PRESIDENTIAL ADDRESS

Revisiting the taxonomy of *Colletotrichum* using multi-locus gene phylogeny*

P. CHOWDAPPA

Central Plantation Crops Research Institute, Kasaragod 671 124, Kerala, India

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Dear members of the Indian Phytopathological Society (IPS) and delegates of the National Symposium.

I am privileged to represent our society as the President and to follow and strengthen the philosophy and scientific contribution of the previous leading scientists, who have served as Presidents. This is a formidable task, yet I derive strength and inspiration from our executive committee. Please join me in welcoming our IPS members and delegates to the IPS 69th Annual Meeting and National Symposium on “Diagnosis and Management of Plant Diseases: Integrated Approaches and Recent Trends” held at ICAR Research Complex for NEH Region, Umiam, Meghalaya during January 09-11, 2017. Moreover, I would like to extend many thanks for the involvement and contribution of the executive committees at Zonal and national levels, who have been essential in keeping our society running actively and soundly. The society will continue to providing support and, in some cases, guidance, for the organization and development of courses, seminars, workshops and zonal meetings in different parts of the India for reducing crop losses caused by plant pathogens.

I am very happy to mention that American Phytopathological Society (APS) and the Indian Phytopathological Society (IPS) exchanged memorandums of understanding (MOUs) at the inaugural ceremony of the 6th International Conference on “Plants, Pathogens, and People” held in New Delhi, India, February 23-27, 2016. This MOU would provide greater engagement between the societies, increase memberships in both societies, joint planning of sessions at each society’s annual meetings, webinar development, and eventually the development of an intergovernmental

funding mechanism modeled after U.S.-Israel BARD for joint research projects. The agreement is valid through September 2019. I consider this is a milestone in the history of IPS. As part of MOU, APS has extended the benefits to IPS by offering travel grant to IPS student members to attend annual APS meetings in the USA every year and joint APS-IPS meeting at International Congress of Plant Pathology, Boston, USA.

Plant pathology has played a key role in ushering “green revolution” and has an equally important role to play in modern agriculture. We must be alert continuously for new ways to position our discipline to address the emerging challenges that affect food security. Producing sufficient food is a major challenge for rising population coupled with declining natural resources and climate changes. Over the past couple of centuries, plant diseases have inflicted severe damage to the cultivated crops, leading to starvation and death of the people. Crop losses due to plant diseases play a significant role in reducing global food production and associated food security. Estimates have shown that 30-40% crop losses occur every year globally and future strategies that reduce these crop losses can improve the food security. Avoiding the spread of diseases between countries is also an important part to reduce the disease impact and biosecurity measures need to be strengthened to reduce the risk of introduction of aggressive pathogens. Among the various diseases of the crops caused by phytopathogens, the challenges posed by fungal diseases are most predominant compared to the combined effects of bacteria, viruses and phytoplasma. Indeed, fungal diseases have been causing relentless economic damage to crops since the mid-20th century. Undoubtedly, fungal diseases potentially could be ascribed as a serious threat to the global food security and natural vegetation.

The genus *Colletotrichum* has been ranked as one of the top 10 economically important fungal pathogens by scientists world-wide (Dean *et al.*, 2012).

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Email: pallem22@gmail.com

Fig. 1. Symptoms of anthracose on different crop plants in India

Colletotrichum causes anthracnose disease in diverse crop plants such as fruits, vegetables, ornamental crops (Fig. 1) and natural vegetation (Cannon *et al.*, 2012; Damm *et al.*, 2012a,b; Weir *et al.*, 2012; Udayanga *et al.*, 2013; Sharma and Shenoy, 2016). Besides, *Colletotrichum* has been attributed as a causal organism for widespread post-harvest diseases in many fruits such as apple, banana, chilli, coffee, grape, mango and strawberry (Bailey and Jeger, 1992; Chowdappa *et al.*, 2009). The fungal genus is so diverse that some of the species of this genus are endophytes while saprobes were also documented (Cannon *et al.*, 2012; Hyde *et al.* 2009; Jayawardena *et al.* 2016). Also, multiple *Colletotrichum* species have been reported to infect a single host or on the contrary, a single *Colletotrichum* species can cause infection in multiple hosts (Cannon *et al.*, 2012).

Historical perspectives

The genus *Colletotrichum* belongs to the family *Glomerellaceae* (Glomerellales, Sordariomycetes), and is a monotypic genus of this family (Jayawardena *et al.*, 2016). Initially, Tode (1790) described the genus *Colletotrichum* under the name *Vermicularia*; it was later renamed by Corda (1831) as *Colletotrichum*. It was

placed in the order “Melanconiales” under “Coelomycetes” by Hawksworth (1983). The generic epithets *Colletotrichum* and *Vermicularia* encompassed a range of species for many years; however, presently they are all classified under the genus *Colletotrichum* (Sutton, 1992). A major morphological distinction is the presence of marginal setae in *Colletotrichum* whereas *Vermicularia* is characterized with dispersed setae throughout the conidiomata (Clements and Shear, 1931). Nonetheless, the variable nature of conidiomata in terms of its structure, form, setae and their arrangement within the acervulus has been remarked as of little taxonomic significance (Duke, 1928) at the genus level. These conclusions lead to the transfer of large number of species from *Vermicularia* to *Colletotrichum* (Cannon *et al.*, 2012). Interestingly, a morphologically similar anamorph, *Gloeosporium*, which does not produce setae, could not be separated from the genus *Colletotrichum* (Baker *et al.*, 1940). However, *Gloeosporium lindemuthianum* has been placed in *Colletotrichum* (Briosi and Cavara, 1889). Recently, *Gloeosporium kaki hori* has been renamed as *Colletotrichum horii* (Weir and Johnston, 2010) and *G. pedemontanum* has been merged with *C. gloeosporioides* (Weir *et al.*, 2012).

The anamorph-teleomorph associations in *Colletotrichum* have been described in detail by Cannon *et al.* (2012). While *Glomerella* has been designated as its teleomorph, the anamorphic features are found in *Colletotrichum*. Moreover, the occurrence of *Glomerella* has been observed only infrequently in nature/culture media (Cannon *et al.*, 2012; Damm *et al.*, 2012a,b; Hyde *et al.*, 2009; Sutton, 1992) and morphological identification of many *Glomerella* species still remains uncertain. In the light of these facts, uniform code of “one fungus: one name” has been adopted after modifying Article 59 of the International Code of Nomenclature for algae, fungi and plants (Norvell, 2011). Hence, all the fungal species are henceforth to be identified with one formal name even though the species may show separate asexual and sexual life cycles. International sub-commission on *Colletotrichum* Taxonomy (ISCT) has been established under the International Commission on the Taxonomy of Fungi (ICTF, <http://www.fungaltaxonomy.org/subcommissions>) in order to resolve the issues associated with *Colletotrichum* nomenclature. Accordingly, the epithet *Colletotrichum* is preferred over *Glomerella* by the mycologists (Cai and Weir, 2012). Readers are advised to see a detailed review by Cannon *et al.* (2012) for more information on the history of classification and nomenclature.

Colletotrichum taxonomy

The shape of conidia, its size, setae and appressoria and host-specificity are the traditional characteristic features which have been used to identify *Colletotrichum* species (Sutton, 1980, 1992; von Arx, 1957). The period from the 1880s through 1950s witnessed description of hundreds of *Colletotrichum* species based on the impression that *Colletotrichum* species were host-specific. When the first monograph of *Colletotrichum* was

published by von Arx (1957), around 750 names existed (Cannon *et al.*, 2012). Thus, description and identification based on morphological criteria alone resulted in 11 *Colletotrichum* species (von Arx, 1957). It was followed by further addition of 12 species by Sutton (1980); the addition was based not only on morphology but also on the host-specificity. Later on, it went up to 39 species (Sutton, 1992). Nevertheless, identification and classification of *Colletotrichum* species purely based on morphological characters have led to many inconsistencies. The problem was further compounded when *Colletotrichum* species complexes were observed due to the presence of overlapping morphological characters (Cai *et al.*, 2009; Hyde *et al.*, 2009). Hyde *et al.* (2009) questioned the veracity of 19 doubtful species in the genus and proposed the necessity for taxonomic revision of this genus employing molecular techniques (Hyde *et al.*, 2009a).

A repertoire of molecular methodologies *viz.*, sequencing and analysis of the *ITS* region of the rDNA region (Mills *et al.*, 1992; Sreenivasaprasad *et al.*, 1994; Brown *et al.*, 1996), restriction enzyme digestion-based restriction fragment length polymorphism analysis and sequence analysis of [A+T rich] mitochondrial DNA have been employed to study *Colletotrichum* species. Furthermore, the efficiency of molecular tools such as arbitrarily primed (AP)-PCR or random amplified polymorphic DNA fingerprints (Freeman *et al.*, 1993, 1998, 2000; Talhinhas *et al.*, 2005) have been compared and employed to differentiate *Colletotrichum* species. Recent years have witnessed crucial developments and changes in the taxonomy of *Colletotrichum* (Cai *et al.*, 2009; Cannon *et al.*, 2012; Damm *et al.*, 2012 a,b; Hyde *et al.*, 2009; Prihastuti *et al.*, 2009; Phoulivong *et al.*, 2010; Wikee *et al.*, 2011; Weir *et al.*, 2012). Hence, a polyphasic approach, comprising morphological characteristic features and multiple-locus sequence comparisons, is advised. Various fungal genes, of genomic origin, effectively employed for multi-locus sequence typing (MLST) include the commonly used

internal transcribed spacers (*ITS*) region, along with other genes such as actin (*ACT*), Apn2/MAT1GS (*Ap/Mat*), partial β -tubulin (*TUB2*), calmodulin (*CAL*), chitin synthase (*CHS-1*), histone (*CYLH3*), glutamine synthase (*GS*) and glyceraldehyde-3-phosphate-dehydrogenase (*GAPDH*), manganese-superoxide dismutase (*SOD2*), mating type gene (*Mat1*).

The utilization of molecular approaches has unraveled that many species were aggregates or complexes of morphologically indistinguishable, closely related cryptic species (Cannon *et al.*, 2012). Including *C. acutatum* (Damm *et al.*, 2012b), *C. boninense* (Damm *et al.*, 2012a), *C. caudatum* (Crouch, 2014), *C. destructivum* (Damm *et al.*, 2014), *C. gloeosporioides* (Weir *et al.*, 2012), *C. gigasporum* (Liu *et al.*, 2014), *C. graminicola* (Crouch and Beirn 2009; Du *et al.*, 2005), *C. orbiculare* (Damm *et al.*, 2013) and *C. truncatum* (Damm *et al.*, 2009). Hence, the combined efforts of MLST (based on the analysis of *ITS*, *GAPDH*, *CHS-1*, *ACT*, *HIS3*, *TUB2* and *CAL* sequences) and morphology based taxonomy has placed 190 species of *Colletotrichum* under eleven species complexes (Fig. 2) (Jayawardena *et al.*, 2016). Further, doubts have been raised against *Colletotrichum phaseolorum* (whereas *Colletotrichum corchori-capsularis* has been excluded from the list of species).

Colletotrichum species complexes

The molecular sequence analysis works at two level-species complexes could be distinguished from one another based on the analysis of *ITS* sequence data, whereas sequence analysis of additional genes is required for further resolution of the species placed within the same complex.

***Acutatum* species complex:** Around 34 species were recognized in this species complex, which includes *C. acutatum* and its close associates. *Acutatum* species complex is the causal agents of the fruit rot diseases (Damm *et al.*, 2012b). Generally, the species of this

Fig. 2. Eleven species complexes of *Colletotrichum*

complex are characterized with conidia with the acute end (Damm *et al.*, 2012b). They recommended both *TUB2* and *GAPDH* for differentiating species within this complex effectively.

Boninense species complex: Boninense species are either pathogens or endophytes. This species complex has 18 closely related species of *C. boninense*. The conidia of species in this complex are characterized with a obvious scar at base and periclinal thickening is observed in the conidiogenous cells. The periclinal thickening may sometimes extend to form a new conidiogenous cell (Damm *et al.*, 2012a). *GAPDH* alone can separate all the species within this complex.

Caudatum species complex: This species complex comprises seven related species and a collection of *C. caudatum*. The differentiating conidial feature of this complex is a filiform appendage placed at the conidial apex (Crouch, 2014).

Dematium species complex: *Dematium* species complex is observed in the regions where temperate climate prevails (Cannon *et al.*, 2012). This species complex consists of *C. dematium* and 10 closely related species. The conidia are angular in shape with truncate base and abrupt bent at the apex and straight central part (Damm *et al.*, 2009).

Destructivum species complex: As the name indicates, the *destructivum* species complex are a collection of pathogens that belongs to *C. destructivum* and 14 of its closely related species (Damm *et al.*, 2014). The distinctness of this complex and its monophyletic character has been demonstrated by O'Connell *et al.* (2012). The conidia produced by species of this complex are slightly curved characteristic with tapering ends. The acervuli produced are small, and inconspicuous but show diffused growth (Damm *et al.*, 2014). The species in this complex could be differentiated using molecular techniques by analyzing the sequences of *TUB2* and *GAPDH* genes (Damm *et al.*, 2014).

Gigasporum species complex: Species of *Gigasporum* complex are either endophytes or pathogens and the complex comprise *C. gigasporum* and its five related species. Morphologically, the species of this complex are characterized with the large conidial formation (> 20 μ m) (Liu *et al.*, 2014). The distinction of species within this complex could be performed by studying any of the following four genes such as *ACT*, *CHS-1*, *GAPDH*, and *TUB2* besides characterizing *ITS* region (Liu *et al.*, 2014).

Gloeosporioides species complex: Comprising mainly of phytopathogens (Weir *et al.*, 2012), this species complex includes a few endophytes too (Liu *et al.*, 2015). This species complex includes a collective of *C. gloeosporioides* and about 37 species, which are closely related. The cylindrical conidia possess rounded ends which taper, to a certain extent, towards the base (Weir *et al.*, 2012). Two subclades viz., kahawae and musae, have been identified within this species complex (Weir *et al.*, 2012). Liu *et al.* (2015) have reported the requirement of both *ApMat* and *GS* sequences to differentiate species within this complex.

Graminicola species complex: Comprising of predominantly pathogens on grasses, the graminicola species complex consists of *C. graminicola* and 14 closely related species. Cannon *et al.* (2012) have reported that this species complex forms a monophyletic clade. A characteristic feature of this species in this complex is falcate conidia (Crouch *et al.*, 2009a).

Orbiculare species complex: Comprising of *C. orbiculare* and seven closely related species, members of this species complex are pathogens on specific herbaceous plants (Damm *et al.*, 2013) and are hemibiotrophic (Damm *et al.*, 2013). Conidia appear straight and are moderately short and broad. Identification of species under orbiculare species complex is possible solely based on *GS* sequences (Damm *et al.*, 2013).

Spaethianum species complex: Comprising of *C. spaethianum* and nine closely related species, members of this species complex form complex appressoria (Damm *et al.*, 2009).

Truncatum species complex: Members of this species complex are known pathogens and consist of *C. truncatum* and three closely related species (Damm *et al.*, 2009; Wikee *et al.*, 2011). Conidia are characteristically curved; the base of conidia is acute and truncated with a strongly curved apex. One of the distinctive traits is the formation of appressoria in groups and in dense clusters (Damm *et al.*, 2009; Crouch *et al.*, 2009).

Taxonomy of *Colletotrichum* isolates associated with anthracnose diseases in India

Several taxonomic studies undertaken have resulted in the identification of several new *Colletotrichum* species from varied hosts. Therefore, it is all the more vital to undertake detailed studies of *Colletotrichum* taxonomy in India. Authentic identification of postharvest pathogens will have a noteworthy bearing on agriculture, biosecurity and quarantine, given the variety of fruits and vegetables produced, exported and consumed in countries of the tropics (Phoulivong *et al.*, 2012; Than *et al.*, 2008).

Chilli anthracnose: Chilli (*Capsicum annum* L.) is a spicy vegetable which is popular in Asia; it is extensively cultivated in different regions of the world (Makari *et al.*, 2009). India constitutes the largest producer, consumer and exporter of chillies (Singhal, 1999). Worldwide, the crop occupies an area of 1,832 thousand hectares with production reaching up to 2,959 thousand tons (Source: FAO). In India, chilli occupies an area of 792.1 ha with production reaching to the tune of 1.2 million metric tonnes (Kumar *et al.*, 2011). Anthracnose is a main production constraint in tropical and subtropical areas. Although anthracnose appears on leaves and stems, acute damage can be observed in mature fruits in the field; rampant damage can also occur during transit and storage (Chowdappa, 2013).

A number of species viz., *C. acutatum* (Simmonds), *C. gloeosporioides* (Penz.) Penz. & Sacc., *C. capsici*

(Syd.) Butler & Bisby and *C. coccodes* (Wallr.) S. Hughes have been implicated as causal organisms of chilli anthracnose (Chowdappa, 2013; Than *et al.*, 2008). According to the classification given by Damm *et al.* (2009), *C. capsici* has been placed in *C. truncatum* clade and is no longer considered as a recognized species. In a recent study from India, Sharma and Shenoy (2014)

have reported the involvement of *C. siamense* and *C. fruticola* in chilli anthracnose. In a subsequent study, Chethana *et al.* (2015c), providing morphological evidence and multilocus gene phylogeny, have reported *C. truncatum* and *C. fruticola* causing fruit anthracnose of chilli in Karnataka. Setae and conidiophores were present in both species. *C. truncatum* produces falcate

Fig. 3. Morphological features of *Colletotrichum* isolates associated with various hosts in India, a) culture on potato dextrose agar, b) Conidia, c) appressoria. 1) *C. aeschynomenes*, 2) *C. aotearoa*, 3) *C. asianum*, 4) *C. communis*, 5) *C. cordylinicola*, 6) *C. dianesei*, 7) *C. endomangiferae*, 8) *C. endophytica*, 9) *C. fruticola*, 10) *C. gloeosporioides*, 11) *C. horii*, 12) *Glomerella cingulata* f. sp. *camelliae*, 13) *C. hymenocallidis*, 14) *C. kahawae*, 15) *C. musae*, 16) *C. nupharicola*, 17) *C. queenslandicum*, 18) *C. siamense*, 19) *C. syzygicola*, 20) *C. ti*, 21) *Colletotrichum* sp. indet. 1

conidia with tapering towards the ends, while Conidia of *C. fruticola* cylindrical, sometimes oblong with or without guttules (Fig. 3).

Onion anthracnose: Onion (*Allium cepa*) is a chief fresh market vegetable, with a world production, including shallots, of 66.82 million tonnes in 3.73 million ha (FAO, 2011). Anthracnose, also called 'twister disease' or 'seven curls disease', is a serious production constraint, causing considerable yield losses to onion and shallot (*A. ascalonicum*) worldwide (Galvan *et al.*, 1997). Disease symptoms appear on leaves, neck and bulbs of onion plants (Chowdappa *et al.*, 2014). They consist of white, sunken, oval spots that may increase in size with time, turning in sunken necrotic spots on which concentric rings of grey-coloured acervuli develop (Fig. 1). Die-back can occur on severely infected leaves, leading to collapse of the plants (Ebenebe, 1980).

World-wide, there are reports of five *Colletotrichum* species, i.e. *Colletotrichum dematium* f. *circinans* (Berk) (John *et al.*, 1987; Shumway *et al.*, 1983), *C. gloeosporioides sensu lato* (sl) (Penz.) Penz. and Sacc (Galvan *et al.*, 1997; Nischwitz *et al.*, 2008; Rajasab and Chawda, 1994), *C. acutatum* (Alberto and Aquino, 2010), *C. circinans* (Jiehr *et al.*, 2012; Kim *et al.*, 2008) and *C. coccodes* (Rodriguez-Salamanca *et al.*, 2012) being associated with anthracnose of onions. However, *C. gloeosporioides* has been reported to be associated with anthracnose in India (Rajasab and Chawda, 1994). Detailed cultural characteristics, growth rates, conidial shapes and sizes, appressorial morphology and combined sets of eight gene sequences (*CYLH3*, *ACT*, *GAPDH*, *TUB2*, *CAL*, *CHS-1*, *GS* and *ITS*) comparisons revealed association of *C. siamense* and *C. truncatum* with onion anthracnose in India (Chowdappa *et al.*, 2015).

In comparison to *C. truncatum*, *C. siamense* possess considerably enhanced growth rate; also the size and shape of conidia are features which can be utilized to distinguish these two species. Isolates of *C. siamense* have fusiform conidia with obtuse slightly rounded ends (slightly different from fusiform conidia in *C. acutatum*), while those of *C. truncatum* produced with curved conidia (Fig. 3). Appressoria of *C. siamense* were clavate, while those of *C. truncatum* were irregular or lobed. Morphological characteristics of *C. truncatum* examined falls within the range detailed for *C. truncatum* (Damm *et al.*, 2009), supported by multi-locus phylogeny, although Damm *et al.* (2009) mentioned that *Colletotrichum* isolates causing disease of onion bulbs are likely to be *C. circinans*.

Mango anthracnose: Mango (*Mangifera indica* L., Anacardiaceae) is a popular fruit crop, considered as the 'King of Fruits' and grown mainly in tropical and subtropical countries. Anthracnose affects the inflorescence, leaves, twigs, branches and fruits with dark brown or black necrotic spots causing major economic loss mainly by post-harvest fruit-rots which directly affect the export of the fruit (Chowdappa and Mohan Kumar, 2012). *C. gloeosporioides* has been implicated as a major pathogen in decaying of mango worldwide (Chowdappa and Mohan Kumar, 2012).

Based on evidence generated from morphology and molecular data, *C. gloeosporioides* has been reported to be associated with mango anthracnose in India (Chowdappa and Mohan Kumar, 2012; Gupta *et al.*, 2010). In addition to *C. gloeosporioides*, association of *C. frgariae*, *C. melanocaulon* *C. jasmine-sambac* and *C. fruticola*, with mango tissues/anthracnose has been proved via molecular tools (Sharma *et al.*, 2013).

Multi-locus probing utilizing rDNA-ITS (*ITS*), chitin synthase 1 (*CHS-1*), actin (*ACT*), glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*), β -tubulin (*TUB2*), histone (*CYLH3*) and *ApMat* gene regions revealed the involvement of six species: *C. asianum*, *C. communis*, *C. dianesei*, *C. fruticola*, *C. hymenocallidis*, and *C. siamense* (Chowdappa *et al.*, Unpublished). In *C. asianum*, conidia are guttulate, hyaline, cylindrical with obtuse ends (oblong) with slight narrowing at the centre. *C. communis* produced hyaline conidia, smooth, cylindrical with rounded ends. Conidia of *C. dianesei* are cylindrical with obtuse to slightly rounded ends, sometimes oblong. Conidia are fusiform, straight, obtuse at the ends in isolates of *C. hymenocallidis*. In isolates of *C. siamense*, conidia were found to be guttulate, hyaline and fusiform, with ends obtuse to somewhat rounded, often cylindrical or oblong.

Small cardamom anthracnose: Small cardamom (*Elettaria cardamomum* Maton, Zingiberaceae) is the third most valuable spice in the world (Reyes *et al.*, 2006). It is broadly grown in the Western Ghats of South India. In India, small cardamom anthracnose, popularly known as "Chenthal", has been described as the most devastating foliar disease affecting the crop (Biju *et al.*, 2015; Praveena *et al.*, 2013). The anthracnose disease is initially apparent as yellowish lesions on the leaves; the lesions coalesce to develop as large blighted areas later (Fig. 1). In later stages, the infected foliage dries up, presenting a burnt appearance. Based on morphological characters, *Colletotrichum gloeosporioides* has been reported as the sole casual organism responsible for small cardamom anthracnose (Govindaraju *et al.*, 1998; Praveena and Biju 2012; Saju *et al.*, 2013). Chethana *et al.* (2015a) had undertaken comprehensive morphological and also multi-locus phylogenetic analyses using eight genes viz., *ACT*, *ITS*, *CYLH3*, *CHS-1*, *GAPDH*, *TUB2*, *ApMat* and *GS* of *Colletotrichum* isolates from small cardamom; the analysis uncovered six species: *C. karstii*, *C. gloeosporioides*, *C. siamense*, *C. syzygicola*, *Colletotrichum* sp and *C. guajavae*. The foliage of the small cardamom cultivar Appangala1 was inoculated with the isolates of these six species; all the isolates formed characteristic symptoms (oval and sunken streaks with reddish margins, which are bounded by a yellow halo).

Black pepper anthracnose: Black pepper (*Piper nigrum* L.), considered "King of Spices" or "Black Gold", had its origins in the tropical forests of Western Ghats, India. The area under cultivation of black pepper in India is about 2,01,381 hectares, with an annual production of 55,000 tonnes. India produced 15,363 tonnes of black pepper products and exported worth of Rs. 63,810 lakhs

during 2012-13 (Anandaraj and Sarma, 1995). The causal organism of anthracnose/spike shedding/fungal pollu is *C. gloeosporioides* (Penz.) Penz. and Sacc. (Biju *et al.*, 2013). Anthracnose is a severe problem, particularly during August to September months, causing losses up to 100 per cent if infection occurs on berries. The fungus causes severe damage both in the nursery and field, attacking all the aerial parts including foliage (Fig. 1), stem, spikes and berries (Biju *et al.*, 2013).

In India, *C. endophytica*, *C. queenslandicum*, *C. siamense*, *C. syzygicola* and *C. guajavae* have been reported to be associated with anthracnose of black pepper based on evidences derived from morphology and multi-locus gene phylogeny of *ACT*, *ITS*, *GAPDH*, *CHS-1*, *CYLH3*, *TUB2*, *ApMat* and *GS* gene regions (Chethana *et al.*, 2015b). When leaves of black pepper were inoculated with the above five isolates, typical brown necrotic centers, surrounded with yellow halo lesions, were noticed five days post inoculation.

Orchid anthracnose: Orchids, a highly commercial industry, constitute about 10% of the global floriculture trade (Medhi and Chakrabarti, 2009). Anthracnose has been implicated as a major cause of losses incurred in both field-grown and nursery-grown orchids (Duff and

Daly, 2002). A few studies have been undertaken to decipher the etiology of the disease. *Colletotrichum cymbidiicola* on *Cymbidium*, *C. oncidii* on *Oncidium* and a species of *C. boninense* complex on *Dendrobium* (Damm *et al.*, 2012a), *C. gloeosporioides* on *Cymbidium sinense* in China (Huang *et al.*, 2012) and *C. karstii* on *Phalaenopsis* in USA (Jadrane *et al.*, 2012) have been associated with the disease. Anthracnose caused by *Glomerella cingulata* was first reported on *Vanda coerulea* in India as early as 1952 (Ramakrisnan *et al.*, 1952). In subsequent studies, *C. orchidacearum* and *C. gloeosporioides* were associated with anthracnose on *Phalaenopsis* hybrids, *Dendrobium nobile*, *Bulbophyllum cylindrum*, *Cymbidium aloifolium* and *Coelogyne flaccida* from Assam and Uttarakhand (Chowdappa *et al.*, 2012; Roy, 1979; Roy and Barman, 1979; Sohi, 1992), *Colletotrichum dendrobii* on *Dendrobium latifolium* and *Phalaenopsis* sp. in Maharashtra, (Yadav, 1980), *Glomerella cingulata* on *Oncidium* sp. in Kerala (Shreedharan *et al.*, 1994) and *G. cingulata* in Sikkim (Srivastava, 1999). Bag (2007), based on surveys undertaken in Sikkim, reported anthracnose on 85 species of 29 orchid genera; however, only a single isolate was recently identified as *C. cymbidiicola* (Sharma and Shenoy, 2013). *Colletotrichum* spp. recovered from

Table 1. Identity of *Colletotrichum* isolates associated with anthracnose diseases of crop plants in India

<i>Colletotrichum</i> species	Host
<i>C. aeschynomene</i>	Brinjal (<i>Solanum melongena</i>)
<i>C. aotearoa</i>	Taro (<i>Colcasia esculenta</i>), Lemon (<i>Citrus limon</i>) Drum stick (<i>Moringa oleifera</i>), Clove (<i>Syzygium aromaticum</i>)
<i>C. asianum</i>	Mango (<i>Mangifera indica</i>)
<i>C. cordylinicola</i>	Clove (<i>Syzygium aromaticum</i>)
<i>C. communis</i>	Mango, Passion fruit (<i>Passiflora edulis</i>)
<i>C. dianesi</i>	Mango
<i>C. endophytica</i>	Black pepper (<i>Piper nigrum</i>)
<i>C. endomangiferae</i>	Cow pea (<i>Vigna unguiculata</i>), Elephant foot yam (<i>Amorphophallus paeoniifolius</i>), Drum stick (<i>Moringa oleifera</i>), Citrusinensis (Orange), Taro (<i>Colocasia esculenta</i>)
<i>C. fruticola</i>	Chilli (<i>Capsicum annuum</i> L), Taro, Banana (<i>Musa acuminata</i>), Lemon (<i>Citrus limon</i>), Karando (<i>Dioscorea esculanta</i>), Ivy gourd (<i>Coccinia grandis</i>), Arecanut (<i>Areca catechu</i>), Ginger (<i>Zingiber officinalis</i>), Mango.
<i>Glomerella cingulata</i> f. sp. <i>camelliae</i>	Cinnamon (<i>Cinnamomum zeylanicum</i>), Tea (<i>Camellia sinensis</i>), Rubber (<i>Hevea brasiliensis</i>), Vanilla (<i>Vanilla planifolia</i>)
<i>C. gloeosporioides</i>	Cardamom (<i>Elettaria cardamomum</i>)
<i>C. horii</i>	Garlic (<i>Allium sativum</i>)
<i>C. hymenocallidis</i>	Mango
<i>C. kahawae</i>	Cardamom, Castor (<i>Ricinus communis</i>)
<i>C. musae</i>	Papaya (<i>Carica papaya</i>), banana (<i>Musa</i> sp)
<i>C. nupharicola</i>	Arecanut
<i>C. queenslandicum</i>	Black pepper, betelvine (<i>Piper betel</i>), Avocado (<i>Persea Americana</i>), Basil (<i>Ocimum basilicum</i>), Sesame (<i>Sesamum indicum</i>)
<i>C. siamense</i>	Avocado, Betelvine, Drum stick, Orange, Taro, Black pepper, Cardamom, Snake gourd (<i>Trichosanthes cucumerina</i>)
<i>C. syzygicola</i>	Black pepper, Cardamom
<i>C. ti</i>	Lily (<i>Lilium</i>)
<i>Colletotrichum</i> sp. <i>indet. 1</i>	Anthurium (<i>Anthurium andraeanum</i>), Cassava (<i>Manihot esculenta</i>), Chilli, Castor, Arecanut, Tea (<i>Camellia sinensis</i>), Taro

different orchids such as *Cymbidium* hybrid, *Eria bambosifolia*, *Bulbophyllum hirtum*, *Eria emica*, *Dendrobium fimbriatum*, *Oncidium spacealatum*, *Coelogyne clala*, *Liparis longipes* and *Cymbidium dendulum* in North eastern India showing typical symptoms of anthracnose were reported as *C. cymbidiicola* and *C. cliviae*, based on evidence derived from morphology and multi-locus gene phylogenies (Chowdappa *et al.*, 2014).

Characterization of Colletotrichum isolates associated with anthracnose on 35 hosts in India

Comprehensive phylogenetic analyses have been undertaken for 161 *Colletotrichum* isolates associated with anthracnose disease on 35 hosts (Table 1) in India (Chowdappa, Unpublished). These isolates were subjected to morphological analysis as well as multi-locus probing with seven genes (*ITS*, *GAPDH*, *ACT*, *CHS-1*, *TUB2* and *CYLH3* and *ApMat*) (Fig. 3). The phylogenetic analysis could delineate 21 *Colletotrichum* species (Table 1).

We have made an attempt to resolve taxonomic complexities of *Colletotrichum* isolates from 35 hosts in India, mainly utilizing molecular phylogenetic analyses. Details molecular studies to identify *Colletotrichum* isolates on cereals, cucurbit and legumes have not yet been undertaken. The identification of a new *Colletotrichum* species causing anthracnose on different crop plants in India and the lack of identification of important species that occur on other hosts reflects the importance for further research in *Colletotrichum* taxonomy to mitigate the risk to the Indian agriculture.

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