Identification of ethnomedicinal plants (Rauvolfioideae: Apocynaceae) through DNA barcoding from northeast India

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ABSTRACT

Background: DNA barcode-based molecular characterization is in practice for plants, but yet lacks total agreement considering the selection of marker. Plant species of subfamily Rauvolfioideae have long been used as herbal medicine by the majority of tribal people in Northeast (NE) India and at present holds mass effect on the society. Hence, there is an urgent need of correct taxonomic inventorization vis-à-vis species level molecular characterization of important medicinal plants. **Objective:** To test the efficiency of *matK* in species delineation like DNA barcoding in Rauvolfiadae (Apocynaceae). **Materials and Methods:** In this study, the core DNA barcode *matK* and *trnH-psbA* sequences are examined for differentiation of selected ethnomedicinal plants of Apocynaceae. DNA from young leaves of selected species was isolated, and *matK* gene (~800 bp) and *trnH-psbA* spacer (~450 bp) of Chloroplast DNA was amplified for species level identification. **Results:** The ~758 bp *matK* sequence in comparison to the *trnH-psbA* showed easy amplification, alignment, and high level of discrimination value among the medicinal Rauvolfioidae species. Intergenic spacer *trnH-psbA* is also exhibited persistent problem in obtaining constant bidirectional sequences. Partial *matK* sequences exhibited 3 indels in multiple of 3 at 5 end. Evidently, generated *matK* sequences are clustered cohesively, with their conspecific Genbank sequences. However, repeat structures with AT-rich regions, possessing indels in multiple of 3, could be utilized as qualitative molecular markers in further studies both at the intra-specific and shallow inter-specific levels like the intergenic spacers of CpDNA. **Conclusion:** *matK* sequence information could help in correct species identification for medicinal plants of Rauvolfioideae.

Keywords: Apocynaceae, DNA barcoding, ethnomedicinal, indels, *matK*

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INTRODUCTION

DNA barcoding is emerged as powerful technique of species identification and exemplified with its wide application in monitoring and documentation of bio-resource.[1-4] The technique utilizes ~650 bp region of mitochondrial COI in animals[5] and various chloroplast regions (*matK, rbc*L, and *trnH-psbA*) in plants.[6-8] The application of the technique emphasizes some thrust areas, like documentation of the important and vulnerable ethnomedicinal plant bio-resources, dealing with which is recently defined as the subject "Ethnobotany Genomics."[9] The principal issues in ethnobotany emphasized the importance of correct species identification and deciphering of indigenous and conventional knowledge of restorative plant usage and their transfer for the promotion of bio-prospect in human health care. Apocynaceae is one of the 10 largest angiosperm families (including Asclepiadaceae) and comprises of several prominent medicinal plants, like Rauvolfioideae subfamily of Apocynaceae is known for the rich source of typical laticiferous tissues, which produce various alkaloids and cardenolides being used in traditional medicines for stomach ulcer, fever, asthma, whooping cough, etc. Similarly, *Catharanthus roseus* is the source of very important drug *viz.* vinblastine, vincristine used in cancer chemotherapy.[10] *Calotropis gigantea* is also a potential candidate source for anti-cancer drugs,[11] and *Allamanda cathartica* possess a remarkable wound healing function.[12]

Indian saga has a long heritage of using numerous medicinal and aromatic plants (MAPs) for human health care, and the nation is bestowed with rich resources of plant

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bio-diversity distributed in various ecological conditions. It is the home of about 17,000 of global plant species and expected to be fully explored. It is reported that above 2000 species of ethnobotany plants have been utilizing by various medicines in Northeast India.[13] Amidst, the galaxy of rich traditional knowledge of herbal medicine in use by the majority of tribal people in NE India, there is an urgent need of correct taxonomic inventorization vis-à-vis species level molecular characterization of medicinal plants from this region in the globe. The conventional morphological techniques involve difficulties in species identification from any unstructured plant part. Thus, the ethnomedicinal resources of NE India seem least explored and found fragmentary. It entails the need of intervention of modern tools to characterize the molecular marker of important and vulnerable medicinal plants for correct species-level identification as well as their inventorization.

The DNA barcoding is rapidly evolving, but yet provides full agreement on which region(s) of DNA should be universally used for plants. In the current study, we have explored the effectiveness of *matK* and *trnH-psbA* spacer in differentiation of selected ethnomedicinal plants (*Catharanthus roseus* (L.) G. Don*, Alstonia scholaris* (L.) R. Br.*, Thevetia Peruviana* (Pers.) Merrill*, Allamanda cathartica* L. Allamanda*, Tabernaemontana divaricata* (L.) Alston*, Calotropis gigantea* L. R. Br. Ex Ait) belonging to the family Apocynaceae inhabiting in NE India. The *matK* is located in the large single-copy region of chloroplast genome, nested between the 5´ and 3´ exons of *trnK, t-RNA* –lysin. In *matK*, rates of substitution among all the 3 codon positions are reported almost equal,[14] leading to the high rate of substitution, which results from non-synonymous mutations, but amino acid replacements occur as chemically-conserved, preserving its structural and biochemical properties.[15] The *trnH-psbA* spacer is among the most variable plastid regions in angiosperms. It is a popular tool for plant population genetic and species-level authentication.[16,17] The study shows the efficiency of *matK* in species delineation like DNA barcoding in Rauvolfiadae, and bears insights of effective utilization of *matK* indels in multiple of 3 for studies both at the intra-specific and shallow inter-specific levels in the entire family Apocynaceae.

MATERIALS AND METHODS

Sample collection, DNA Isolation, and PCR amplification

Young leaves of selected ethnomedicinal plants of Rauvolfioideae were collected aseptically from different sources in Southern Assam, India. All the species examined in the study were carefully identified by expert. About 40 mg, wet young leaves were homogenized in the DNA extraction buffer (50 mM Tris HCl pH 8.0, 25 mM EDTA pH 8.0, 150 mM NaCl, and 2 μL/mL β- mercaptoethanol). Genomic DNA was extracted through successive steps using 5 M Potassium acetate (pH 9.0), Phenol:Chloroform:Isoamylalchol (25:24:1), Chloroform:Isoamylalchol (24:1). To obtain high-quality DNA, free from polysaccharides and other metabolites that might interfere during PCR amplification, purified DNA concentration of each sample was estimated both fluorometrically and by comparison of ethidium bromide-stained band intensities against standard λ DNA. PCR was performed using primers pair, *matK*-F 5´-TAATTTACGATCAATTCATTC-3´, *matK*-R 5´-GTTCTAGCACAAGAAAGTCG-3´ and *trnH-F 5´*-CGCGCATGGTGGATTCACAATCC-3´ and *psbA-R 5´*-GTTATGCATGAACGTAATGCTC-3´ for *matK* and *trnH-psbA,* respectively.[18] The PCR reaction of 30 μl mixture contained 20 ng genomic DNA, 20 pmole each primer, 0.2 mM of each dNTPs, 0.5 units of high fidelity *Taq polymerase* enzyme (Applied Biosystem), 1Xbuffer, and 1.5 mM $MgCl_2$. PCR thermal conditions were 94ºC for 3 minutes, 30 cycles at 94ºC for 1 minute, 48ºC for 45 seconds, 72ºC for 45 seconds in the case of *matK,* and 94ºC for 3 minutes, 30 cycles at 94ºC for 1 minute; 51ºC for 45 seconds, 72ºC for 45 seconds for *trnH-psbA* and a final extension at 72ºC for 10 minutes for both the cases. The PCR products were checked by 1.5% agarose gel electrophoresis.

Purification of PCR Products and DNA sequencing

The PCR products of presumed size were extracted using QIA quick PCR purification kit (QIAGEN, Cat. No.28704). The purified PCR products were sequenced both bi-directionally using automated DNA sequencer (ABI 3700).

Sequence analysis

Raw traces were manually edited, and both forward and reverse sequences were subsequently aligned to generate targeted sequences. The 3´ and 5´ terminals were clipped to generate consensus sequences for each taxon for sequence length of ~ 758 bp (Nt. 520-1278) for *matK* and ~450 bp for *trnH-psbA*. The Open Reading Frame (ORF) for *matK* was checked, and correct amino acid sequences were determined by online software ORF prediction (http://www.ncbi.nlm.nih.gov/gorf/gorf.html). These *matK* and *trnH-psbA* sequences were aligned individually for combined data set using the ClustalX program.[19] The aligned sequences were corrected manually, and nucleotide compositions were calculated using BioEdit program.[20] Neighbor-joining (NJ) method was used for calculating intra- and interspecies divergence. In addition, 20 sequences of *matK* and 13 sequences of *trnH-psbA* intergenic spacer for same or related taxa of the studied specimen were

obtained from GenBank (http://www.ncbi.nlm.nih.gov/genbank/) [Table 1]. The generated sequences of both *matK* and *trnH-psbA* for the studied species of Apocynaceae were subsequently submitted to NCBI.

Phylogenetic analysis

Pair-wise nucleotide sequence divergences were calculated using the Kimura-2-parameter (K2P) model to generate the distance matrices, and the neighbor-joining (NJ) analysis was done in MEGA 4.2 [21] to examine phylogenetic relationship between 14 taxa from a subfamily Rauvolfioideae, and two taxa from the subfamily Asclepiadaceae of Apocynaceae. K2P distances were used following the guidelines of the Consortium for the Barcoding of Life (CBOL) to evaluate performance barcoding locus (http://www.barcoding.si.edu/protocols.html). A total of 1000 bootstraps replicates were calculated for the NJ tree construction.

RESULTS

In this study, we uncovered 8 sequences of the *matK* region and 6 sequences of *trnH-psbA* spacer from the studied specimens, which include the few sequences that have been determined for the first time. The *matK* sequences of *Allamanda cathartica* (JN228933, JN228935) and *Calotropis gigantea* (JN228932), and *trnH-psbA* spacer of *Catharanthus roseus* (JN245984 and JN245989), *A. cathartica* (JN245987), *C. gigantea* (JN245986) *T. peruviana* (JN245983) are the novel sequences contributed from the study [Table 2].

Due to length variations in the *matK* sequences, only 758 aligned nucleotide positions were used in sequence analysis, of which a total of 189 variable and 157 parsimony-informative positions were found. However, the *trnH-psbA* sequences were not included in the subsequent analysis because the alignment was impossible across the Apocynaceae family [Figure 1].

Table 1: *matK* and *trnH-psbA* sequences from NCBI with their Accesion No also given

Species	Subfamily	Accession No. of *matK*	Accession No. of *trnH-psbA*
Catharanthus roseus	Rauvolfioideae	DQ660507, AM295068,	—
Vinca minor	Rauvolfioideae	AM295076, DQ660553	FJ493259
Alstonia scholaris	Rauvolfioideae	FJ449631, Z70189, AJ429321	GQ435037, GQ435038
Alstonia microphylla	Rauvolfioideae	GU135061, GU135060	GU135394, GU135392
Thevetia ahouai	Rauvolfioideae	GQ982112	GQ982387
Thevetia peruviana	Rauvolfioideae	Z70188,	—
Allamanda schottii	Rauvolfioideae	DQ660495	—
Nerium oleander	Rauvolfioideae	EF456295, GQ997641	FJ493258, EU531690, GU135391, FN675803
Tabernaemontana bufalina	Rauvolfioideae	DQ660548	—
Tabernaemontana divericata	Rauvolfioideae	Z70187	—
Plumeria rubra	Rauvolfioideae	Z70191	—
Plumeria cubensis	Rauvolfioideae	DQ660536	—
Carissa ovate	Rauvolfioideae	DQ660506	—
Asclepias curassavica	Asclepiadeae	DQ026716	—
Asclepias incarnata	Asclepiadeae	—	GQ248250, DQ006139
Asclepias syriaca	Asclepiadeae	—	HQ596608

Table 2: List of Plant sample of Apocynaceae examined in this study scientific name, subfamily, Voucher, Accession Number of sequences of *matK* and *trnH-psbA* also given

Species	Subfamily	Sample ID	Accession No. of *matK*	Accession No. of *trnH-psbA*
Catharanthus roseus (L.) G. Don	Rauvolfioideae	AUS-MP-03, AUS-MP-36	JN228930, JN228936	JN245988*, JN245984*
Alstonia scholaris (L.) R. Br.	Rauvolfioideae	AUS-MP-05	JN228931	JN245985
Thevetia peruviana (Pers.) Merrill	Rauvolfioideae	AUS-MP-01	JN228929,	JN245983*
Allamanda cathertica L. Allamanda	Rauvolfioideae	AUS-MP-29, AUS-MP-33	JN228933*, JN228935*	JN245987*
Tabernaemontana divaricata (L.) Alston	Rauvolfioideae	AUS-MP-32	JN228934	-
Calotropis gigantea L. R. Br. Ex Ait	Asclepiadeae	AUS-MP-22	JN228932*	JN245986*

* Sequence submitted first time in GenbanK

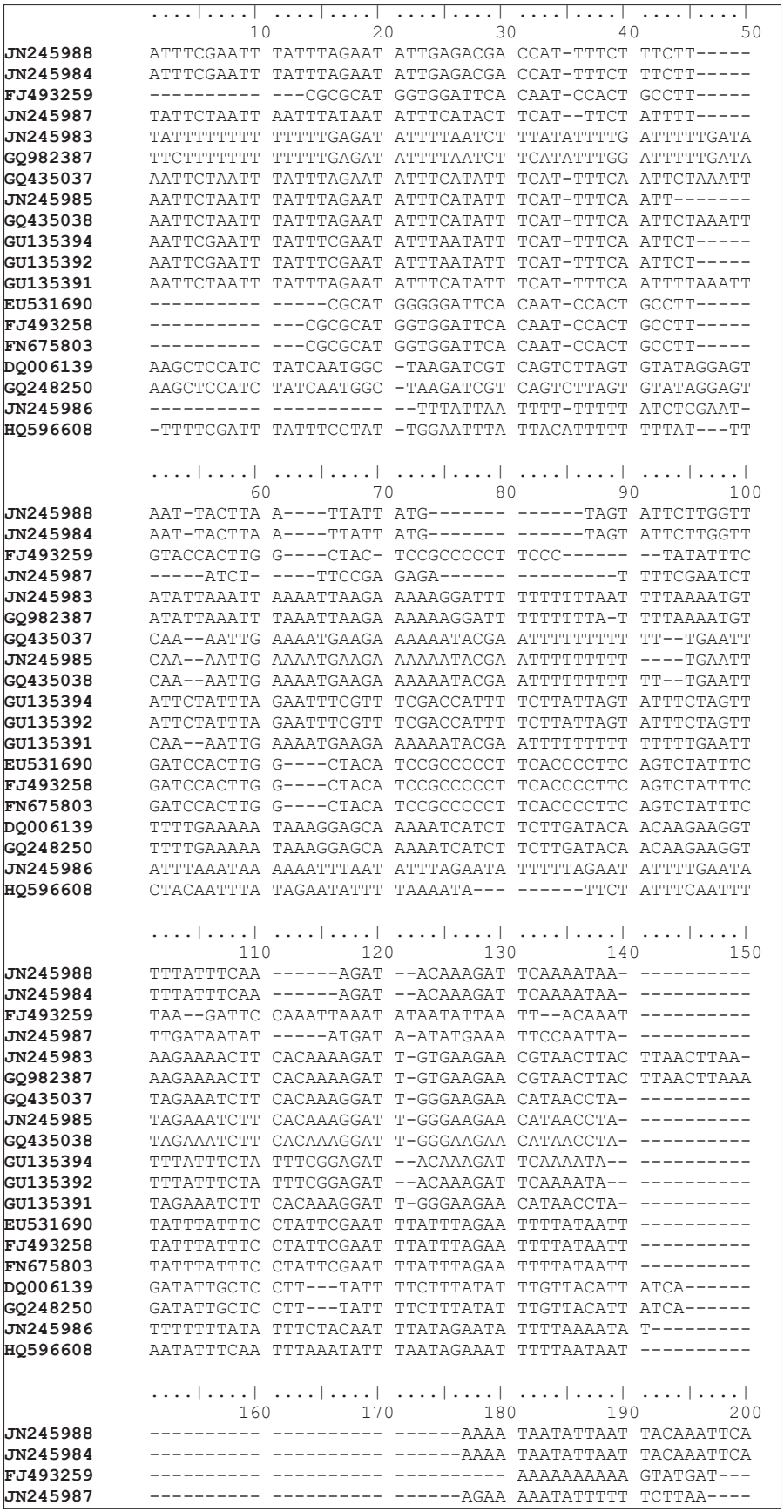

Figure 1: Showing Alignment of 19 sequences of trnH-psbA of Apocynaceae, containing indels of different regions

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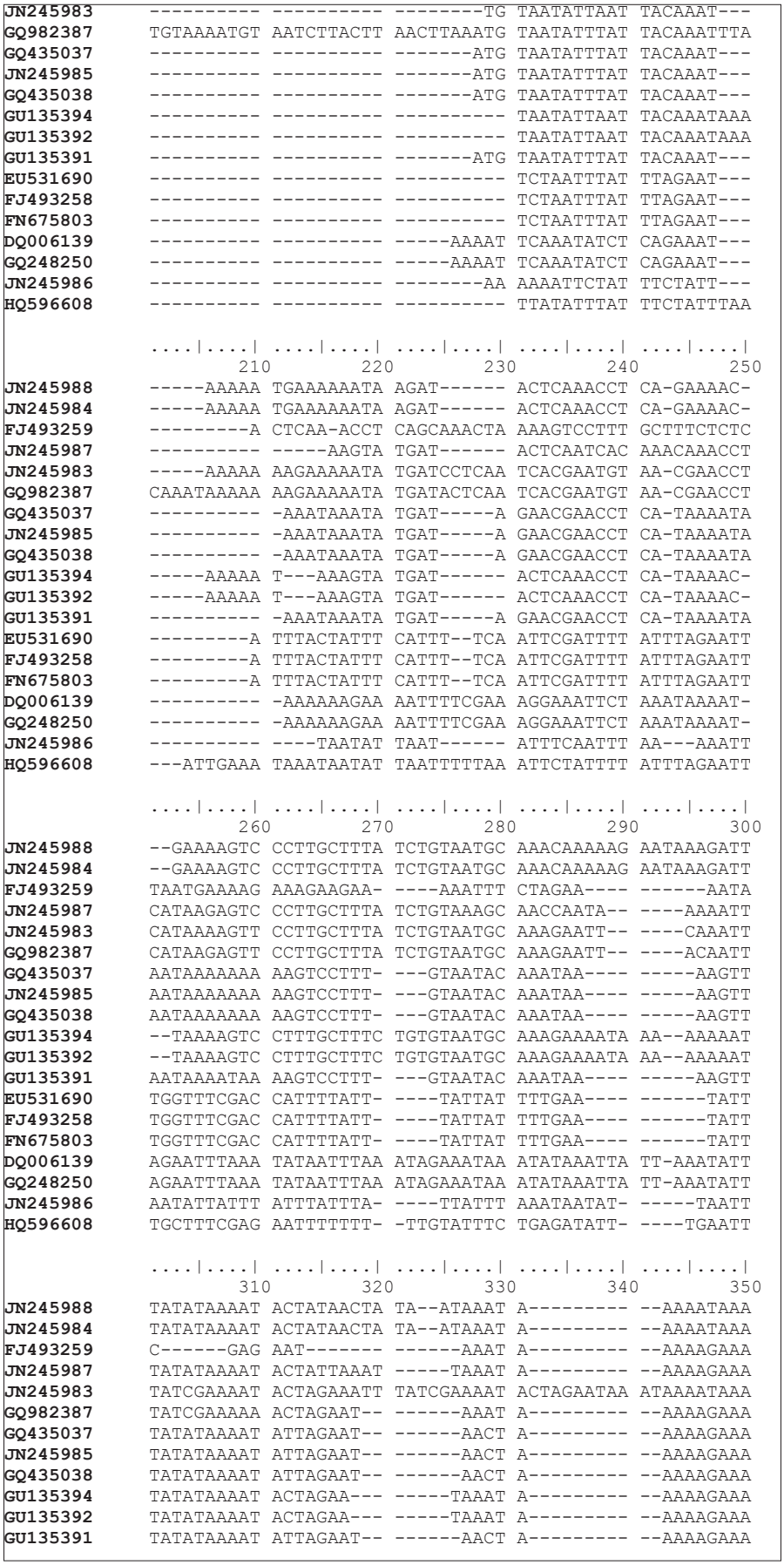

Figure 1: Contd....

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EU531690      T------GAT AATGTAAC-- ------AAAC A--------- --AAAATAAA
FJ493258      T------GAT AATGTAAC-- ------AAAC A--------- --AAAATAAA
FN675803      T------GAT AATGTAAC-- ------AAAC A--------- --AAAATAAA
DQ006139      TCTATTAAAT ATTTAAATTG ------AAAT AT-------- -TAAATCGAA
GQ248250      TCTATTAAAT ATTTAAATTG ------AAAT AT-------- -TAAATCGAA
JN245986      TTT---AAAT TCTATTTT-- ------ATTT A--------- ---TAATTTT
HQ596608      TTT----GAT AATGTAAC-- ------AACT A--------- --TAAAGAAA

                       360        370        380        390        400
JN245988      ATAAAGGAGC AATA-CCACC CTCTTGATAG AAGAAGAAGG TGA-TTATTG
JN245984      ATAAAGGAGC AATA-CCACC CTCTTGATAG AAGAAGAAGG TGA-TTATTG
FJ493259      ATAAAGGAGC AATA-CCACC CTCTTGATAG AACACGAAGG TGA-TTATTG
JN245987      ATAAAGGAGC AATA-CCCCT TTCTTGATAG AACAAGAAGG TGA-TTATTG
JN245983      ATAAAGGAGC AATA-CTC-C CTCTTGATAG AACAAGAAGG TGGATTATTA
GQ982387      ATAAAGGAGC AATA-CTC-C CTCTTGATAA AACAAGAGGG TGG-TTATTG
GQ435037      ATAAAGGAGC AATA-CCAAC CTCTTGATAG AACAAGAAGG TGA-TTATCG
JN245985      ATAAAGGAGC AATA-CCAAC CTCTTGATAG AACAAGAAGG TGA-TTATCG
GQ435038      ATAAAGGAGC AATA-CCAAC CTCTTGATAG AACAAGAAGG TGA-TTATCG
GU135394      ATAAAGGAGC AATA-CCACC CTCTTGATAG AACAAGAAGG TGA-TTATTG
GU135392      ATAAAGGAGC AATA-CCACC CTCTTGATAG AACAAGAAGG TGA-TTATTG
GU135391      ATAAAGGAGC AATA-CCAAC CTCTTGATAG AACAAGAAGG TGA-TTATCG
EU531690      ATAAAGGAGC AATA-CCGCC CTCTTGATAG AACAAGAAGG TGA-TTATTG
FJ493258      ATAAAGGAGC AATA-CCGCC CTCTTGATAG AACAAGAAGG TGA-TTATTG
FN675803      ATAAAGGAGC AATA-CCGCC CTCTTGATAG AACAAGAAGG TGA-TTATTG
DQ006139      ATAGAATATT TTCAAATATT CTATAAATTG TAGAAATAAA AAAAATGTAA
GQ248250      ATAGAATATT TTCAAATATT CTATAAATTG TAGAAATAAA AAAAATGTAA
JN245986      CTAAAGGAGC AATA-TCAAC TTCTTGTTCT ATCAAGAAG- ------TTTG
HQ596608      ATAAAGGAGC AAAAATCACC TTCTTGTTCT ATCAAGAAGA TGC-TTTTTG

                       410        420        430        440
JN245988      CTCCTTTATT TTTCAAAAAC TCCTATACAC TAAGAACAGG G-TCTTAG
JN245984      CTCCTTTATT TTTCAAAAAC TCCTATACAC TAAGAACAGG G-TCTTAG
FJ493259      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCGAG G-TCTTAG
JN245987      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCTGG G-TCTTAG
JN245983      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCAGT G-TCTTAG
GQ982387      CTCCTTTATT TTTCAATAAC TTCTATACAC TAAGACCAGT G-TCTTAG
GQ435037      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCAGA G-TC----
JN245985      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCAGA G-TCTTAG
GQ435038      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCAGA G-TC----
GU135394      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCAGG G-TCTTAG
GU135392      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCAGG G-TCTTAG
GU135391      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCAGA G-TCTTAG
EU531690      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCGGG G-TCTTAG
FJ493258      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCGGG G-TCTTAG
FN675803      CTCCTTTATT TTTCAATAAC TCCTATACAC TAAGACCGGG G-TCTTAG
DQ006139      TAAATTTCAA TAGGAAATAA ATCGAAAAAT AAATAGAAAT AGAACCAG
GQ248250      TAAATTTCAA TAGGAAATAA ATCGAAAAAT AAATAGAAAT AGAACCAG
JN245986      CTCCTTTATT TTTCAAAAAC TCCTATACAC TAAGACTGGC GGTCTTAG
HQ596608      CTCCTTTATT TTTCAAAAAC TCCTATACAC TAAGACTGGC GATCTTAG
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Figure 1: Contd....

Also, very few sequences are available from Rauvolfioideae in GenBank. Nucleotide composition of *matK* sequences of Apocynaceae is strong A+T bias (average 65.6% for all codon) where a percentage of T (36.5%) is higher than A (29.1%). The rates of substitution among the 3 codon position were almost equal [Figure 2].

matK sequences exhibited indels in multiple of 3 at 5´ end where a 12 bp insertion (641-652 region) was found in *Tabernaemontana divaricata, Tabernaemontana bufalina, Calotropis gigantea,* and *Asclepias curassavica*; next 12 bp insertion (677-688 region) was found in *Tabernaemontana divaricata* and *Tabernaemontana bufalina*, while the other 6 bp insertion (1124-1129 region) was found only in *Calotropis gigantea* and *Asclepias curassavica* of a subfamily Asclepiadaceae [Figure 3].

To evaluate the degree of DNA polymorphism, sequence divergence between and within species were calculated by Kimura 2-parameter (K2P) that revealed high average inter-specific and low intra-specific distances. Highest inter specific distance was 0.119 between *Catharanthus roseus* and *Calotropis gigantea. Thevetia peruviana, Tabernaemontana divaricata, Allamanda cathartica,* and *Alstonia scholaris* also showed high distance with *Calotropis gigantea*. Minimum inter-specific (0.065) was found between *Catharanthus roseus and Tabernaemontana divaricata*; maximum mean divergence within species (0.029) was found in

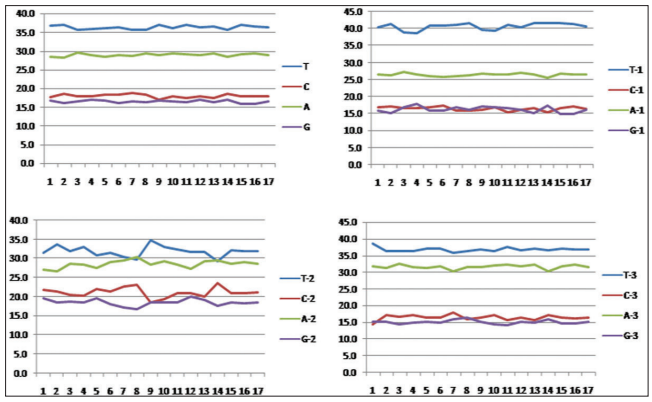

Figure 2: Nucleotide compositions of ~758 bp partial *matK* for the different species of Apocynaceae plants. The frequencies of nucleotide in sequences are present as the total average value for the all the codon positions and for each codon position separately with the accuracy to tenths of a percent. (A, T, G, C shown average value for all codon positions. A-1, T-1, G-1, C-1 shown average value for first codon position. A-2, T-2, G-2, C-2 shown average value for second codon position. A-3, T-3, G-3, C-3 shown average value for third codon position. A+T, A1+T1, A2+T2, A3+A3 represent the average value of A+T bias of total and each codon position.)

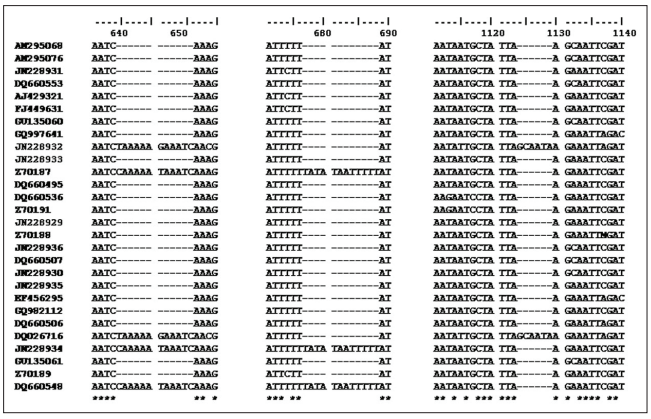

Figure 3: Showing Alignment of 28 sequences of *matK* of Apocynaceae, containing indels of 3 different regions. A 12 bp insertion found in *Tabernaemontana divaricata* (Z70187, JN228934), *Tabernaemontana bufalina* (DQ660548), *Calotropis gigantea* (JN228932), *Asclepias curassavica* (DQ026716) (641-652 region) and in *Tabernaemontana divaricata* (Z70187, JN228934), *Tabernaemontana bufalina* (DQ660548) (677-688 region) and 6 bp insertion in *Calotropis gigantea* (JN228932), *Asclepias curassavica* (DQ026716) (1124-1129 region). * indicate conserve nucleotide

Table 3: Mean divergence (K2P) within (bold number on diagonal) and among (below diagonal) the 6 species of Apocynaceae from southern Assam. (n/c indicates comparable due to only one accession number)

	Species	1	2	3	4	5	6
1	*Catharanthus roseus*	0.001					
2	*Alstonia scholaris*	0.068	0.000				
3	*Calotropis gigantea*	0.119	0.094	n/c			
4	*Allamanda cathertica*	0.089	0.068	0.109	0.001		
5	*Tabernaemontana divaricata*	0.075	0.065	0.113	0.080	0.005	
6	*Thevetia peruviana*	0.083	0.068	0.103	0.070	0.073	0.029

Thevetia peruviana, and minimum mean divergence (0.00) was found in *Alstonia scholaris* [Table 3]. The accuracy of barcoding depends on the barcode gap between intra-specific and inter-specific variation. Sequence variation between species has to be high enough to tell them apart, while the distance within species must be low for them to cluster together.

The different species of Apocynaceae have formed distinctive clusters. Evidently, all the database sequences and the conspecific generated sequences of *Catharanthus roseus, Thevetia peruviana, Tabernaemontana divaricata, Allamanda cathartica,* and *Alstonia scholaris* with Genbank accession numbers are clustered cohesively. However, the members of Asclepiadaceae subfamily, *Calotropis gigantea* and *Asclepias curassavica,* were located at the basal position, hence used as an out group of the phylogenetic tree [Figure 4].

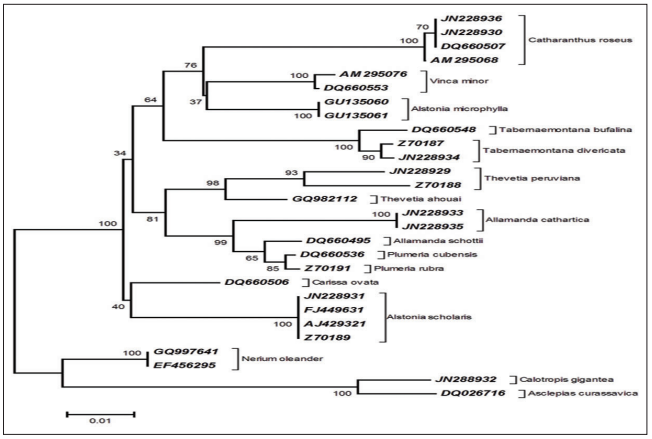

Figure 4: Neighbor-Joining analysis of Kimura2-parameter (K2P) distance of *matK* sequences of Apocynaceae ~758 aligned nucleotide positions of *matK* (Nt. 520-1278) were used in phylogenetic analysis. A total of 1000 bootstrap replicates were calculated for the NJ tree construction.

DISCUSSION

Analyzes of the targeted single loci *matK* (~ 750 bp, Nt. 520-1278) sequences depicted repeat structures with AT-rich regions possessing indels in multiple of 3, and high rate of substitution contributed a considerable number of characters for resolving the phylogeny of

the ethnomedicinal plants of Apocynaceae. Occurrences of indels in *matK* sequences have also been explored to the extent of their applicability as qualitative molecular markers depending upon the size, position, and influence of open reading frame.[22] Several molecular processes are known to create indels, *viz.*, polymerase slippages during DNA replication so called slipped-strand mispairing,[23] and due to addition or subtraction of short repeat sequences, which are primarily AT rich.[22] In general, microstructural changes in DNA, such as, insertions and deletions (indels), and inversions in introns and intergenic spacers, have been importantly used both for resolving phylogenetic relationships among the angiosperms[24,25] and for inferring relationships among more closely related taxa.[26] Imperatively, these changes in protein coding gene are very rare phenomenon, because these changes would lead into non-synonymous mutation. But, the observed indels in the presumed barcode region of *matK* happened in multiple of 3 nucleotides, thereby reduced the chances of frameshift mutation and did not interrupt the site of maturase activity in X domain. So, *matK* indels could be utilized as qualitative molecular marker for studies both at the intra-specific and shallow inter-specific levels like the intergenic spacers of CpDNA.

The sequence divergence among the studied ethnomedicinal plants of Apocynaceae revealed the highest divergence (0.119) between *Catharanthus roseus* and *Calotropis gigantea* [Table 3]. Moreover, *Calotropis gigantea* being a member of subfamily Asclepiadoideae always consistently high rate of divergences with other 5 studied members of subfamily Rauvolfioideae. Thus, following the notional DNA barcode concept, it can be justifiably infer that use of the partial *matK* sequence having reliable barcode gap as characterized in the study would be appreciably applicable to the species level discrimination of the important ethnomedicinal plants belonging to the family Apocynaceae.

Furthermore, NJ tree showed that the member of Rauvolfioideae subfamily Apocynaceae formed one clade where different species clustered into different subclade. The generated sequences of *Allamanda cathartica* is found closely related to *Allamanda schottii*. It is also close to genera *Thevetia* and *Plumeria*. Although *Alstonia microphylla* and *Alstonia scholaris* are the congeners but placed in different clades, which may be due to polyphyletic nature of Alstonieae.[27] Two sequences from *Neruim oleander* of subfamily Apocynoideae, and two members, *viz. Calotropis gigantea* and *Asclepias curassavica* of subfamily Asclepiadoideae, formed two distinct clades at the basal position of phylogenetic tree. Large sample sizes are required to increase the power of the test in Asclepiadaceae subfamily members, but the poor number of *matK* sequences of Asclepiadaceae in the database remained a limitation of the study, which entail the study using large sample sizes from different geographical location.

Recently, the CBOL Plant Working Group (2009) confirmed and suggested the combination of *matK* with *rbcL* as a universal plant DNA barcode[28] though the low discriminating power of *rbcL* gene is severally reported.[6,8] On the contrary, insertions, deletions, and short sequence repeats were common and often more numerous than single base pair substitution that has been the limitation on the part of *trnH-psbA,* hence remained unable to fulfill the criteria of plant DNA barcoding.[7] Nevertheless, in the present study, intergenic spacer *trnH-psbA* also exhibited persistent problem in obtaining constant bidirectional sequences. Our study showed that species identification of Rauvolfioideae subfamily is possible using phylogenetic analyzes constructed from partial *matK* sequences (Nt. 520-1278), which is comparable to that of the full-length sequences, also had species discrimination power. The observed divergences among the studied species using the partial *matK* sequences maintained a reliable gap, which holds good to the concept of species discrimination through DNA barcoding.[29] Furthermore, the NJ phylogenic tree, based on K2P model, also efficiently distinguished the species under study using the partial *matK* sequence. This gene has been identified as a universal DNA barcode for flowering plants.[30]

CONCLUSION

The *matK* sequences within and among the Rauvolfioideae sub-family have shown indels in multiple of 3, particularly N-terminal regions. The *matK* indels could be utilized as studies both at the intra-specific and shallow inter-specific levels like intergenic spacers of CpDNA. To evaluate the indel containing regions, a more powerful algorithm is needed to calculate the intra- and inter-species comparisons. Our result suggests that *matK* sequence information could help in correct species identification for medicinal plants of Rauvolfioideae and in providing diagnostics for rapid and easier identification of mal species forensics in herbal formulation, which bear insights of similar application in family Apocynaceae.

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