



Data Article

Dataset on intergenic spacer regions of chloroplast genome and potential DNA barcode of *Hoya verticillata* var *verticillata* in Vietnam



Cuong Viet Hoang^a, Tan Quang Tu^a, Thu Thi Mai Lo^b,
Mau Hoang Chu^{a,*}

^a Thai Nguyen University of Education, Thainguynen City, 24000, Viet Nam

^b Tay Bac University, Son La City, 34100, Viet Nam

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ABSTRACT

Hoya verticillata var *verticillata*, an epiphytic plant, is both an ornamental and a valuable medicinal plant. However, *H. verticillata* has a similar morphology to other species belonging to the *Hoya* genus, so it is challenging to distinguish the *H. verticillata* var *verticillata*, plant accurately. Alternatively, if *H. verticillata* var *verticillata*, is deformed or powdered, it is more challenging to identify. This dataset includes information on *H. verticillata* var *verticillata*, samples collected from the natural environment and four chloroplast DNA markers to support *H. verticillata* var *verticillata*, species identification. Phylogenetic analysis based on sequences of intergenic spacer regions (trnK-rps16, rps16-trnQ, psbl-atpA, and ndhC-trnV) shows that *H. verticillata* var *verticillata*, is very closely related and distributed in the same group as *Hoya carnosa* with a Bootstrap coefficient of 99–100 %. Four intergenic spacer region sequences, trnK-rps16, rps16-trnQ, psbl-atpA, and ndhC-trnV from the chloroplast genome are potential DNA barcoding candidates to distinguish *H. verticillata* var *verticillata*, from different species in the *Hoya* genus.

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* Corresponding author.

E-mail address: chuhoangmau@tnu.edu.vn (M.H. Chu).

Specifications Table

Subject	Biological Sciences
Specific subject area	Biotechnology, Genetics diversity, Molecular Phylogenetics, Evolution
Type of data	Raw, sequence data, tables, figures, text files
Data collection	Illumina NovaSeq 6000 (Illumina) sequencer
Data source location	GenBank: OR475244.1 NCBI Reference Sequence: NC_085236.1
Data accessibility	Repository name: NCBI Data identification number: Not applicable Direct URL to data: The NCBI links to the sequenced data can be accessed at: https://www.ncbi.nlm.nih.gov/nuccore/OR475244.1 https://www.ncbi.nlm.nih.gov/nuccore/NC_085236.1

1. Value of the Data

- *Hoya verticillata* var *verticillata*, an epiphytic plant, has significant medicinal value. *H. verticillata* var *verticillata* contains many biologically active medicinal substances, effective in treating some for human diseases.
- A dataset on intergenic spacer region sequences, *trnK-rps16*, *rps16-trnQ*, *psbI-atpA*, and *ndhC-trnV* from the chloroplast genome can be used to develop potentially useful molecular markers and support species identification, especially when plant specimens are deformed and in powder form.
- The analysis of molecular phylogeny and evolution of *Hoya* genus based on the intergenic spacer regions sequences.

2. Background

Hoya verticillata var *verticillata*, an epiphyte that climbs and belongs to the Apocynaceae family [1], is a precious medicinal plant. *H. verticillata* var *verticillata* widely used in traditional medicine to treat kidney diseases, urinary tract disorders, rheumatism, jaundice, fever and diarrhea [2]. Therefore, accurate species identification is the basis for the effective use of *H. verticillata* var *verticillata* in medical treatment in traditional medicine in Vietnam.

Chloroplast DNA has a double circular structure, and different regions in the DNA molecule have different mutations [3]. Therefore, it is possible to determine close or distant relationships of plant objects based on the different levels of variation of a particular DNA region. So, regions with high variability are used for phylogenetic analysis and selected as potential DNA barcodes to support species identification. The complete chloroplast genome of *H. verticillata* var *verticillata* has been sequenced, analyzed and registered on GenBank with code OR475244.1 [4]. Accordingly, some intergenic spacer regions belonging to the large single-copy region (LSC) with high nucleotide diversity (Pi), such as *trnK-rps16*, *rps16-trnQ*, *psbI-atpA*, and *ndhC-trnV*, were identified. So, these IS regions may be potential DNA markers for identification and phylogenetic analysis of *Hoya* that need to be explored.

3. Data Description

The present work employs data on *H. verticillata* var *verticillata* specimens. The leaf samples and specimens of *H. verticillata* var *verticillata* samples (Voucher HOYP202305TN) were collected in May 2023 at Hang Trai area, Tan Long commune, Dong Hy district, Thai Nguyen province, Vietnam, in the coordinates of 21°43'34" N, 105°50'52" E (Fig. 1). The *H. verticillata* var *verticillata* plant has a cylindrical root with a strongly developed main root and lateral roots. The small tree trunk is climbing and has 5–20 mm long aerial roots. Leaves are simple, growing oppositely on

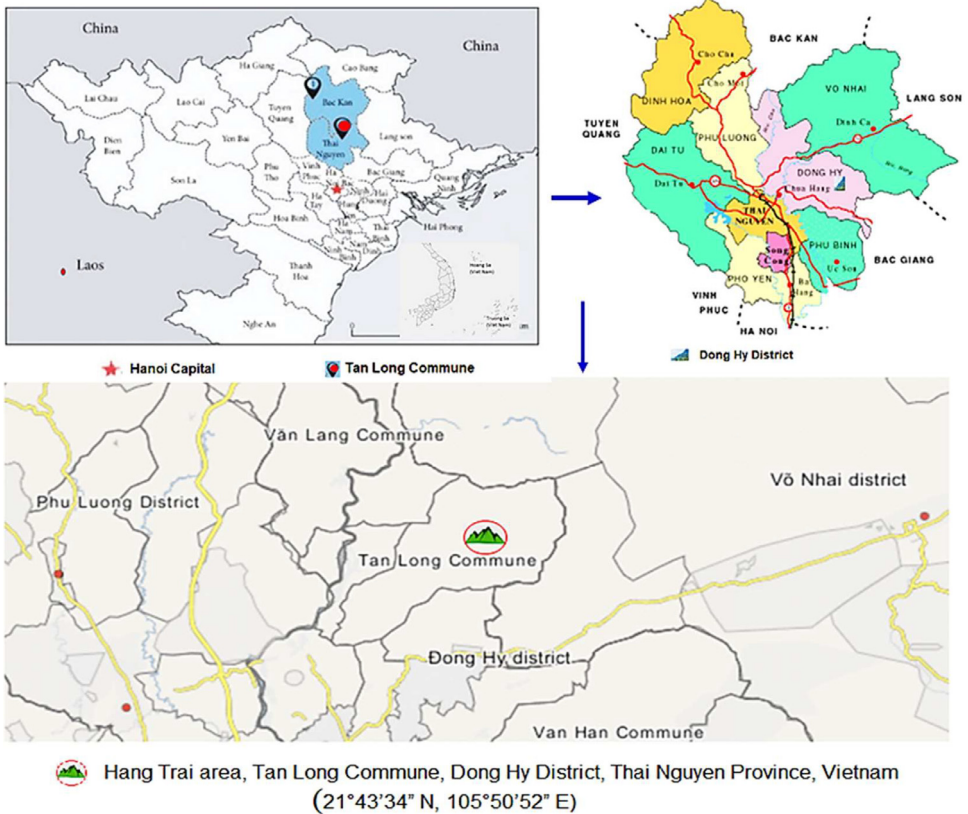


Fig. 1. Map showing *Hoya verticillata* var. *verticillata* sample collection location Hang Trai area, Tan Long commune, Dong Hy district, Thai Nguyen province, Vietnam, in the coordinates of 21°43'34" N, 105°50'52" E.

the trunk and branches. Fat leaves, oval blades up to 7 cm long, 1.3–2.5 cm wide. Leaf stalks are 10–20 mm long, with sparse fine hairs (Fig. 2).

Four intergenic spacer regions of *H. verticillata* var. *verticillata* chloroplast genome (cp) [1] with high Pi, *trnK-rps16*, *rps16-trnQ*, *ndhC-trnV* and *psbI-atpA* were selected as cp DNA barcodes with nucleotide sequences as shown in Table 1. *H. verticillata* var. *verticillata* is distributed in the same group as *Hoya carnososa* with a Bootstrap coefficient of 99–100 % on the phylogenetic tree established based on the four regions *trnK-rps16*, *rps16-trnQ*, *ndhC-trnV* and *psbI-atpA* (Fig. 3 and Table S1, Fig. 4 and Table S2, Fig. 5 and Table S3, Fig. 6 and Table S4).

4. Experimental Design, Materials and Methods

4.1. Sample collection and data source creation for analysis

The *Hoya verticillata* var. *verticillata* samples (Voucher HOYP202305TN) were collected in May 2023 at Hang Trai area, Tan Long commune, Dong Hy district, Thai Nguyen province, Vietnam, in the coordinates of 21°43'34" N, 105°50'52" E. The *Hoya verticillata* var. *verticillata* was identified by comparative morphological methods at the Botany Department in the Faculty of Biology, Thai

Table 1

Sequence characteristics of four intergenic spacer regions of *Hoya varticillata* var *verticillata* chloroplast genome.

Intergenic spacer regions	Sequence length(bp)	Sequence
trnK-rps16	793	<p>GAAAAGAAGAAACCAATTATAGAAGATAATCTATCGACTATAAAAATATATGTATAAAT AAAAGTATAATAAAAAGAAGTGCATAAATACAATCGGAATTATAAAAAATTAACA ATAAATTAACCAAAGAAATTTAGACGGAAGCAATTAACCCATTAAGCTAACAAATCGAA AAAAATGGATTTTCTAATGAATTCGGAACATAAAAAAATATATAGATCGGATGACAAAT ATAAGAAATTTCTCAGATAAAATTATATTTAGATAAAGCAAAACAAAAGAAAAA AAAAATGAAAAATAGAGATTCAAAATTTATGAACGGATCCTTTTGTATCCCTCTTTT CAATCACAAAAAAAGCTCGTGTATCAAAGAACCCTGTCGACGTAAGTAAAAAATCA AACAAACCAAATAACTAGATCTAACTTCACCTTATCATGATGAATTTATTTGTTCAA TACACTGTTGTCAATATAAATGTTACGAAAAAAGAATAAAAAAAGAAAAAGAA TTCAATTTGAATTTCTTTTTTTTTTATTCTTTTTTGTAGTTAAATTCAAAATAAAAA TGAAACCATCAAGTTTAAAGTTGTGCGGAATGCCTAAATTTCTAGGATCAAGGAA ATAGGGTTTTGTGTTATAGAACAAGGATTCGAAGAAAAACAATGATAAATAGATAC GAATAGAACGGGAAAGGAAAAAAGGGGGGTAATAAAAAAGAGTAGAGAAAGGTT ATCCAAAGTTATATACAATAACTGCCCCCTTTTTGTATTCCTTAATCC AACATCCCTCTAATTTGGAACCGATGGAATTTGATCAATTTATGGAATCATGAATA GTCATTTGGTTGTAGACATCATAACTATATCCCTTTGTCTATATAGTTCTTTAGA ATATAGAAGAGAGATTTTATATATAGCTATAGATCGGTAATAAAGAATATAGCTAC AAATCGGTAAAGAAGTTTCTGAATAAGTTTTAGCAAGTCCCTCTTAATTTAAATGAA AAAGAATTTCTATTTAATAATATATTTAATAATAGATTAAGTTAGGGTTAAATAT TTGTTAAATATTTTCATTTTTAAATTCAAAATCGAGGGGTCAAACCTTTTTAC AAAAATAGAATAGAAGGATACATACGTTAAACATTTCTCGTTTTTTTTTATTTT GTTTAAAGCTGTGAGGTGAGCAAGATTTCCGCTAATCGAATCTTCCATACATAAAT AATATCCATACATAAAGAATAGAAGTGAATAAAGAGAATAAAGATATAAATA TAAACACCCCTTTTTAAGTGTACATAAATTTACAATTTATTTATTTATTAGGG CCAAACAGGAAATACTTATTCAAAGAAAATACATCGGATTCGGATAGATATATTCGG ATAGATATATAAATACATATATAATTTATAAATTTGATTTTTTGTAAATGCAATTCAG GCAGACAGAAAATTTAATATCTTCGGTTAATGTATTCCGCCCCGGGGTATACAG GACTAATGGACATAAGAGAAAAAATGGGAATTTATGCTCGGGATCGGACTGAC TAGGTACAAAATCCCAACAGTCCAAAATTAAGTTGCTCCTTTTTTTTTTATTTAGTC TAACCCCTTAGGGAATTAATCCTATCGGCTTTGAATGAATTTCAATTTAGTAAAAA TAGTTAGAATTAATAAATCTATATAAAAAAATAAATTCCTAAAAATATAGTTTCTAG GATACGAAATAATAGATAGGATCGTTGAAAATCAAATAATTGATAAATAATAAATC AATATGGGACGGAATTTTTTCTAAATAACTAACTTCCCGAAACAAGATGGGATGGA GCATTAGGATGAAAAGACCCCTTTTTTAAATTCCAACTCGGAAACCGATTTTCC AATTTACCTGGATCAGAAATAGAGTCAATTACATTTGCGTGTCTTTTGTACGCGATT CAATTCAGTTTGTGTAATAAAGATATGATTCATGCATAAAGATAAAAAAAGAA ATAAATCCAGCTAACATTAGACGTTACCCCAATCAACAAAATCTTTATTTCTATTTCT AAGATAATGAATATGCT</p>
rps16-trnQ	1328	<p>AGACACACTCCCATGAACGTGAAAAATATACCGAATTTCTCGATTGCAATTTGCAAG TCATCCATAACTGTTTAGTCAAATCAAACAAGAATTCATTTTTATCGAATTTACT AGTTTCCTTTGTTTACTTATCCCATTTCAAGACAAAATCCTATTTAGATTACTTA TTTCTTTTTTTTCAGTTAGTAACTTTAGATCTATATCTTATCTTATACAAATAT AAAAATGAAAAATTTCTCTTATTTTCACCTAGAATCTCTGTGAAAGAAAGAAAGGAAT TCAAAAAAATATGGAATTTCCAAGGGGAATTTGGAACCTCTTTATTTTTTTTTA ATTAATAAATTTTTATTACTATCTATTATATATTTATCTATTATATATTTATATTTT TTGAAATTGATGAAATGAAATAAATCAATTTGAAATAAATGAAAAAATAATATAGA TTATTTCTTAATTTCTATAAATTTCTATAAATTTATAGCTATATTTATATATTTAT AGATTTCTTTATTTTTTTTTTTCATTTATTTATTAATAAATATATATATTTCTAGA TTATTTATTTATTTTTATTTCTATTTTTTTTATTAATAAATTTGAATTTAATAATTA AAATTTTTTATTTAATAACAATCTAATAATAACAATTTAAATTTCTATTTTCATTTCC AATTTGAAATGTTTTTAAATGAAATGCTAATTTTTTTTTTATTTGAAATTTCAAT CTTTTTCTTTATAGATTTGACTTTTATGAATAGAATCGACAGGCTCTTTGGTTTTT TTCTTAGTATTTAGAATAAGAACAAGCAAGAGACTGGCTAGAAATTTCCATTTGAC AATTTAGAATCTTTGGTGTGTATTTCTTTTTTATTAATCTAGGCTAGGAGACCT TCTCTTGATTTGAATATAAAAAAAGAAGACAGACTACCCCTCGTGTCTCGTAGGCT AGGTAAGGTATATGGCGAGCCTATTTACATTTTACATTGTTAATAATGAGACTTAC CAAGATATTTACATTTTTTAACTTTGTACACAAGCAGCAGGCTTTTTCTAGATCCA TATTTTGACTTCAAAAAATTCACCAACATTGGCTATACCAAAGAAAGGGAGTCTCAAG AACTCCTGAAATATGAATTCGCCTCTACCCCAAGATTAATGCCCAAGATTAATA</p>
ndhC-trnV	1492	<p>AGACACACTCCCATGAACGTGAAAAATATACCGAATTTCTCGATTGCAATTTGCAAG TCATCCATAACTGTTTAGTCAAATCAAACAAGAATTCATTTTTATCGAATTTACT AGTTTCCTTTGTTTACTTATCCCATTTCAAGACAAAATCCTATTTAGATTACTTA TTTCTTTTTTTTCAGTTAGTAACTTTAGATCTATATCTTATCTTATACAAATAT AAAAATGAAAAATTTCTCTTATTTTCACCTAGAATCTCTGTGAAAGAAAGAAAGGAAT TCAAAAAAATATGGAATTTCCAAGGGGAATTTGGAACCTCTTTATTTTTTTTTA ATTAATAAATTTTTATTACTATCTATTATATATTTATCTATTATATATTTATATTTT TTGAAATTGATGAAATGAAATAAATCAATTTGAAATAAATGAAAAAATAATATAGA TTATTTCTTAATTTCTATAAATTTCTATAAATTTATAGCTATATTTATATATTTAT AGATTTCTTTATTTTTTTTTTTCATTTATTTATTAATAAATATATATATTTCTAGA TTATTTATTTATTTTTATTTCTATTTTTTTTATTAATAAATTTGAATTTAATAATTA AAATTTTTTATTTAATAACAATCTAATAATAACAATTTAAATTTCTATTTTCATTTCC AATTTGAAATGTTTTTAAATGAAATGCTAATTTTTTTTTTATTTGAAATTTCAAT CTTTTTCTTTATAGATTTGACTTTTATGAATAGAATCGACAGGCTCTTTGGTTTTT TTCTTAGTATTTAGAATAAGAACAAGCAAGAGACTGGCTAGAAATTTCCATTTGAC AATTTAGAATCTTTGGTGTGTATTTCTTTTTTATTAATCTAGGCTAGGAGACCT TCTCTTGATTTGAATATAAAAAAAGAAGACAGACTACCCCTCGTGTCTCGTAGGCT AGGTAAGGTATATGGCGAGCCTATTTACATTTTACATTGTTAATAATGAGACTTAC CAAGATATTTACATTTTTTAACTTTGTACACAAGCAGCAGGCTTTTTCTAGATCCA TATTTTGACTTCAAAAAATTCACCAACATTGGCTATACCAAAGAAAGGGAGTCTCAAG AACTCCTGAAATATGAATTCGCCTCTACCCCAAGATTAATGCCCAAGATTAATA</p>

(continued on next page)

Table 1 (continued)

Intergenic spacer regions	Sequence length(bp)	Sequence
psbl-atpA	1878	<p>ACAAAAGGTTCTTTGTTATCCGCGATTGGAAAACATCAATTTGGGTCCACTGAAA CGCCTTTTTTTTTTTATTTCCGGGTTTATGTTCTGTTTTAAAAGCTTCCGGCTGAGTAA ACTTATGGGAAAAATTTAGATTTTCGATTAACCAACCCGACAGTTCCAAGCAACAAAC AATAATGAAAAAATTATACAATTTTCATTTTTGTATTTGAGTTTTCCCTTAATCATTT TGTTTTATTTTTATATAAAAATTTTTATATATATATAGTATATAAATTATAGTAAT AGTAATAGTA</p> <p>GGGTTTTCTTTCTATTTTCTCCGATTTTTGTTTTATATAAAAAATGCCAAATTTG AAAAAAAATAAATAAATAAATAAAGTCATCAAGGAAAGCGGAAAGAGAGGGATTCCGA ACCCTCGGTACGAATAACTCGTACAACGGATTAGCAATCCGCGCTTTAGTCCACT AGCCATCTCTCCTAATTGAAAATTTGGGTTAGATTACACATAAAAAAATAAGGAGTA TTTCTTTCTCTATTATATAGATATGTACCATTTTTATCAGTAAATTTTTTTTCGATAA ATAAAGAAATAAAGAATAAATAAAGAGAAGGGCTCGAAAGTGCCAACAATATAAAGA AAACCAAAAAGCGACCCCTTCGTATTTTGTTCGAAAGCCCTTCTTATTGTTATTGAC ACGGCTGGTCTGGTCAGTACCCAGCCGGGCTCTTTTTGTTTTGTTCCAACTAATT ATAGAAAAAATAATGATAAATTTTCATTTATCTGATTTGAAAACAAAAATGCTTAGTA TTTTTAGTATTAATATA TAATAAAGGAATAGGCAATATTCAAGCACGAACAAAAAAGAAAGAAAGGATTTTC CATCCGCGAAAACGAAAAAAGAGGGTAAATACGCTAAATTTTTGGATTCCTTGA TGATCCCATCTTATTATACCCATTTTCCGGTTCGACAAAAGTCCAGTTGTATACAA TAATCGAATTTGAGCGGGTATAGTTTAGTGGTAAAAGTGTGATTCGTTTTTTAAAC CTTTGATAGTTAAAGGTCTTTGTTTTCCGGTTTGATTTCGTATCCGACCAAAAACTT TATTTGAAAAAGAAAAGGATTTAATCCTTTACCTCTCAATCAGGGATTCCGAGAAAA AATATACATCTCGTATTTGTATCCAAGGATCACTTAGAAAGTGACAAAATTTGGATT ATGAAATTCAGAAAACATAATTTTGAATTGGATTAATACTTCCAATTTGAATCAGTAT GAGTAAAGGATCCATGGATAAAGATAGCAAGTAGGTTTCTAATCGTAACTAAATCTT CAATTTTTGCTTTACAAAACAAAATTTGAATAAAAAATAGCTATTAATGATGACTCT GGTTTACTAGAGGCATCGACCTGTTTTTTTAGCTCGGTGGAAAACAAAATCCCTTTCC TCAGGACCGTCTCAAAAATAAAGATAAGAACGAAGTAACTAGAAAAGTGTGAGATT ACTCTCTTCTAGAGGGATCATCTAGAAAAGAAAATAGTAGTCAGACAAAAGTTGACAT AGATGTTATGGGTAGAATTTTTTTTGTAAAGTTTGTTCACATCCATCCATAAAGGA GCCGAATGAAACCAAGTTTCATGTTCCGGTTTTGAATTAGAGACGTTCAAAAATGCTG AATCGACGTCCGACTATAACCCCTAGCCTTCCAAGCTAACGATGCGGGTTCGATTCCC GCTACCCGCTTCAATCTTTTTTTTTTATTCGCAATTTGAAATTTATATATATTCTAA TCTAGACTTAATGCATCATTTAATATACAGTTTCAAAAATTTATCTCACATACAAT CGATCTCTGTTTTTTTCGGCGAAAAAGTGGGAAAGTCAAAAATACGAAAAAATCCG AATGAAAAGCGTCCATTTGCTAATGGATAGGACAGGGGCTTCTAAACCTTTGGTAT AGGTTCAAATCCTATTGGACGCAAAATTTTTCCATATATCTATTTTTTTTTTATTTTG ATACCACGAAAGCCTTTTTGAATAACTTTGAATTTGAGTGGATTTGAGACCCTTAAT ACATTACCATTACCTTTTTAAGATAAAATTTAAGATAAAAAGAAATCCTTTTTGTGC</p>

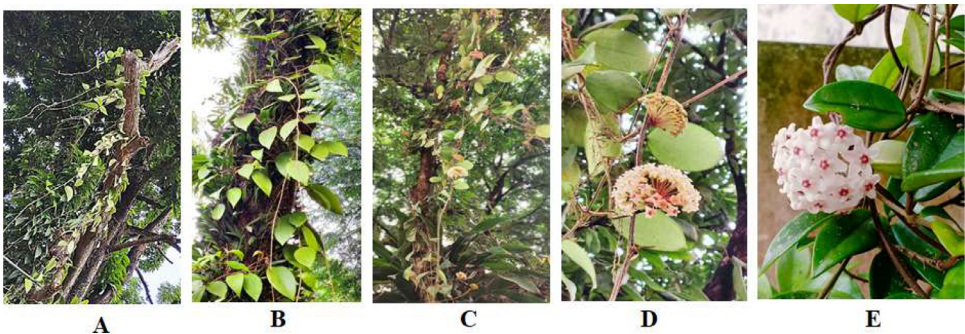


Fig. 2. *Hoya verticillata* var. *verticillata* plant growing in natural environment (A, B, C, D) were collected at Hang Trai area, Tan Long commune, Dong Hy district, Thai Nguyen province, Vietnam and kept at the experimental garden (E) of the Department of Biology, Thai Nguyen University of Education, Vietnam.

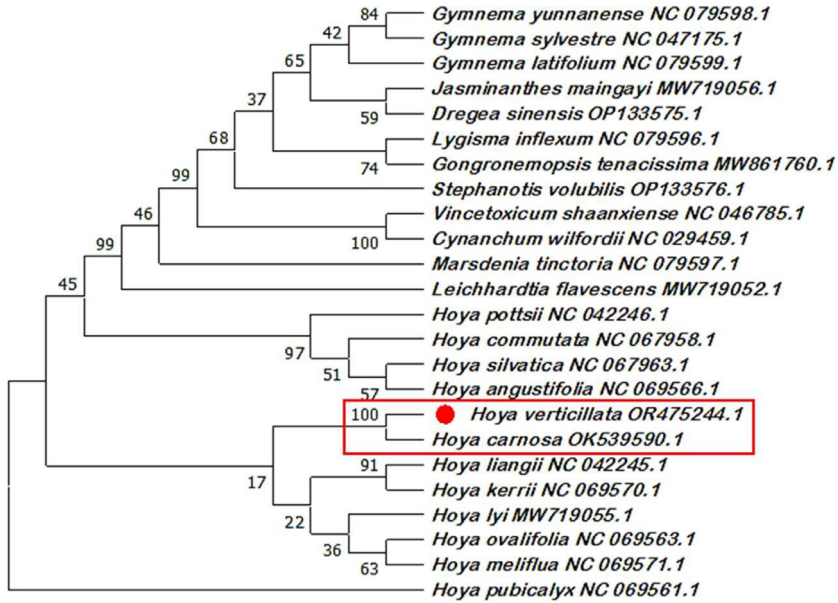


Fig. 3. Phylogenetic tree construction using the trnK-rps16 intergenic spacer region of *Hoya verticillata* var *verticillata* chloroplast genome and of other species belongs the Apocynaceae family.

Nguyen University of Education. The voucher specimens were placed in the Herbarium of the Department of Biology, Thai Nguyen University of Education, Vietnam.

Total DNA extracted from leaves was used for chloroplast DNA sequencing. The chloroplast genome of *H. verticillata* var *verticillata* is registered on GenBank. Nucleotide diversity (Pi) of DNA regions in chloroplast DNA was calculated by sliding window analysis performed in DnaSP v.6.11.01 [14], and DNA regions with high nucleotide diversity were selected for analysis.

The intergenic spacer regions of other species belonging to the Apocynaceae family were obtained by a Basic Local Alignment Search Tool (BLAST) search on the National Center For Biotechnology Information (NCBI) [5].

4.2. Phylogenetic analysis

Evolutionary analyses of some gene regions were conducted in MEGA v11.0.13 [6]. The evolutionary history was inferred using the Maximum Likelihood method and the Tamura-Nei model [7]. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa analyzed [8]. For the trnK-rps16 intergenic spacer region, the analysis was performed with 24 species (Table S1), for rps16-trnQ with 44 species (Table S2), for ndhC-trnV with 47 species (Table S3), and for with psbI-atpA with 46 species (Table S4).

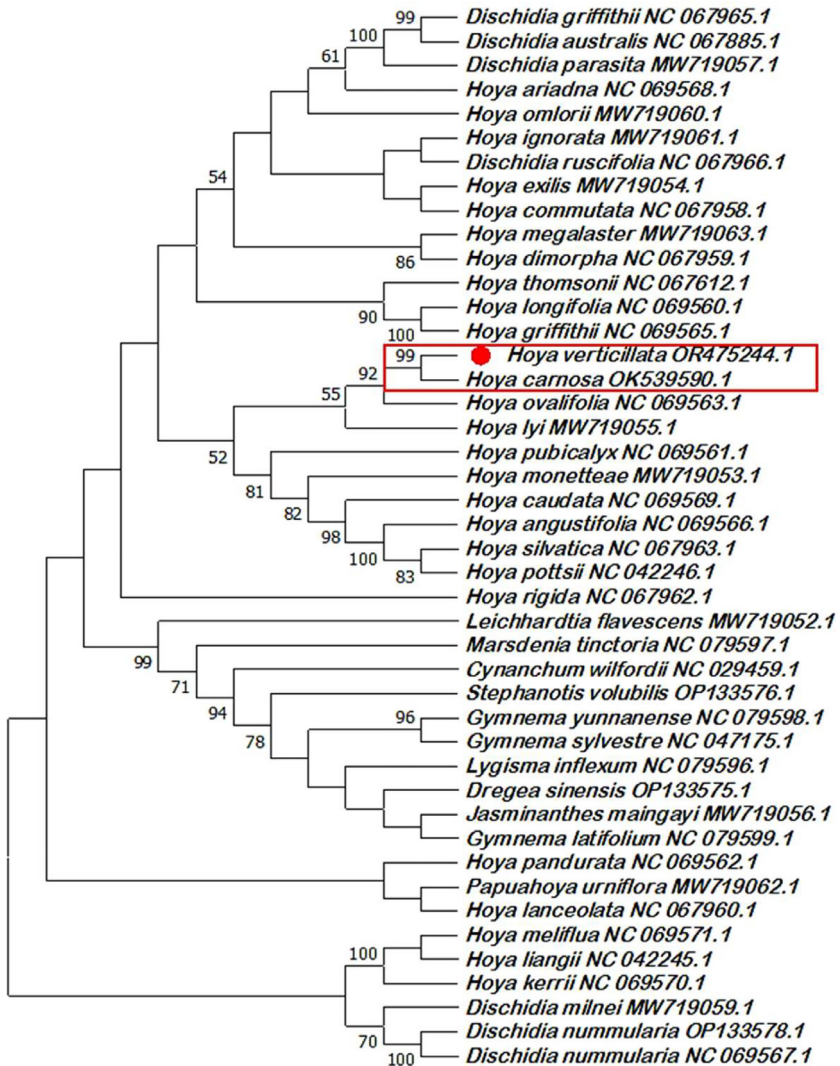


Fig. 4. Phylogenetic tree construction using the rps16-trnQ intergenic spacer region of *Hoya verticillata* var *verticillata* chloroplast genome and of other species belongs the Apocynaceae family.

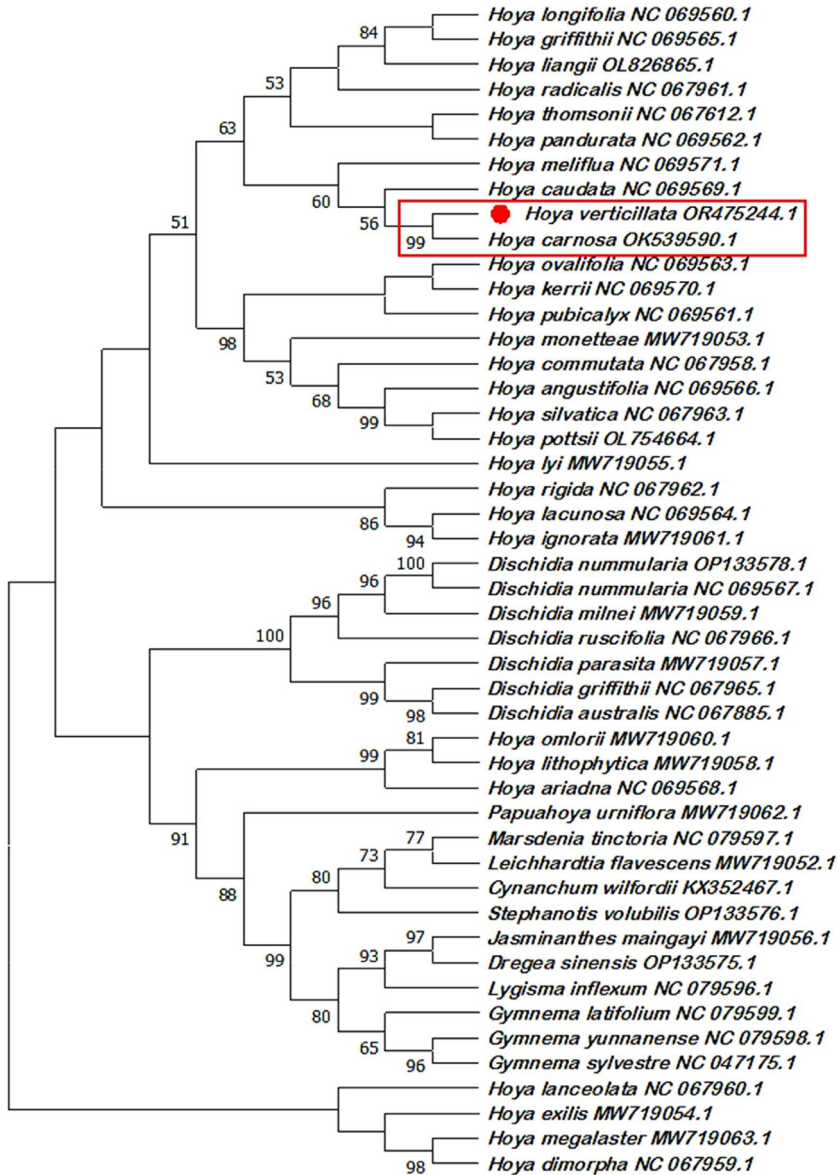


Fig. 5. Phylogenetic tree construction using the ndhC-trnV intergenic spacer region of *Hoya verticillata* var *verticillata* chloroplast genome and of other species belongs the Apocynaceae family.

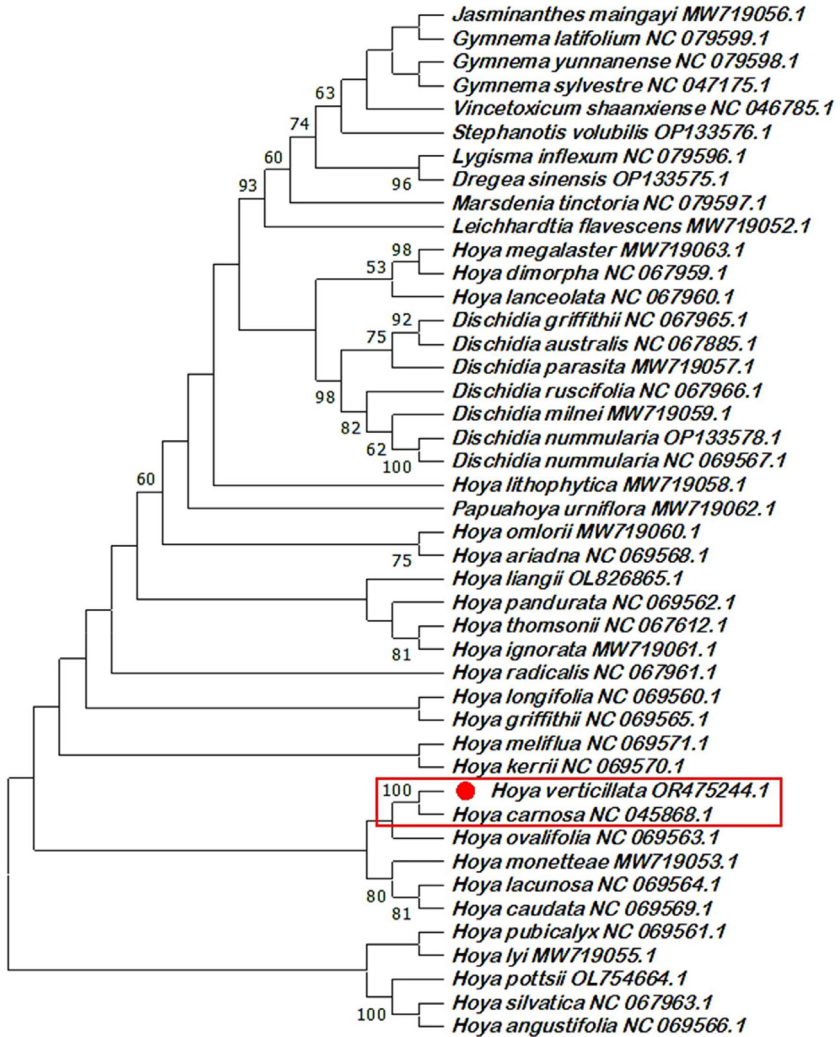


Fig. 6. Phylogenetic tree construction using the psbI-atpA intergenic spacer region of *Hoya verticillata* var *verticillata* chloroplast genome and of other species belongs the Apocynaceae family.

Limitations

None.

Ethics Statement

The authors have read and followed the ethical requirements for publication in Data in Brief and confirmed that the current work does not involve human subjects, animal experiments, or any data collected from social media platforms.

Data Availability

[Hoya verticillata chloroplast, complete genome \(Original data\)](#) (chloroplast genome)

CRedit Author Statement

Cuong Viet Hoang: Conceptualization, Formal analysis, Investigation, Resources, Writing – original draft; **Tan Quang Tu:** Data curation, Investigation, Writing – original draft; **Thu Thi Mai Lo:** Formal analysis, Resources, Writing – original draft; **Mau Hoang Chu:** Conceptualization, Data curation, Methodology, Supervision, Writing – review & editing.

Data Availability

Hoya verticillata chloroplast, complete genome. GenBank: OR475244.1 (Original data) (NCBI).

Hoya verticillata chloroplast, complete genome. NCBI Reference Sequence: NC_085236.1 (BioProject: PRJNA927338) (NCBI).

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper

Supplementary Materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.dib.2024.110471](https://doi.org/10.1016/j.dib.2024.110471).

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