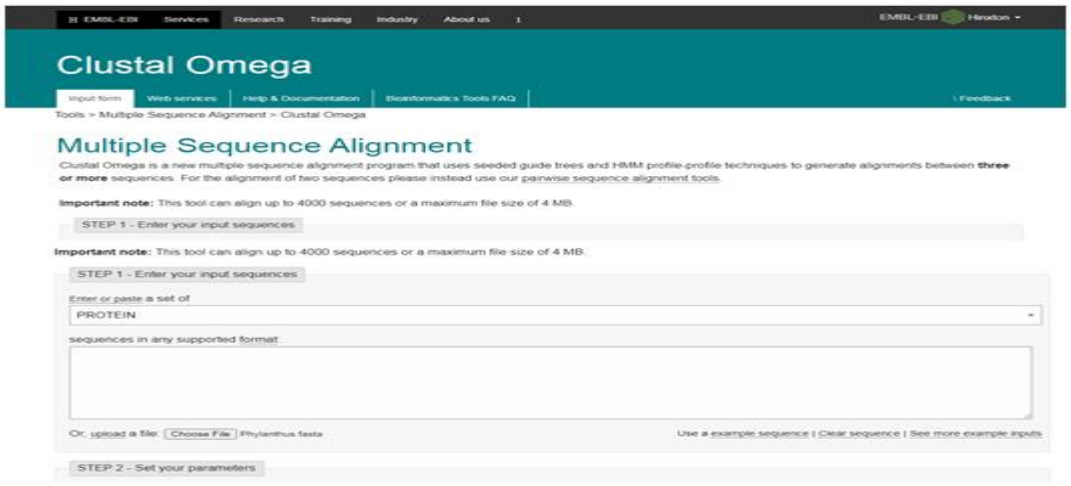

Fig:3 *Phyllanthus amarus and Phyllanthus tenellus* species FASTA document sent to server.

Multiple sequence alignment in Clustal omega HMM profile

ISSN PRINT 2319 1775 Online 2320 7876

Research paper **© 2012 IJFANS. All Rights Reserved, UGC CARE Listed (Group -I) Journal Volume 11, S Iss 1,2022**

```
UNA06836.1          LVQTLRYWVKDTSSLHLLRFFLHEYWNWNSLIFPNNFISFFSKSNPR--LFLFLYNSHVY      58
QBJ26842.1          ---------KETSSLHLLRFFLHEYWNWNSLIFPNNLISFFPKSNPR--LFLFLYNSHVY      49
YP_009776627.1      -------------------MAIHLYKTST-PSTRNGAVDSQVKSNTRNTRKNLIYGQHRC      40
AWA46134.1          ------------------------------------------------------------      0
UNJ21533.1          ------------------------------------------------------------      0
UIE35002.1          ------------------------------------------------------------      0
AUW55867.1          ----------------------------------------------TET-----------      3
AWX41228.1          ------------------------------------------------------------      0
AWX41226.1          ------------------------------------------------------------      0
AWX41220.1          ------------------------------------------------------------      0

UNA06836.1          EYE----SIFFFLRKQSFHLRSTFFRVLLERIFFYGKIEHFAEVFANDFQAILLLF---K      111
QBJ26842.1          EYE----SIFFFLRKQSFHLRSTFFRVLLERIFFYGKIEHFAEVFANDFQAILWLF---K      102
YP_009776627.1      GKGRNARGIIT-ARHRGGGHK-----------RLYRKID-----FRRNEKDIYGRI----      79
AWA46134.1          ---------------------K-----------LTYYTPD-----YETKDTDILAAFRVTP      24
UNJ21533.1          ------------------------------LTYYTPE-----YETKDTDILAAFRVTP      23
UIE35002.1          ---------------------K-----------LTYYTPE-----YETKDTDILAAFRVTP      24
AUW55867.1          ---KASVGF----KAGVKEYK-----------LTYYTPD-----YETKDTDILAAFRVTP      40
AWX41228.1          ----------------VKEYK-----------LTYYTPD-----YETKDTDILAAFRVTP      28
AWX41226.1          ----------------VKEYK-----------LTYYTPD-----YETKDTDILAAFRVTP      28
AWX41220.1          ----------------VKEYK-----------LTYYTPD-----YETKDTDILAAFRVTP      28
                                                    * . :     : .   *   :

UNA06836.1          DPFMHYVRYQGKSILASKDTPLLIKKWKNYLVNL----CQCHFSVWFQPA---KICINPL      164
QBJ26842.1          DPFMHYVRYQGKSILGSKDTPLLIKKWKNYIVNL----CQCHFSVWFQPA---KICINPL      155
YP_009776627.1      ------------------------------------------VTIEY-DPNRNAYICLIH-      96
AWA46134.1          QPGVP-PEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPVAGEENQYIAYVA-      82
UNJ21533.1          QPGVP-PEEAGAAVAAESSTGTWTTVWTDGLTSLDRDKGQCYHIEPVAGEETQFIAYVA-      81
UIE35002.1          QPGVP-PEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPVAGEETQFIAYVA-      82
AUW55867.1          QPGVP-PEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPVAGEETQFIAYVA-      98
AWX41228.1          QPGVP-PEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPVAGEETQFIAYVA-      86
AWX41226.1          QPGVP-PEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPVAGEETQFIAYVA-      86
```

Fig: 4 Multiple sequence alignment of the *Phyllanthus amarus and Phyllanthus tenellus* species in Clustal Omega

Phylogeny analysis- Clustal omega

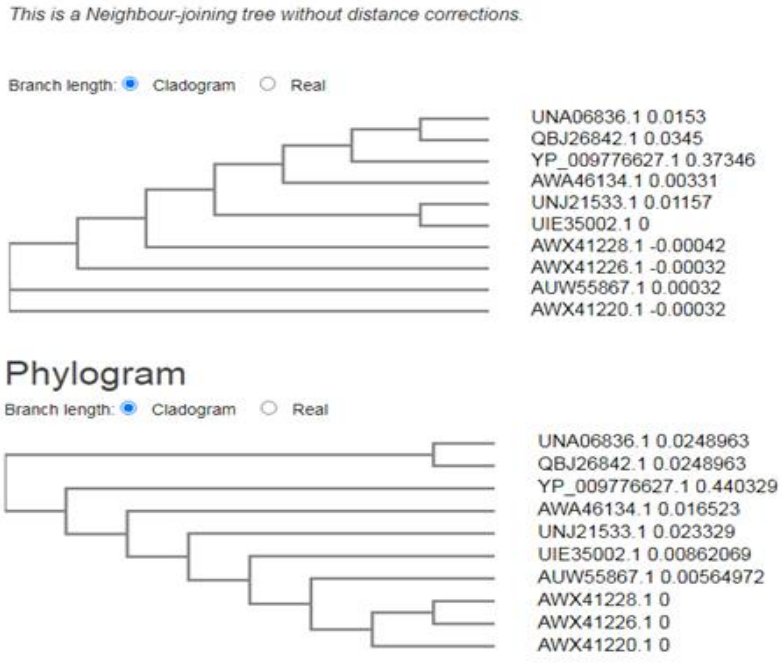

Fig:5 Phylogenetic tree for the species *Phyllanthus amarus* and *Phyllanthus tenellus*, shown graphically.

ISSN PRINT 2319 1775 Online 2320 7876

Research paper **© 2012 IJFANS. All Rights Reserved, UGC CARE Listed (Group -I) Journal Volume 11, S Iss 1,2022**

Phyllanthus amarus and *Phyllanthus tenellus'* phylogenetic tree is shown graphically in Figure 5 with the hypothetical root of a straight line indicating 100% sequence similarity and branch length signifying non-sequence similarity. Neighbor-joining is used to create dendograms. The findings demonstrate the evolution of the many kinds of medicinal plants.

CONCLUSION

The evaluation of molecular markers based identification and categorization of a considerable range of medicinal plants is the first research of its type. By using the neighbor-joining approach, a cladogram based on the nucleotide sequences of these three medicinal plants—*Phyllanthus amarus, Phyllanthus tenellus* was produced. Comparative examination of these two medicinal plants from the Phyllanthus family was conducted, and it was discovered that the *Phyllanthus tenellus* group is closely linked, as previously discussed in the current taxonomic systems. Additional application studies will be conducted in the future with regard to *Phyllanthus tenellus* almost all of the plant's components have been utilized and eaten as food. The majority of plant parts are consumed as food in traditional medicine to treat inflammatory-mediated illnesses including gastrointestinal and cardiovascular conditions. According to reports, the plant's seeds and leaves have anticancer, anti-hypertensive, cardio protective, wound-healing, and other beneficial characteristics. They are also used to treat eye disorders. High sequence similarity was found in the plant during blast analysis. They are used in additional *Phyllanthus tenellus* research on drug design, molecular docking and dynamics, and system biological research on network prediction.

REFERENCE

1. Unander, D.W., Webster, G.L., Blumberg, B.S., 1995. Usage and bioassays in Phyllanthus (Euphorbiaceae) IV. Clustering of antiviral uses and other effects. Journal of Ethnopharmacology 45, 1–18.
2. Jayaram, S., Thyagarajan, S.P., Sumathi, S., Manjula, S., Malathi, S., Madanagopalan, N., 1997. Efficiency of Phyllanthus amarus treatment in acute viral hepatitis A. B and non A and non B: an open clinical trial. Indian Journal of Viorology 13, 59–64.
3. Foo, L. Y., & Wong, H. (1992). Phyllanthusiin D, an unusual hydrolysable tannin from Phyllanthus amarus. *Phytochemistry*, *31*(2), 711-713.
4. Sievers F, Wilm A, Dineen D, Gibson TJ, Karplus K, Li W, Lopez R, McWilliam H, Remmert M, Soeding J, Thompson JD, Higgins DG (2011) Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Mol Syst Biol 7:539.
5. Thompson JD, Higgins DG, Gibson TJ (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting,

ISSN PRINT 2319 1775 Online 2320 7876

Research paper UGC CARE Listed (Group -I) Journal Volume 11, S Iss 1,2022

position-specific gap penalties and weight matrix choice. Nucleic Acids Res 22:4673–4680.

6. Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 25: 4876–4882.
7. Edgar RC (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res 32:1792–1797.
8. Katoh K, Kazuharu M, Kuma K, Miyata T (2002) MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res 30:3059–3066.
9. Notredame C, Higgins DG, Heringa J (2000) T-Coffee: A novel method for multiple sequence alignments. J Mol Biol 302:205–217.
10. Higgins DG, Bleasby AJ, Fuchs R (1992) CLUSTAL V: improved software for multiple sequence alignment. Comput Appl Biosci 8:189–191.