

DIVERSITY OF FUNGAL ENDOPHYTES FROM PHLOGACANTHUS THYRSIFORMIS (ROXB.EX HARDW.) MABB., A PROMISING MEDICINAL PLANT IN ARUNACHAL PRADESH, NORTHEAST INDIA.

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The findings of the present study deals with the first type of its report, as presented in the current study, on the diversity of fungal endophyte from ethno medicinal plant-*Phlogacanthus thyrsiformis* (Roxb.ex Hardw.) Mabb., (Acanthaceae). The plant is growing wildly in the forest of Papum Pare, Arunachal Pradesh, India. The samples of the fungal endophytes were collected randomly from the study area and identified based on the morphological, cultural, and reproductive structures (hyaline, ellipsoidal, aseptate, pycnidia, beta conidia, perithecia, asci and ascospores). Further, the phylogenetic analysis of the isolated species was made, using the sequences of 5.8S and 28S rDNA internal transcribed spacer sequence 1 and 4. Overall, 41 fungal spp have been isolated, out of which 37 species belong to the class Ascomycetes; 01 species belong to the each class Zygomycota, Oomycota and Basidiomycota, respectively; however 01 fungal endophyte couldn't identified properly. The maximum number of fungal isolates were recorded from leaves (37%), followed by stems (33%) and root (30%). The observations shows that *Colletotrichum siamense* was the most dominant endophytic fungi, isolated from the selected plant (*P. thyrsiformis*); followed by *Chaetomium globosum*, *Sordaria fimicola, Aureobasidium* sp., *Pythiopsis cymosa* etc. However, *Colletotrichum siamense, Aspergillus fischeri, Plenodomus wasabiae, Aspergillus fumigatus, Nigrospora oryzae*, Saccharomycetales sp., *Epicoccum nigrum., Curvularia borreriae, Colletotrichum guajavae* were the common fungal endophytes recorded from all the plant parts viz., leaf, stem and roots. Besides this, the density of colonization (rD%) was also recorded chronologically as *Colletotrichum siamense* (12.66%) < *Chaetomium globosum* (3.33%) < *Sordariomycetes* sp., *Sordaria fimicola* and *Aureobasidium* sp. (2.66%) followed by the other remaining endophytes (0.66% to 2.00%), respectively.

Keywords: Biodiversity, ethno medicinal plant, endophytic fungi, Molecular identification, Phylogenetic analysis.

De Barry (1866) coined the term 'endophyte' to detect fungi which lives intercellularly and intracellularly in plants tissues, without causing any harm to the plant (Compant et al. 2017, Jeewon et al. 2017). Further, on the bases of their interaction with host plants, fungal endophytes may be divided into three groupscommensalists, parasites and mutualists (Jia et al 2016, Kirschner 2018). In mutualism, definite fungal endophytes gives tolerance to abiotic and biotic stresses on their host plants, improve their growth, and restrain diseases (Redman 2002, Rodriguez 2008). These Endophytes protect their hosts from infectious agents and adverse conditions by secreting bioactive secondary metabolites (Nath et al. 2012, Nongalleima et al. 2013). Endophytic fungi were reported in almost all the plants spp viz. algae, ferns, mosses and mainly in gymnosperms, angiosperms, reported from

various parts of the world (Radic and Strukelj 2012, Doilom et al. 2017). Many researchers have proven that endophyte are the potential source of novel natural products for exploitation in modern medicine, agriculture and industry (Kaul et al. 2013). Till date it has been found that taxol can be produced by endophytic fungi Metarhizium anisopliae and Cladosporium cladosporioides (El-Maali et al 2018). Moreover, since, fungal endophytes can easily be grown in laboratories under routine culture techniques, hence, the potential for discovering virtually inexhaustible supply of metabolites is high. Fungal endophytes are capable of producing compounds similar to their host plants, and are capable in the preservation of world's diminishing biodiversity (Bender et al. 2016, Mane et al. 2017). However, the practicality of commercial production of compounds by endophytic fungi still remains unproven. The reduction of secondary metabolite production on repeated sub-culturing under axenic monoculture conditions is one of the key challenges that need to be addressed in order to establish, restore and sustain the *in vitro* biosynthetic potential of endophytes (Strobel and Daisy 2003).

Studies on fungal endophytes concentrated on medicinal plants have shown that the curative property of the medicinal plant is not only because of the chemicals present in the plant but also because of the fungal endophytes that present in the plant (Verma 2011, Suryanarayanan 2013). Thus, there is enormous need to isolate and identify more number of fungal endophytes and explore the potency of their secondary metabolites. Although, number of studies have already been reported in the association of fungal endophytes with medicinal plants from India viz., *Clerodendron serratum, Pongamia, Withania somnifera* (Ashwagandha) *Taxus* brevifolia, Azadirachta indica, Terminalia arjuna, Trigonella foenum, Labelia nicotinifolia, Adhatoda zeylanica, Bauhinia phoenicea, Catharanthus roseus, Parthenium hysterophorus, Ficus religiosa, Coffea arabica, Crataeva magna, Silybum marianum, Allium sativum, Mamordica chaeantia, and Nothapodytes nimmoniana, (Mane et al. 2017, Mane and Vedamurthy 2018).

It is useful for curing coughs, colds and asthma and is easy to administer. It has also been reported to have antimicrobial properties (Singh and Singh 2010). Fruits and leaves are taken after burning as specific for fevers. Fruits and leaves are taken by the Karbi tribes of Assam after burning them as a specific treatment for fever (Patwari 1992); and also been used in jaundice (Khanikar 2005).

MATERIALS AND METHODS Study area and Sample collection

The study area Papum Pare is located at the N $26^{\circ}56'11''$ to $27^{\circ}35^{\circ}44''$ and E $93^{\circ}12'45''$ to $94^{\circ}13'30''$ is one of the important hotspots in

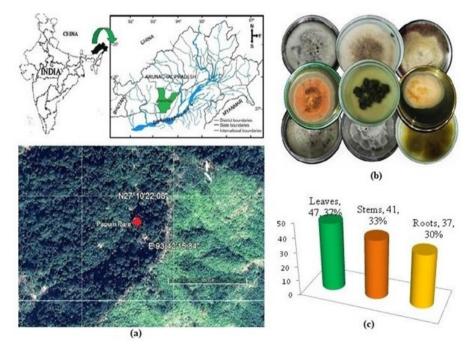


Figure 1 (a) Sample collection site of *Phologacanthus thyrsiformis* Roxb.ex Hardw.Mabb., in Arunachal Pradesh, India (satellite image from Google Earth), where, red circle indicates collection site. **(b)** Isolated endophytic fungi (some) on the culture plates, separately **(c)** Percentage fungal endophytes isolated from different parts of *P. thyrsiformis*

the world, ranked 25th (Chowdhery 1999) and among the 200 globally important eco-regions (Olson and Dinerstein 1998). It covers an area of 2875 sq. km, having annual rainfall 2694 mm. Major part (75%) of this district is sheltered by thick forest which has subtropical, deciduous and humid type of vegetation (Fig.1-a). The selected plant, P. thyrsiformis is an evergreen shrub grows up to 2.4 m high, branchlets quadrangular; leaves 13 to 35 cm long, oblanceolate, elliptic-oblong, acute or acuminate, entire. Flowers in terminal elongated, thyrsoid panicles, up to 30 cm long; corolla tubular, curved; orange or brick red villous. Capsule 3.8cm long, linear clavate (Phurailatpam et al 2014).

Samples of leaves, stems and roots were collected during the period of Dec 2016 to Dec 2018 from the healthy plant of *P. thyrsiformis*; in sterile bags and brought to the laboratory for processing within 24 hours after sampling.

Surface sterilization and isolation: During investigation, total 150 sample segments (50 leaf, 50 stem, and 50 root) were collected from 15 different P. thyrsiformis plants. The samples thus collected were washed gently in running tap water to remove the soil and debris. Further, isolation of fungal endophytes was determined, using the method of Suryanarayanan et al (1998). Samples were chopped into small pieces of (0.5-1.0 cm), and surface-sterilized by dipping them serially in 70% ethanol for 5 sec followed by 4% NaOCl for 90 sec; and finally rinsed in sterile distilled water for 10 sec. The samples thus processed (150 segments) were placed in petriplates (7.5 cm diam; @ ten samples in each plate) already contained potato dextrose agar (PDA) medium (supplemented with 150 mg/L chloramphenicol). The petriplates were sealed properly using parafilm and incubated (12 h dark: 12 h light cycle) for 25 days at the temperature $25\pm2^{\circ}$ C, following the method of Suryanarayanan (1992). After incubation period, the germinated hyphal tips were

isolated and sub cultured on PDA medium, and preserved at 4°C to get the purified sample(s), for further investigation.

Besides this, the density of colonization (rD%) of a single endophyte species was calculated, using the formula as suggested by Fisher and Petrini (1987).

$$rD\% = (Ncol/Nt) \times 100$$

Where,

Ncol = Number of segments colonized by each fungus Nt = Total number of segments inoculated

Morphological identification: The endophytes thus isolated, were identified based on their macroscopic and microscopic characteristics. The fruiting structures and spore morphology were assessed, as per the expertise available at the laboratory as well as confirmed using primary and secondary literature (Ellis 1976, Domsch *et al.* 1980, and Nagmani 2005, Jia *et al.* 2016).

Molecular Identification:DNA Extraction And PCR Amplification of rDNA : Genomic DNA was extracted from fungal mycelia (5-8 days old culture) growing on PDA plates (at $25\pm 2^{\circ}$ C), using Qiagen microbial extraction kit. Fragments of 18S rRNA gene were amplified by PCR, using forward ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') and ITS4 (5'revers TCCTCCGCTTATTGATATGC-3') primer (White et al. 1990). Each PCR amplification reaction was performed in a final volume of 25 uL containing 25 ng template DNA, 10X PCR buffer (10 mM Tris-HCl, 50 mM KCl, pH 8.3), 1.5 mM MgCl2, 200 µM of each dNTP, 50 pM of each primer, 1 unit of Taq polymerase (Genei, Banglore) and distilled water (Sigma, USA). The conditions of the PCR was initial denaturation at 95°C for 5 min followed by 35 cycles of 95°C for 45 s, annealing at 56 °C for 1 min and primer extension at 72 °C for 1 min (again 35 cycles), final extension at 72 °C for 7 min (1 cycle) and hold (cooling) at 4 °C. PCR

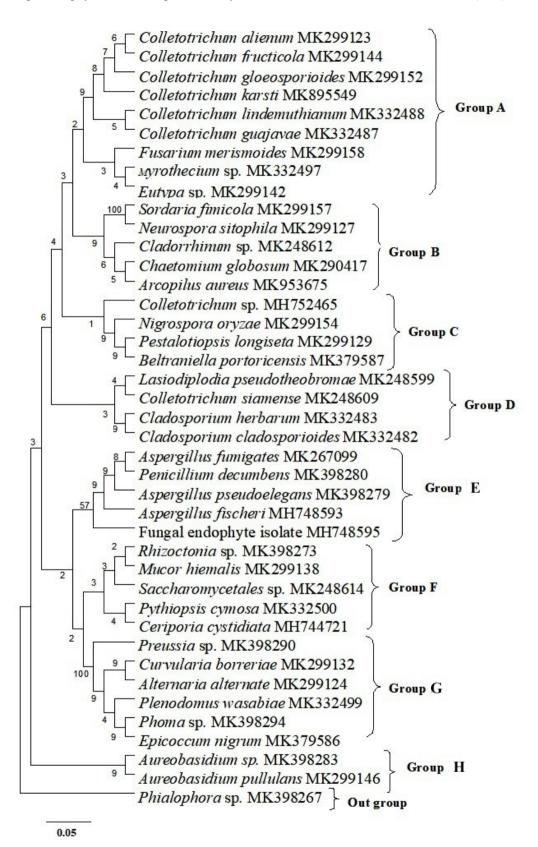


Figure 2 Joining tree based on rDNA of ITS sequences of the different fungal endophytes species isolated of the present study. Numerical value indicates bootstrap percentile from 1000 replicates.

Table 1: Fungal endophytes isolated from different parts of P. thyrsiformis., its number of isolated fungal endophytes
spp and density (rD%)

S.N	Isolated of fungal Endophytes	Plant parts			No. of isolated	rD
		Leaf	Stem	Root	fungal spp	(%)
1	Colletotrichum siamense	Leaf	Stem	Root	19	12.66
2	Aspergillus fischeri	Leaf	Stem	Root	2	1.33
3	Ceripora cyctidia		Stem		1	0.66
4	<i>Eutypa</i> sp.	Leaf			1	0.66
5	Plenodomus wasabiae	Leaf	Stem	Root	2	1.33
6	Neurospora sitophila	Leaf	Stem		2	1.33
7	Colletotrichum fructicola	Leaf			1	0.66
8	Alternaria alternata		Stem	Root	2	1.33
9	Pythiopsis cymosa	Leaf		Root	3	2.00
10	Colletotrichum gloeosporioides		Stem		1	0.66
11	Colletotrichum sp.	Leaf			2	1.33
12	Arcopilus aureus	Leaf	Stem		2	1.33
13	Mucor hiemalis	Leaf		Root	1	0.66
14	Colletotrichum alienum	Leaf	Stem		2	1.33
15	Aspergillus pseudoelegans	Leaf	Stem		1	0.66
16	Penicillium decumbens	Leaf		Root	3	2.00
17	Cladosporium cladosporioides		Stem	Root	2	1.33
18	Myrothecium sp.	Leaf		Root	3	2.00
19	Cladosporium herbarum	Leaf	Stem		2	1.33
20	Aspergillus fumigatus	Leaf	Stem	Root	1	0.66
21	Chaetomium globosum	Leaf			5	3.33
22	Fusarium merismoides		Stem		3	2.00
23	Nigrospora oryzae	Leaf	Stem	Root	2	1.33
24	Saccharomycetales sp.	Leaf	Stem	Root	4	2.66
25	Cladorrhinum sp.			Root	1	0.66
26	Epicoccum nigrum	Leaf	Stem	Root	3	2.00
27	Colletotrichum karstii		Stem		2	1.33
28	Beltraniella portoricensis	Leaf			2	1.33
29	Sordaria fimicola		Stem	Root	4	2.66
30	Curvularia borreriae	Leaf	Stem	Root	1	0.66
31	Fungal Endophyte sp.	Leaf		Root	1	0.66
32	Pestalotiopsis longiseta		Stem		3	2.00
33	Aureobasidium pullulans	Leaf		Root	3	2.00
34	Colletotrichum guajavae	Leaf	Stem	Root	2	1.33
35	Colletotrichum lindemuthianum		Stem		3	2.00
36	Rhizoctonia sp.	Leaf		Root	1	0.66
37	Lasiodiplodia pseudotheobromae		Stem	Root	1	0.66
38	Preussia sp.	Leaf		Root	3	2.00
39	Phialophora sp.	Leaf			2	1.33
40	Phoma sp.		Stem	Root	2	1.33
41	Aureobasidium sp.	Leaf	Stem		4	2.66

--- indicates absences of the fungal endophytes.

products were checked on 1.2 % Agarose gel in Tris-acetate-EDTA buffer (TAE) at pH 8.0, stained with ethidium bromide (0.3 lg/mL) and visualized under UV light by using Gel documentation system. Sequencing was done by GeNei Labs Private Limited, Bengaluru; using PRISM® BigDyeTM Terminator Cycle

Sequencing Kits with AmpliTaq® DNA polymerase, as per the manufacturer's instructions.

Phylogenetic analysis: The sequences thus obtained, were subjected to BLAST and submitted to Genbank of NCBI as well as got

the accession number. Further, to get the homology, search and multiple sequence alignments were made using Clustal W (Thompson *et al.* 2003). However, sequences were analyzed for generating phylogenetic tree, using neighbour joining methods of MEGA 5 (Tamura *et al.* 2011). The robustness of the inferred phylogeny was assessed using bootstrap value at 1,000 replications (Fig. 2).

RESULTS

The findings of the present investigation deals with the isolation of endophytic fungi, from P. thyrsiformis; an ethnomedicinal plants commonly used for the treatment of various ailments in human beings. The observations showed that total 105 isolates of endophytic fungi were isolated from the 150 sample segments. The maximum number of fungal isolates were recorded from leaves (37%), followed by stems (33%) and root (30%) (Fig.1-c), respectively. Overall 41 fungal endophytes were recorded, which belongs to 29 genera. Colletotrichum siamense was the most dominant endophytic fungi, followed by Chaetomium globosum, Sordaria fimicola, Aureobasidium sp., Pythiopsis cymosa and others. However, Colletotrichum siamense, Aspergillus fischeri, Plenodomus wasabiae, Aspergillus fumigatus, Nigrospora oryzae, Saccharomycetales sp., Epicoccum nigrum., Curvularia borreriae, Colletotrichum guajavae were the common fungal endophytes recorded from all the plant parts viz., leaf, stem and roots (Fig. 1-b). Besides, the density of colonization (rD%) was recorded in the chronology of Colletotrichum siamense (12.66%) < *Chaetomium globosum* (3.33%) < Sordariomycetes sp., Sordaria fimicola and Aureobasidium sp. (2.66%) and 0.66% to 2.00% for the remaining endophytes (Table 1). Further, it was observed that out of 41 fungal endophytes; 20 belongs to the class-Sordariomycetes; 11 belongs to Dothideomycetes; 05 belongs to

Eurotiomycetes; 02 belongs to Agaricomycetes; and 01 belongs to class Zygomycetes and Oomycetes, each; however, 01 couldn't identified properly. While categorizing up to the order level; it was recorded that Colletotrichum sigmense, C. fructicola, C. gloeosporioides, Colletotrichum sp., C. alienum, C. karstii, C. guajavae and C. lindemuthianum, belongs to the order Glomerellales; Plenodomus wasabiae, Alternaria alternata Epicoccum nigrum, Curvularia borreriae, Preussia sp. and Phoma sp. belongs to the order Pleosporales; A. fischeri, A. pseudoelegans, Penicillium decumbens and A. fumigatus belongs to the order Eurotiales; Neurospora sitophila, Arcopilus aureus, Chaetomium globosum and Sordaria fimicola belongs to order Sordariales; Eutypa sp., Beltraniella portoricensis and Pestalotiopsis longiseta belongs to order Xylariales; Cladosporium cladosporioides and C. herbarum belongs to order Capnodiales; Myrothecium sp. and Fusarium merismoides belongs to order Hypocreales; Aureobasidium sp. and A. pullulans belongs to order Dothideales; Sordariomycetes sp. and Cladorrhinum sp. belongs to order Saccharomycetales. Besides this, 01 fungal endophytes belong to order Cantharellales viz. Rhizoctonia sp.; Ceripora cvctidia belongs to order Polyporales; Mucor hiemalis belongs to order Mucorales; Pythiopsis cymosa belongs to order Saprolegniales; Lasiodiplodia pseudotheobromae belongs to order Botryosphaerial; Phialophora sp. belongs to order Chaetothyriales and Nigrospora orvzae belongs to order Trichosphaeriales, respectively.

Furthermore, the isolated samples of the fungal endophytes (41 samples) were used for extraction of the DNA, molecular characterization as well as phylogenetic analysis. The observations of the neighbour joining tree as constructed based on the sequence structure alignment, shows clearly

eight well separated groups. Group 'A' consisted Colletotrichum fructicola, C. gloeosporioides, C. alienum, C. karstii, *Colletotrichum guajavae*, *C. lindemuthianum*, Fusarium merismoides, Myrothecium sp. and Eutypa sp. Similarly, group 'B' consisted Sordaria fimic, Neurospora sitophila, Cladorrhinum sp., Chaetomium globosum, Arcopilus aureus; group 'C' consisted Colletotrichum sp., Nigrospora oryzae, Pestalotiopsis longiseta, Beltraniella portoricensis; group 'D' consisted Lasiodiplodia pseudotheobromae. Colletotrichum siamense, Cladosporium herbarum, Cladosporium cladosporioides; group 'E' consisted Aspergillus fumigatus, Penicillium decumbent, Aspergillus pseudoelegans, Aspergillus fischeri, fungal endophyte isolate; group 'F' consisted Rhizoctonia sp., Mucor hiemalis, Saccharomycetales sp., Pythiopsis cymosa, Ceriporia cystidiata; group 'G' consisted Preussia sp., Curvularia borreriae, Alternaria alternata, Plenodomus wasabiae, Phoma sp., Epicoccum nigrum; and group 'H' consisted Aureobasidium sp., Aureobasidium pullulans; however Phialophora sp. was used for outer group (Fig. 2).

DISCUSSION AND CONCLUSION

Literature revels that diversity of fungal endophytes have already been reported from several medicinal plant species viz., Fomitopsis sp. Penicillium sp., Diaporthe sp., Arthrinium sp. Phomopsis sp. and Schizophyllum sp. have been reported from Garcinia mangostana and G. parvifolia (Sim et al 2010); Mortierella minutissima, N. sphaerica, Acremonium strictum, Humicola Grisea, Mortierella hyaline, Oidiodendron echinulatum, O. griseum, Humicola fuscoatra and Arthroderma tuberculatum reported from Elaeocarpus sphaericus (Shukla et al. 2012); P.citrinum, A. alternata, Aspergillus niger, Cladosporium sp., Rhizopus sp., C.vermiformis reported from Helicteres isora

(Gayathri and Chandra 2017); Periconia hispidula, Allomvces arbuscula, N. sphaerica, A. falciforme, P. chrysogenum Aureobasidium sp. Chaetomium sp. from Litsea cubeba (Deepanwita and Dhruva 2018); and Fusarium spp, Aspergillus sp., Chaetomium sp., Penicillium sp., Setosphaeria rostrata, F.solani, Bipolaris maydis, D.phaseolorum, Rhizoctonia bataticola, and Macrophomina reported from Chlorophytum phaseolina borivilianum (de Carvalho et al. 2019) as well as Alternaria alternata, Aspergillus terreus, Alpestrisphaeria reported from Vitex rotundifolia (Yu-Hung and Roland 2019). Similarly, in the current study, we have reported total 41 fungal endophytes, out of which Aspergillus fischeri, A. fumigatus, Colletotrichum guajavae, Colletotrichum siamense, Curvularia borreriae, Epicoccum nigrum., Nigrospora oryzae, Plenodomus wasabiae, Saccharomycetales sp., were the common fungal endophytes recorded from all the plant parts viz., leaf, stem and roots. Colletotrichum siamense was the most dominant endophytic fungi having 12.66% density of colonization (rD%) (Table 1). Besides this, extraction of the DNA and its molecular characterization as well as phylogenetic analysis based on the ITS1-ITS4 sequencing data of the isolated 41 fungal endophytes, have also been investigated and recorded (Figure 2).

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