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Lasiodiplodia indica - A new species of coelomycetous mitosporic fungus from India

Indu Bhushan Prasher* and Gargi Singh Department of Botany, Mycology and Plant Pathology Laboratory Panjab University, Chandigarh, India * Corresponding author email: chromista@yahoo.co.in (Submitted in November, 2014; Accepted on December 20, 2014)

ABSTRACT

Lasiodiplodia indica sp. nov. is described as a new species based on morphological characteristics and DNA sequence data of ITS1 and ITS4. It differs from other species in the nature of the conidiomata, conidial septation, branching and septation of paraphyses. Detailed description, taxonomical remarks, and illustrations are provided.

Keywords: Coelomycetes, conidiomata, ITS, phylogeny, taxonomy

INTRODUCTION

Lasiodiplodia species are widespread, most commonly found in tropical and subtropical regions where they cause variety of diseases (Punithalingam, 1980). However, only a single species viz: *L. theobromae* has been reported from different geographical regions of India (Bilgrami *et al.*, 1991; Jamaluddin *et al.*, 2004). The presence of pycnidial paraphyses and longitudinal striations on mature conidia are the typical characteristics of this genus that distinguishes it from other closely related genera.

This report is a part of the ongoing study to inventorize anamorphic and telomorphic fungi of North West India including Himalaya (Sohi and Prasher, 1981; Prasher and Sharma, 1997; Prasher et al., 2003; 2004; 2005; 2008; Prasher and Verma 2012a; b; Prasher and Ashok, 2013; Prasher and Lalita, 2013; Prasher and Singh, 2012; 2013; 2014; Ashok and Prasher, 2014a; b; Prasher and Sushma, 2014). An interesting coelomycetous fungus was isolated from fallen twigs near the trees of Morus alba L. collected from the Botanical Gardens, Department of Botany, Panjab University, Chandigarh, India. A thorough review of literature (Sutton, 1980; Abbas et al., 2004; Pavlic et al., 2004; 2008; Burgess et al., 2006; Damm et al., 2007; Alves et al., 2008; Abdollahzadeh et al., 2010; Begoude et al., 2010; Úrbez-Torres et al., 2011; Ismail et al., 2012; Phillips et al., 2013) and detailed examination using both morphological characteristics and DNA sequence data of the rDNA internal transcribed spacers, ITS1 and ITS4, revealed it to be an undescribed species of Lasiodiplodia.

MATERIALAND METHODS

Fungal isolation: The fungus was isolated from fallen twigs collected from Botanical Gardens, Panjab University, Chandigarh. The isolations were made by directly plating out pieces of the fungal tissue after surface sterilization (2 min in 90% ethanol). The conidiomata were cut through horizontally and the contents were transferred on plates of PDA. The plates were incubated at 25 °C.

Morphology and cultural characteristics: To induce sporulation the isolates were transferred on 2% PDA (HiMedia) and incubated at 25 °C for 4-6 weeks in the dark. Culture colours (upper surface and reverse) were described using the colour charts of Rayner (1970). Morphological characters were studied from the isolates sporulating on PDA as well as from the fungal material on

the host tissue. Cross-sections of conidiomata were made by hand, stained in Cotton blue (Cotton blue 0.01g+Lactic acid 100 ml) and mounted in glycerol to observe conidiophores and paraphyses morphology. Conidial masses were mounted in Amann's Lactophenol (Phenol-20 g, Lactic acid-20 g, Glycerol-40 g, Distilled water 20 ml). All digital images were recorded with Matrix VL-Z60 stereo triocular microscope and Matrix VRS-2f transmission microscope. Measurements were made using dgsoft ProMed software.

DNA extraction, amplification and sequencing: The molecular characterization of *Lasiodiplodia indica* was done by employing the technique of White *et al.* (1990) by amplifying the entire ribosomal internal transcribed spacer (ITS) using ITS1 (5'- TCCGTAGGTGAACCTGCGG-3') and ITS 4 (5'-TCCTCCGCTTATTGATATGC-3'). Mycelium was harvested from colonies on PDA grown at 25 °C for 7 days in the dark and total genomic DNA was extracted using HiPurATM SP Fungal DNA mini kit (HiMedia) by following the manufacturer's instructions. DNA was stored at -20 °C for further use.

Fragment containing the region encoding ITS 1, 5.8 s rDNA and ITS 4 was amplified using primer pair ITS 1 and ITS 4 (White et al., 1990). DNA amplification was performed in a 25 µl reaction using 2 µl of template DNA (30 ng), 1U of Taq DNA polymerase (Genei, Bangalore India), 2.5 µl of 10 x Taq DNA polymerase buffer, 1µl of 10 pmol primer, H₂O (Sterile Ultra Pure Water Sigma) to make up volume 25 µl. For the amplification of ITS region following PCR condition were used: 3 min at 95 °C, 1 min at 56 °C, 1 min at 72 °C and final 7 min extension step at 72 °C. The PCR product was purified with an Axygen PCR cleanup kit (Axygen Scientific, CA, USA) and sequenced with the same primers using the BigDye Terminator v3.1 Cycle Sequencing kit (Applied Biosystems, USA). The sequencing reactions were run on an ABI 3730/3730XL-1409-023 automated DNA sequence (Applied Biosystems, USA). The sequencing step was done by Xcelris genomics, An Abellon Company.

Phylogenetic analysis: ITS sequences of 19 isolates of *Lasiodiplodia* species, 2 isolates representing 2 species of *Diplodia* and *Botryosphaeria dothidea* were retrieved from GenBank (**Table 1**) and compared with *Lasiodiplodia indica*. Fungal sequences were aligned using the ClustalW multiple alignment program (Thompson *et al.*, 1994). Manual adjustments of sequence

Species	Isolate	Origin	Host	Collector	GenBank accession no
Lasiodiplodia	CBS 164.96	New Guinea	Fruit	-	NR 111174
theobromae					_
L. viticola	CMM4014	Brazil	Mangifera indica	-	JX464098
L. hormozganens is	CMM3987	Brazil	M. indica	-	JX464094
L. brasiliense	CMM2320	Brazil	Carica papa ya	-	KC484814
L. eg yptiacae	CB S130992	Egypt	Mangifera indica	A Ismail	NR 120002
L. mahajangana	CMW 27801	Madagascar	Terminalia catappa	-	FJ900595
L. irani ensis	WAC1 3297	Australia	Mangifera indica	-	GU172379
L. missouriana	UCD2199MO	Missouri, USA	Vitis sp.	K Striegler & GM	HQ288226
			-	Leavitt	-
L. parva	CBS 456.78	Colombia	Cass ava-field soil	O Rangel	NR 111265
L. pseudotheobromae	CBS 116459	Costa Rica	Gmel ina arbore a	J Carranza-Velásquez	NR ⁻ 111264
L. gilanensis	IRAN1501C	Iran	-	J Abdollahzadeh & A	GU945352
				Javadi	
L. pluri vora	STE-U5803	South A frica	Prunus s alic ina	U Dam m	EF445362
L. citricola	7E80	Califomia, USA	-	-	KC357300
L. margaritacea	CB S122065	Australia	Adansoni a g ibbosa	TI Burgess	EU144051
L. rubropurpurea	WAC1 2538	Australia	Eucalyp tus grandis	TI Burgess & G Pegg	DQ103556
L. venezuelensis	P1	Venezuela	-	0 00	JX 545103
L. crassispora	WAC 1 25 33	Australia	Santalum al bum	TI Burgess & B Dell	NR 111194
L. gonubiensis	CBS 115812	South A frica	Syzygium cordatum	D Pavlic	NR 111218
L. ligni cola	MFLUCC 11-	Thailand	Wood	AD Ariyawansa	NR ⁻ 111795
0	0435			5	—
L. indica	IB P 01	India	Angiospermous	IB Prasher & G Singh	KM376151
			wood		
Dip lodia africana	STE-U 5908	South A frica	Prunus persica	U Dam m	NR 119635
D. mutila	B53	Italy	-	-	FJ481586
Botryosphaeria dothidea	CMW 8000	Switzerland	Prunus sp.	B Slippers	NR_111146

Table 1 Isolates of species considered in the phylogenetic study

alignment was done using BioEdit Sequence Alignment Editor Version 7.0.8. (©19972005 Tom Hall). Phylogenetic analyses of sequence data were done using PAUP* v.4.0b10 (Swofford, 2003) for Maximumparsimony (MP) and Neighbour joining (NJ) analyses. The NJ analysis was performed using Kimura-2 parameter nucleotide substitution model (Kimura, 1980). All characters were unordered and of equal weight. Bootstrap values were obtained from 1000 NJ bootstrap replicates. Maximum-parsimony analysis was performed using the Tree-Bisection-Regrafting (TBR) algorithm (Nei and Kumar, 2000) with search level 1 in which the initial trees were obtained by the random addition of sequences (100 replicates). All characters were unordered and of equal weight and all positions containing gaps and missing data were eliminated. Branches of zero length were collapsed and all multiple, equally parsimonious trees were saved. The robustness of the most parsimonious trees was evaluated by 1000 bootstrap replications (Hillis and Bull, 1993). Other measures used were consistency index, retention index and composite index. Evolutionary analyses were conducted in MEGA6 (Tamura et al., 2013). Fungal sequences were deposited in GenBank and the specimen (Holotype) was deposited in the Herbarium of Botany Department Panjab University, Chandigarh, India (PAN). Culture of the novel species described in this study was deposited in the culture collection of the Botany Department, Panjab University, Chandigarh (PAN).

RESULTS

PHYLOGENETIC ANALYSIS

The analysis involved 23 isolates compared on the basis of ITS sequences. There were a total of 424 positions in the final dataset. Maximum parsimony analysis of the final dataset resulted in 10 equal, most parsimonious trees

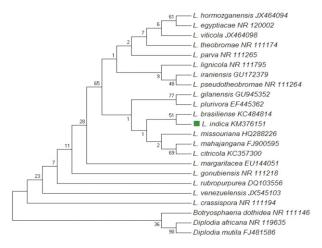


Fig. 1 Maximum Parsimony analysis of taxa. The evolutionary history was inferred using the Maximum Parsimony method. Tree #1 out of 10 most parsimonious trees (length = 90) is shown. The consistency index is (0.611111), the retention index is (0.686567), and the composite index is 0.526368 (0.419569) for all sites and parsimony-informative sites (in parentheses).

(consistency index = 0.611111; retention index = 0.686567and composite index = 0.526368) each with the same topology. One of the 10 most parsimonious tree is presented in **Fig. 1**.

TAXONOMY

Lasiodiplodia indica I.B. Prasher and Gargi Singh sp. nov. Figs. 2-4

MycoBank MB810909

Conidiomata multilocular, with 1-2 ostioles; paraphyses hyaline, with fusoid pointed tip,

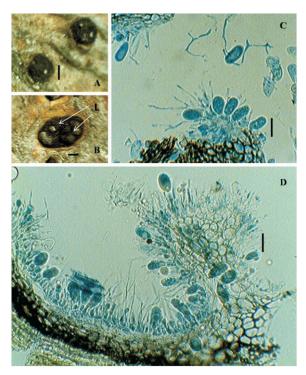


Fig. 2 Lasiodiplodia indica A-Conidiomata erumpent through the host bark, B-Conidiomata cut through horizontally showing locules (L), C & D-Cross section of conidiomata showing paraphyses, conidiogenous cells and conidia. Bars A, $B=200 \,\mu m$; C, $D=20 \,\mu m$.

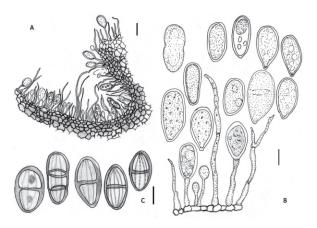


Fig. 4 Lasiodiplodia indica (Line drawings) A-Crosssection of conidiomata showing paraphyses, conidiogenous cells and conidia, B-Conidiogenous cells, paraphyses and hyaline conidia, C-Mature septate conidia with striations. Bars $A=20 \mu m$; B, $C=10 \mu m$.

septate and occasionally branched; conidia initially hyaline, unicellular, later developing one to two septa, with dark brown pigmentation and longitudinal striations from apex to base.

Etymology: After the name of the country of origin.

Mycelium semi-immersed, branched, septate, dark brown. *Conidiomata* eustromatic, semi-immersed, globose, dark brown, multilocular, up to 1 mm, with 1-2 ostioles; wall dark brown, thick-walled, texura angularis, paler and

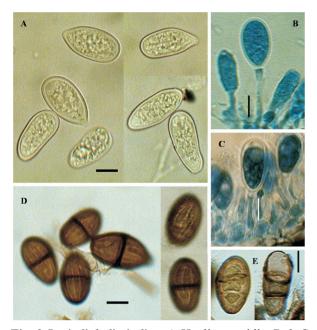


Fig. 3 Lasiodiplodia indica A-Hyaline conidia, B & C-Conidia attached to conidiogenous cell, D-Brown conidia with one septum and striations, E-Brown conidia with two septa. Bars $A-E = 10 \ \mu m$.

thinner towards the conidiogenous region, often with dark brown superficial hyphae over the surface. Paraphyses hyaline, with fusoid pointed tip, septate and occasionally branched, up to 120×1.5 - $3.5 \,\mu$ m. Conidiogenous cells holoblastic, determinate, discrete, cylindrical, hyaline, smooth, formed from cells lining the inner pycnidial walls, 8.5- $15(17.5) \times 1.5$ - $3.5(4) \,\mu$ m. Conidia acrogenous, initially hyaline, unicellular, ellipsoid to obovoid, thick walled, guttulate, rounded at apex, truncate at the base, later developing one to two septa, dark brown pigmentation and longitudinal striations from apex to base, 20- 38×11 - $20.5 \,\mu$ m.

Collection examined: India, Chandigarh 321 m, Botanical gardens, Panjab University, 21.03.2011, on fallen twig of an angiospermous tree, I. B. Prasher and Gargi Singh (Holotype: PAN 30202).

Culture characters: The fungus was isolated on 2% PDA (HiMedia) at 25 °C in the dark. The fungus produced aerial white mycelia initially, turning paler after 7 days and becoming olivaceous black within 20-25 days, reverse side of the colony dark slate-blue, producing pycnidia after 45 days. Optimum temperature for growth 25-30 °C.

DISCUSSION

The presently examined collection was identified as a species of *Lasiodiplodia* based on the typical characteristics of the genus which is the presence of pycnidial paraphyses and longitudinal striations on mature conidia. It can be distinguished morphologically and phylogenetically from the previously described species. The species is differentiated from the rest of the species of the genus described till-to-date by the multilocular nature of the conidiomata. In the septation of conidia it resembles *L. gonubiensis* to some extent. However, the conidia in *L. gonubiensis* are 1-3 septate as compared to 1-2 septate in

Species	Conidia (µm)	L/W ratio	No. of septa	Conidiogenous cell (μm)	Pa raphyses Size (µm)	Septation and branching
Lasiodiplodi a the obromae	21-31× 13-15.5	1.9	1	5-15 × 3	Up to 55 × 3-4	Septate, occasionally
						branched
L. fiorii	24-26 × 12-15	-	1	-	-	-
L. ricinii	$16-19 \times 10-11$	-	1	-	25-35 × 2	-
L. thomasiana	$28-30 \times 11-12$	-	1	-	Up to 90 × 1.5	-
L. gonubiens is	(28)32-36(39) ×	1.9	1-3	(6.5)10-15(18) ×	(14)26.5-47(65)	A sept ate,
	(14)16-18.5(21)			1(2)-4(4.5)	× (1.5)2-2.5(3)	unbranched
L. undulata	20×12	-	1	5-15 × 1.5-3	-	Septate,
L. crass ispora	27-30(33) × 14-17	1.8	1	(6)8-16(19) × 3-7	$(21)30-62(66) \times 225(4)$	unbranched Septate, unbranched
L. rubropurpurea	24-33 × 13-17	1.9	1	7-13(15) × 3-5	2-3.5(4) (30)32-52(58) × 1.5-3.5	A sept ate, unbranched
L. venezuelensis	26-33 × 12-15	2.1	1	(5)7-14(15) × 3- 4.5(5)	$(12)16-41(45) \times (1.5)2-5$	Septate, unbranched
L. pseudoth eobromae	23.5-32 × 14-18	1.7	1	-	Up to 58 × 3-4	A sept ate, oc casionally
L. parva	16-23.5 × 10.5-13	1.8	1	-	Up to 105 × 3-4	branched Septate, unbranched
L. plurivora	(22)26.5-32.5(35) × (13)14.5-17(18.5)	1.9	1	8-13 × 4-7	Up to 130 × 2-5	Septate, occasionally branched
L. marg aritacea	(12)14-17(19) ×	1.3	1	(6)10-11(19.5) ×	(19)28-46(54) ×	Septate,
L. mai gui nuc cu	(12)11-17(12)11-(12)12	1.5	1	(2)3-4 (4.5)	(1.5)2-2.5(3)	unbranched
L. citrico la	(10)11 12(12.5) $(20)22-27(31) \times$ (10.9)12-17(19)	1.6	1	11-16 × 3-5	Up to $125 \times 3-4$	Septate, rarely branched
L. gilanensis	(25.2)28-35(38.8) × (14.4)15-18(19)	1.9	1	11-18 × 3-5	Up to 95 × 2-4	Septate, rarely branched
L. hormozganensis	(15.3)18-24(25.2) × 11-14	1.7	1	9-15 × 3-5	Up to 83 × 2-4	Septate, rarely branched
L. iraniensis	(15.3)17-23(29.7) × 11-14	1.6	1	9-16 × 3-5	Up to 127 × 2-4	Septate, rarely branched
L. mahaj angana	(13.5)15.5-19(21.5) × (10)11.5-13(14)	1.4	1	$\begin{array}{c} (10)10.5 - 18(26) \times \\ (3)3.5 - 5.5(6) \end{array}$	(27.5)33.5 - 52.5(66) × (2)2.5-3.5(5)	Aseptate, unbranched
L. viticol a	(16 5 -)18-20.5 (-23) × (8-)9-10.1(-10.5)	2.05	1	-	Up to $60 \times 2-3$	Aseptate, unbranched
L. lignicola	(15-)16-17.5× (8) 8.5- 10.5(-11)	1.7	1	10-15 × 2.5-3.5	Up to 15	Aseptate
L. missouriana	$(16-)17.5-19.5(-21) \times (8-)9-10.5(-11.5)$	1.9	1	-	Up to 55 × 2-3	Aseptate, unbranched
L. egyptiacae	(17–)20–24(-27) × 1 1–1 2(-13)	2	1	5-11 × 3-5	Up to 57 × 2-3	Aseptate
L. indica	20-38 × 11-20.5	1.8	1-2	8.5-15(17.5) × 1.5- 3.5(4)	Up to 120 × 1.5- 3.5	Septate, oc casionally branched

Table 2 Conidial and paraphyses dimensions of Lasiodiplodia spp.

L. indica. The size of conidia as well as that of conidiogenous cells and paraphyses are different in the two species (**Table 2**). The paraphyses in *L. indica* are septate and branched where as in *L. gonubiensis* these are non septate and unbranched. It differs from rest of the species in which conidia are only single septate. On the basis of above characters it is proposed as a new species.

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