Revision of the genus *Corallomycetella* with *Corallonectria* gen. nov. for *C. jatrophae* (Nectriaceae, Hypocreales)

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**Abstract:** The genus *Corallomycetella* (Ascomycota, Sordariomycetes, Hypocreales, Nectriaceae) has been defined to include red nectrioid fungi associated with rhizomorphs in nature and culture. With the recent collection of an unusual specimen having striated ascospores, the genus was re-examined using this and previously obtained cultures. A multilocus tree was constructed based on three loci (ITS, mcm7, β-tubulin) to determine phylogenetic relationships. Our results indicate that *Corallomycetella repens sensu lato* forms two clades associated with biogeography. *Corallomycetella repens sensu stricto* is restricted to specimens from Asia while *C. elegans* is resurrected for specimens from Africa and America. Minute striations in the ascospores are an overlooked character in species of *Corallomycetella*. *Corallomycetella jatrophae* is related to *Nectria sensu lato* and unrelated to *C. repens* and *C. elegans*; thus, a new genus, *Corallonectria*, is described to accommodate this species. *Corallonectria* is characterized by furfuraceous perithecia and synnematous fusarium-like anamorph.

**Key words:** biogeography, fungal systematics, *Nectria*, plant pathogen

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*Corallomycetella* 属及以 *C. jatrophae* 为模式建立新属 *Corallonectria*（丛赤壳科，肉座菌目）

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INTRODUCTION

The genus *Corallomycetella* Henn. is recognized for two species having large, orange-red to red, smooth to scurfy ascomata arranged in caespitose clusters, and smooth to roughened ascospores (Rossman *et al.* 1999). These species occur primarily in tropical regions. Based on the reddish, KOH+ ascomata this genus is placed in the Nectriaceae, Hypocreales. One species, *C. repens* (Berk. & Broome) Rossman & Samuels, has a synnematal asexual state with red, rhizomorph-like strands at the base that has been referred to as *Rhizostilbella hibisci* (Pat.) Seifert. The reddish rhizomorph-like strands are also produced in culture as well as ellipsoid, non-septate conidia each with a truncate base. This species causes a number of diseases, specifically ‘violet root rot’ of *Theobroma cacao* L., root rot of *Carica papaya* L., and ‘stinking root disease’ of several tropical woody plants (Booth & Holliday 1973). *Corallomycetella jatrophae* (A. Møller) Rossman & Samuels has a similar looking ascomatal state with a reddish synnematal asexual state that produces large, fusiform, multi-septate conidia.

A specimen collected in French Guiana has striate ascospores although otherwise is similar to *C. repens*. As part of a study to determine if this unusual specimen is a distinct species, the phylogenetic placement of *Corallomycetella* within the Nectriaceae was investigated. Previous studies had suggested that it was basal to the genus *Cosmospora* Rabenh., which has recently been shown to be polyphyletic (Gräfenhan *et al.* 2011).

1 MATERIALS AND METHODS

**Herbarium specimens and cultures**

Fresh specimens of *Corallomycetella sensu* Rossman *et al.* (1999) were collected on trips to Brazil, Costa Rica, French Guiana, and Gabon (Kadri Põldmaa). Cultures were obtained by isolating single asc or ascospores and grown in cornmeal dextrose agar (CMD; Difco™ cornmeal agar + 2% w/v dextrose + antibiotics). Dried specimens were deposited at the U.S. National Fungus Collections (BPI), Beltsville, Maryland, USA. Cultures were deposited at Centraalbureau voor Schimmelcultures (CBS), Utrecht, The Netherlands (Table 1) from where additional fungal strains were obtained.
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http://journals.im.ac.cn/jwxtcn
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<td>Microcera rubra</td>
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<td>A.R. 4477, CBS 125165</td>
<td>BPI 879981 Dead twigs of Aesculus sp.</td>
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<td>Nectria pseudotrichia</td>
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<td>BPI 863854 Liana</td>
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Table 1 continued
Table 1 continued

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<td>CBS 122.29</td>
<td>Skin infection of man</td>
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<td>Dacrydium cupressinum</td>
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<td><strong>Viridispora diparietispora</strong></td>
<td>CBS 102797</td>
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</table>

Note: KC479730–KC479789 sequences were produced in this study.

Herbarium specimens of *Corallomycetella* were borrowed from the U.S. National Fungus Collections (BPI), Farlow Reference Library and Herbarium of Cryptogamic Botany (FH), Royal Botanic Gardens Kew (K), and William and Lynda Steere Herbarium, New York Botanical Garden (NY).

**Morphological characterization**

The macro-morphology of the teleomorph was observed using a stereoscope (Olympus SZX12; Olympus, Tokyo, Japan). The color, shape, size, ornamentation, and habit of the perithecia were characterized. To observe their internal structures, the perithecia were rehydrated in 3% KOH and the centrum isolated on a glass slide and covered with a coverslip. Microscopic characters, *e.g.* asci and ascospores, were observed with a compound microscope (Olympus BX50; Olympus, Tokyo, Japan). The color reaction of the perithecial wall was observed using 3% KOH and 100% lactic acid (LA). Sections of perithecia (ca. 10μm in width) were made with the aid of a freezing microtome.

To observe colony morphology strains were grown on Difco™ potato dextrose agar (PDA) in an incubator that alternates between fluorescent light and darkness (12h/12h) at 2°C. Two replicates with two pseudoreplicates were grown for each isolate. Culture growth was measured weekly for two weeks. Colony color is described using the terms in
Rayner (1970). To observe the mononematous anamorph isolates were grown in synthetic nutrient-poor agar (SNA; Nirenberg 1976) under the conditions described above. A block of agar was cut, placed on a microscope slide, covered with a coverslip, and examined by light microscopy (Olympus BX50; Olympus, Tokyo, Japan).

Measurements of continuous characters, e.g. length and width, were made with Scion Image software beta 4.0.2 (Scion Corp., Frederick, Maryland), and summarized by descriptive statistics, e.g., minimum, maximum, mean and standard deviation.

**DNA extraction, PCR, and sequencing**

The detailed DNA extraction protocol is described in Hirooka et al. (2010). Briefly, the strains were grown in Difco™ potato dextrose broth (PDB) for one week, and the mycelial mat harvested for DNA extraction. DNA was extracted with PowerPlant® DNA Isolation Kit (MO BIO Laboratories Inc., Solana Beach, California). DNA of *Corallomycetella jatrophae* (P.C. 1300) was amplified directly from the several centra of the perithecia because the isolate did not survive −80°C storage. The centra were isolated in antibiotics, transferred to a micro centrifuge tube with 10 μm RNAse-free water, incubated for 10 min at 65°C, and homogenized using a micropestle. The sample was centrifuged, and 5 μm of the supernatant was transferred to a new tube. DNA was amplified with Illustra GenomiPhi V2 DNA Amplification Kit (GE Healthcare Bio-Sciences Corp., Piscataway, New Jersey) following the manufacturer’s instructions.

Four partial loci were amplified. These loci include ITS ribosomal DNA (ITS; White et al. 1990) and three protein coding regions: α-actin (*act*; Samuels et al. 2006), *mcm7* (a DNA replication licensing factor; Schmitt et al. 2009), and β-tubulin (*tub*; O’Donnell & Cigelnik 1997). The PCR reaction mixture (25 μL total volume) consisted of 12.5 μL GoTaq® Green Master Mix 2× (Promega Corporation, Madison, Wisconsin), 1.25 μL 10 mmol/L forward primer, 1.25 μL 10 mmol/L reverse primer, 1.0 μL of dimethyl sulfoxide (DMSO; Sigma-Aldrich, St. Louis, Missouri), 2.0 μL genomic DNA template, and 7 μL of sterile RNAse-free water. PCR amplifications were carried out in an Eppendorf Mastercycler thermocycler (Eppendorf, Westbury, New York) under the cycle conditions listed in Table 2. PCR products were cleaned with ExoSAP-IT® (USB Corp., Cleveland, Ohio). Clean PCR products were sequenced at the DNA Sequencing Facility (Center for Agricultural Biotechnology, University of Maryland, College Park, Maryland) and McLAB DNA sequencing services (San Francisco, California). Sequences were assembled and edited with Sequencher 4.9 (Gene Codes, Madison, Wisconsin). Sequences were deposited in GenBank (Table 1).

**Phylogenetic analyses**

A multiple sequence alignment for each locus was performed in the MAFFT v.6 web service (http://mafft.cbrc.jp/alignment/server/; Katoh & Toh 2008) with the E-INS-i alignment strategy. Alignments were manually edited in Mesquite 2.75 (Maddison & Maddison 2011).

CONCATEPILLAR 1.4 (Leigh et al. 2008) was used to determine which loci could be concatenated and analyzed to generate a phylogeny. Loci were concatenated if the p-value was greater than the default α-level of 0.05, which indicated that the null hypothesis, i.e., congruence of loci, could not be rejected.

JModeltest (Guindon & Gascuel 2003; Posada 2008) was used to infer the model of nucleotide substitution for each locus. Default settings in
Table 2 Genes/loci used in the phylogenetic analyses

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<th>ITS</th>
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<th>mcm7</th>
<th>tub</th>
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<td>73</td>
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<td>TIM1+I+G (nst=6, rates=invgamma)</td>
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<td>HKY+I+G (nst=2, rates=invgamma)</td>
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<td>Primers used (reference)</td>
<td>ITS5, ITS4 (White et al. 1990)</td>
<td>Tact1, Tact2 (Samuels et al. 2006)</td>
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<td>Brub-TI, Brub-T2</td>
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<td>65℃, 30s, 15x</td>
<td>48℃, 30s, 30x</td>
<td>56℃, 50s, 38x</td>
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jModeltest were used: 11 substitution schemes with equal or unequal base frequencies (+F), and with/without invariable sites (+I) and/or rate variation among sites (+G). The base tree for likelihood calculations was ML optimized. Once likelihood scores were calculated, the models were selected according to the Akaike Information Criterion (AIC).

Maximum likelihood (ML) analyses were performed with GARLI v2.0 (Genetic Algorithm for Rapid Likelihood Inference; Zwickl 2006) in the GARLI web service (http://www.molecularevolution.org; Bazinet & Cummings 2011), which uses a grid computing system associated with The Lattice Project (Cummings & Huskamp 2005; Bazinet & Cummings 2008). Fifty independent search replicates were performed to generate the starting tree and search for the best tree with a fast ML stepwise-addition algorithm. Two thousand bootstrap replicates were used in the bootstrap analysis. Bayesian analyses were performed in MrBayes v3.2.1 (Ronquist et al. 2012). A majority rule consensus tree was generated by running four chains for 10,000,000 Markov Chain Monte Carlo generations sampling trees every 100th generation, and discarding the first 25% of the sampled trees as burn-in. Tracer version 1.5 (Rambaut & Drummond 2007) was used to confirm whether the negative log likelihoods had reached convergence.

Species recognition in Corallomycetella sensu stricto was based on genealogical concordance phylogenetic species recognition (GCPSR; Taylor et al. 2000), 95% connection limit in statistical parsimony networks (Posada & Crandall 2001; Templeton 2001), and genealogical sorting index (gsi; Cummings et al. 2008). Haplotype networks based on statistical parsimony were generated for
each locus and the combined multilocus dataset in TCS v1.21 (Clement et al. 2000). Haplotypes are joined by an edge only if the edge has a probability of parsimony greater than or equal to 95% (default settings in TCS). The gsi is a statistic that measures genealogical exclusivity of a group of individuals/species on a rooted tree with 0=polyphyly and 1=monophyly. The gsi was implemented in the gsi web interface (http://www.genealogicalsorting.org/) with single locus trees generated with GARLI (as described above) and 10,000 permutations to test statistical significance of the gsi value (P<0.05). The ensemble statistic (gisT) was estimated from a multi-tree file containing all single locus trees.

2 RESULTS

The analysis performed in CONCATEPILLAR rejected the null hypothesis of congruence among all loci (P-value<0.001), and for this reason act was analyzed separately (Fig. 1). The analysis determined that only ITS, mcm7, and tub were congruent (P-value=0.3), and therefore these loci could be concatenated. The concatenated matrix consisted of 2,304 base pairs of which 799 were parsimony-informative, 236 were parsimony-uninformative, and 345 were invariable (Table 2). The topologies of the generated phylogenetic trees in both ML and BI were congruent. The negative log likelihoods for the phylogenetic trees were −17491.8148 and −17588.5333, respectively. The best tree (ML) is shown in Fig. 2.

The combined analyses of species in Corallomycetella sensu Rossman et al. (1999) revealed that these taxa consisted of three clades, although distantly related, i.e. the genus is polyphyletic. One clade is composed of Corallomycetella repens sensu Rossman et al. (1999) (100% BP, 100% PP), and allied with Cosmospora sensu stricto, Dialonectria (Sacc.) Cooke, Fusicolla Bonord., Macroconia (Wollenw.) Gräfenhan et al., and Microcera Desm. (94.5% PP).

Corallomycetella repens sensu Rossman et al. (1999) clustered into two well-supported subclades that correlated with geographic origin (Fig. 2). One subclade is known only from Asia (99.6% BP, 100% PP), and represented in Fig. 2 by isolates from India, Java, and Sri Lanka. In single gene trees, this clade was present in act, ITS, and mcm7, but only act and mcm7 strongly supported this clade (Fig. 3). This subclade is recognized below as C. repens sensu stricto.

The second subclade of Corallomycetella repens sensu Rossman et al. (1999) is known from tropical regions in the western hemisphere and Africa. It is well supported (87.9% BP, 100% PP; Fig. 2) and referred to as C. elegans (see Taxonomy section). It is present and strongly supported in act, ITS, and tub single gene trees (Fig. 3). Within the C. elegans clade, ITS was the only locus supporting the monophyly of specimens from America, while tub was the only locus strongly supporting the monophyly of specimens from Africa (Fig. 3).

TCS analyses resolved two segregate haplotype networks of Corallomycetella repens sensu Rossman et al. (1999; Fig. 4). The smaller haplotype network comprised two haplotypes from Asia, and the larger one included four haplotypes from tropical America and Africa. Within the larger haplotype network, eight polymorphic sites separated two small subgroups that showed geographic congruence. In single gene haplotype networks, only the analysis of tub reconstructed two separate haplotype networks as seen in the combined haplotype network, although ITS and mcm7 had a relatively high number of mutational differences between the “American” and “African” subgroups (five and six, respectively; Fig. 5).
Fig. 1 Phylogenetic placement of *Corallomyces* sensu Rossman et al. (1999) inferred from act. Best tree generated with ML analysis (−Ln=2514.7837). Values at branches indicate Maximum Likelihood bootstrap (ML BP)/Bayesian posterior probabilities (BI PP).
Fig. 2 Phylogenetic placement of Corallomycetella sensu Rossman et al. (1999) based on a combined 3-loci (ITS, mcm7, and tub) dataset. Best tree generated with ML analysis (−Ln = 17491.8148). Values at branches indicate Maximum Likelihood bootstrap (ML BP)/Bayesian posterior probabilities (BP).
Fig. 3 Phylogenetic relationship of *Corallomyces repens* sensu Rossman *et al.* (1999). Trees with the best log likelihood are presented for (A) *act*, (B) ITS, (C) *mcm7*, and (D) *tub*. Thicker lines indicate well-supported branches (>70% ML BP).
Fig. 4 Multilocus haplotype network for *Corallomycetella repens* sensu Rossman *et al.* (1999). The network was constructed in TCS v1.21. Each colored circle represents a haplotype; size of circle is proportional to haplotype frequency. Within each haplotype circle, geographic origins of isolates are proportionally represented as a pie chart. Empty circles represent intermediate haplotypes inferred by TCS. Each line segment represents a single mutation.

Gsi analyses did not support the monophyly of *Corallomycetella repens* sensu Rossman *et al.* (1999). The ensemble gsi$_F$ value was 1, but not significant (P-value=0.075). Complete sorting was not observed in any of the subclades. The ensemble gsi$_F$ values for the *C. repens* sensu stricto and *C. elegans* subclades were 0.928 (P-value=<0.001) and 0.735 (P-value=0.001), respectively. Gsi values for each locus are reported in Table 3.

The second species included in *Corallomycetella* sensu Rossman *et al.* (1999), *C. jatrophae*, formed a well-supported clade distinct from that genus (100% BP, 100% PP, Fig. 2). This species is closely allied with *Ilyonectria* P. Chaverri & Salgado, *Neonectria* Wollenw., and *Viridispora* Samuels & Rossman, although this inner node is not well supported in the combined analysis (87% PP, Fig. 2). *Act* strongly supports a clade comprising *C. elegans* were 0.928 (P-value=<0.001) and 0.735 (P-value=0.001), respectively. Gsi values for each locus are reported in Table 3.

Fig. 5 Haplotype networks of *act*, *ITS*, *mcm7*, and *tub*. The network was constructed in TCS v1.21. Each colored circle represents a haplotype; size of circle is proportional to haplotype frequency. Within each haplotype circle, geographic origins of isolates are proportionally represented as a pie chart. Empty circles represent intermediate haplotypes inferred by TCS. Each line segment represents a single mutation.
jatrophae, Ilyonectria, and Neoneckria (100% PP, Fig. 1). Given the distinctive morphology of C. jatrophae and the lack of affinity with any known genus, this species is placed in a new genus, Corallonectria (described below).

Three isolates identified as “Nectria” mauritiicola (Henn.) Seifert & Samuels, a name considered a synonym of Corallomycetella repens (Rossman et al. 1999), were distinct from all isolates referred to as Corallomycetella. The ITS sequence of these isolates are identical (Max. Ident.=100% in Blast®; blast.ncbi.nlm.nih.gov/) to the sequence of CBS 122.29, ex-type culture of Sarocladium kiliense (Grütz) Summerb. (76% BP, 82% PP; Fig. 2), and related to other species of Sarocladium W. Gams & D. Hawksw. (100% BP, 100% PP; Fig. 2).

3 DISCUSSION
3.1 Genus concepts
In the prior taxonomic revision by Rossman et al. (1999), Corallomycetella was based on C. repens (neotype of C. heinsenii, designated by Rossman et al. 1999). The genus included nectrioid fungi with scurfy to furfuraceous perithecia with rhizomorphs, roughened or smooth ascospores, and synnematous, fusarium-like or Rhizostilbella anamorphs. The circumscription of Corallomycetella was revised based on the genus-for-genus concept (Rossman 1993) in which a teleomorphic fungal genus correlates with its unique anamorph. Using this concept teleomorphic and anamorphic genera are observed to be monophyletic (e.g., Chaverri et al. 2008, 2011; Gräfenhan et al. 2011; Luo & Zhuang 2010, 2012).

Our phylogenetic analyses of molecular sequence data reveal that Corallomycetella sensu Rossman et al. (1999) consists of two distantly related major clades (Fig. 2). The clade that comprises Corallomycetella sensus stricto is related to Cosmopora sensu Rossman (94.5% PP) as previously shown by Hirooka et al. (2012). The anamorph of Corallomycetella sensus stricto is a synnematos Rhizostilbella. The genus is also characterized by scurfy perithecia that develop from rhizomorphs or at the base of synnemata, and produce finely striated ascospores that appear roughened in median section because the outer wall is often sinuous.

Corallomycetella jatrophae forms a second clade of Corallomycetella sensu Rossman et al. (1999), but it is most closely related to neonectria-like fungi (92% PP; Fig. 2). Although the exact relationship is not well resolved (low node support), the topology of this subclade is similar to that reported by Chaverri et al. (2011) in which the inner nodes are well supported due to the higher number of concordant loci used in the combined analyses. Corallomycetella jatrophae is characterized by its synnematous fusarium-like anamorph, which is unique among neonectria-like fungi. Synnematous fusarium-like anamorphs are also observed in Atractium Link and Microcera (Gräfenhan et al. 2011), but these genera appear to be unrelated to C. jatrophae. Representatives of Atractium were not included in our phylogeny, but Gräfenhan et al. (2011) showed that the type, A. stilbaster Link and a second species of Atractium form a distinct genus allied with Pseudonectria and Volutella. The genus Atractium is not included in the major clade of neonectria-like fungi. Microcera and allies (Cosmospora sensu Rossman et al. 1999) are closely related to Corallomycetella (94.5% PP; Fig. 2). This suggests that the synnematous fusarium-like anamorph has been independently derived three separate times. Based on these results, the clade previously regarded as Corallomycetella jatrophae is segregated into a new monotypic genus
Corallonectria (described below).

Species concepts

The species previously referred to as Corallomycetella repens sensu Rossman et al. (1999) is recognized in this study to comprise two species, namely C. repens sensu stricto and C. elegans, based on our multi-method approach (GCPSR, connection of haplotypes with ≥95% parsimony probability, and gsi). In addition to these criteria the two species are supported by morphological and biogeographical differences. Corallomycetella repens is restricted to isolates from South and Southeast Asia (Fig. 2), while isolates from Africa and America are recognized as C. elegans.

Corallomycetella repens is circumscribed in the strict sense based on our phylogenetic results. The clade is well supported in the combined analyses (99.6% BP, 100% PP; Fig. 2). The ensemble gsi value obtained for this clade (0.902, P-value=0.004; Table 3) suggested that it is approximating monophyly (i.e. complete sorting). The clade is present in all single locus trees except tub, but only supported in act and ITS (Fig. 3). Under GCPSR (Taylor et al. 2000) the clade could not be recognized probably because complete lineage sorting has not occurred. This criterion seems too conserved, and we decided to follow the criterion used by Pringle et al. (2005), which recognizes a species if the clade is well supported in the majority of single gene trees. The segregate network of C. repens haplotypes also suggests that C. repens is not conspecific with C. elegans. A segregate network occurs when the observed mutational differences exceed the maximum number of mutational connections, i.e. the 95% parsimony probability cutoff, between haplotypes. Segregate parsimony networks have been associated to correspond to species boundaries (reviewed in Hart & Sunday 2007).

The case for Corallomycetella elegans is slightly more complicated, but also conforms to the species recognition used in this study. The clade is well supported (87.9% BP, 100% PP; Fig. 2), and exhibits a moderate genealogical exclusivity across single gene trees (gsi_T=0.838, P-value=0.001; Table 3). Monophyly of the clade was supported by ITS and tub single gene trees. Conflicting with the monophyly of this clade is the monophyly of the “American” isolates supported by the ITS locus, while tub supported the monophyly of these isolates for ones from Africa (Fig. 3). Under the applied criterion of GCPSR (Pringle et al. 2005), these populations cannot be segregated into species because

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only a single gene supports its monophyly. Under the 95% parsimony probability, these subgroups were not separated into their own haplotype networks. Thus, this method also supports the hypothesis that isolates from Africa and America are conspecific.

As mentioned above, the recognized species of *Corallomycetella* are correlated to geographic origin. It is possible that the observed distribution of *Corallomycetella* species may be the result of vicariance. Supporting this hypothesis are the plant hosts of *Corallomycetella*, some of which are native to the same geographic region. For example, *C. elegans* parasitizes *Hevea brasiliensis* Müll. Arg. (Table 1), which is native to the Americas. It could explain why haplotypes from Africa are conspecific with those in America (Fig. 3). African haplotypes could be the result of anthropogenic introductions from America into plantations of *H. brasiliensis* in Africa. Vicariance has been used to explain the geographic distribution of species of the biotrophic fungus *Cyttaria* Berk. and their hosts in the plant genus *Nothofagus* Blume (Peterson et al. 2010).

**The incorrect application of a name: “Nectria mauritiicola”**

In our revision of the genus *Corallomycetella*, an isolate labeled CBS 400.52, initially identified as *Nectria mauritiicola*, a synonym of *C. repens*, was determined to be unrelated to the genus *Corallomycetella* sensu Rossman et al. (1999). ITS sequences labeled *Nectria mauritiicola* and retrieved from GenBank were identical to those for CBS 400.52. The source of the GenBank sequences was human blood, which cast doubt on the identity of these fungi because specimens of *Corallomycetella* are reported to be plant pathogens (reviewed in Booth & Holliday 1973). Additionally, the observed anamorph of CBS 400.52 was acremonium-like, unlike the anamorph of species of *Corallomycetella* (described below).

The herbarium specimen of CBS 400.52 listed as IMI 44310 was not observed, and we could not determine whether the name was correctly applied to the original specimen/isolate. Examination of the type specimen of *Nectria mauritiicola* revealed that this name is correctly considered a synonym of *Corallomycetella elegans* (see Taxonomy section). Thus, the name *Nectria mauritiicola* was incorrectly applied to CBS 400.52 and the other sequences in GenBank.

The sequences of CBS 400.52 and others retrieved from GenBank were found to be identical to that of CBS 122.29, ex-type culture of *Sarocladium kiliense* (= *Acremonium kiliense*). The acremonium-like anamorph produced by CBS 400.52 also suggests this species. Therefore, the sequences labelled “*Nectria mauritiicola*” in GenBank are determined to be conspecific with *S. kiliense* (76% BP; Fig. 2). They are incorrectly annotated creating confusion in the scientific community especially those who depend on the database for identification. Novicki et al. (2003) and Jang et al. (2012) are examples of clinical literature where the incorrect identification was assigned, although Novicki et al. (2003) questioned the validity of the GenBank name because their samples did not cluster with CBS 313.72 (a true *Corallomycetella repens* included in our study). This example calls for a method to change annotations in GenBank and highlights the importance of taxonomic studies to correct these crucial errors.

**Taxonomy**

*Corallomycetella* Henn., Hedwigia 43: 245. 1904.

Generic type: *Corallomycetella heinseni* [as *heinesii*] (Henn.) Henn. (= *Corallomyces heinseni* Henn., Bot. Jahrb. Syst. 23: 358. 1897).


Perithecia solitary to gregarious, associated with reddish rhizomorphs or synnemata, obpyriform, scarlet to blood-red, KOH+ blood-red, LA+ yellow, slightly scurfy, uniloculate. Perithecial surface cells forming textura angularis. Perithecial wall of one region of cells forming textura angularis, becoming narrow, compressed towards the centrum, 50–70μm thick. Ascii narrowly clavate, apex with a ring, with eight-ascoспорes arranged uniseriately. Ascoспорes ellipsoid, smooth, one-septate, constricted at septum, thick-walled, outer wall sometimes sinuous, appearing rough (optical section), finely striated (surface view), yellow-brown.

Anamorph synnematous Rhizostilbella. Synnemata on natural substrata solitary or gregarious, 2–5 caespitose, arising laterally or as terminal extension of the rhizomorphs or directly from the substratum, cylindric-capitate, subulate-capitate, cylindrical, slender to robust, straight, curved or sinuous, unbranched or once or twice branched, hisurate, pale luteous to luteous, KOH+ livid red to purple, LA+ yellow. Marginal hyphae echinulate to verrucose, pale luteous, KOH+ livid red, with clavate terminal cells, covering entire surface of stipe. Conidiophores unbranched, or once simple monochasial or monoverticillate. Phialides cylindricl, terminal, lateral and terminal, collarettes not flared, periclinal thickening conspicuous. Conidial mass white to yellow, subglobe. Conidia ellipsoidal, ovoidal with a truncate base, non-septate, smooth-walled, hyaline.

Habitat: On bark and roots of decaying or living (diseased) tropical trees, and also isolated from soil.

Distribution: Africa, Asia, America (pantropical).

Notes: Species of Corallomycetella are unique nectriaceous fungi in that they have a synnematous Rhizostilbella anamorph. Corallomycetella is similar to Corallonectria in that species in these genera produce rhizomorphs in PDA, but Corallonectria has a synnematous, fusarium-like anamorph.

Corallomycetella elegans (Berk. & M.A. Curtis) C. Herrera & P. Chaverri, comb. nov. Fig. 6

Mycobank No. MB803107


=Corallomycetella heinsenii (Henn.) Henn., Hedwigia 43: 245. 1904.


=Nectria coccinea (Pers: Fr.) Fr. var. platyspora Rehm, Ann. Mycol. 7: 137. 1900.
Fig. 6 Corallomyctella elegans. A, B: Perithecia on natural substrata; C: Perithecium in 3% KOH; D: Median section of perithecium; E: Perithecial surface cells; F: Asci; G: Ascospores (optical section); H: Ascospore (surface view); I: Synnemata on PDA; J: Conidia produced by synnemata; K: Conidium produced by mononematous anamorph; L: Synnema in 3% KOH; M: Marginal hyphae of synnema; N–O: Conidiophores/phialides of synnema; P: Mononematous anamorph; Q–S: Colonies after 2 wks at 25℃ on PDA; T–U: Colony reverse after 2 wks at 25℃ on PDA. Scale bars: A–C, I=500μm; D=200μm; E, G, H, J, K, O=20μm; F, M, N, P=50μm; R–U=10mm.

http://journals.im.ac.cn/jwxtcn

[≡ *Corallomyces mauritiicola* Henn., Hedwigia 43: 244. 1904, genus illeg., Art. 53].


Anamorph: synnematous *Rhizostilbella*.

Teleomorph: Perithecia solitary to gregarious, associated with reddish rhizomorphs and/or synnemata, obpyriform, scarlet, KOH+ blood-red, LA+ yellow, with concolorous scurf, 512–940 (–1073)×309–634 μm (mean=711×486; SD 127, 70; n=30). Ascii narrowly clavate, apex with a ring, with eight-ascospores arranged uniseriately, (123–)145–211×8.6–14.3 μm (mean=162×11; SD 21, 1.6; n=24). Ascospores ellipsoid, ovoidal with a truncate base, non-septate, smooth-walled, hyaline, 13–26(–28.4)×7–13 μm (mean=19×10; SD 2.5, 1.1; n=270).

Culture and anamorph: Colonies 42–69 mm diam. (mean=54; SD 7; n=34) after 14 d at 25°C on PDA. Colony surface with synnemata forming near the inoculum or scattered, aerial mycelium white to pale-luteous, cottony to velvety; below aerial mycelium greenish oliveaceous; sometimes agar discoloring yellow-green; reverse isabelline at center becoming buff toward colony edge, with isabelline dichotomously branching rhizomorphs immersed in agar. Synnemata cylindrical-capitate, cylindrical, slender to robust, straight, hirsute, orange to luteous, KOH+ livid red, 876–2,536×248–621 μm (mean=1,394×424; SD 545, 108; n=19). Marginal hyphae of synnemata, septate, echinulate, covering entire surface of stipe, with clavate terminal cells, 15–29×7.6–9.9 μm (mean=21×8.5; SD 5.1, 0.8; n=7).

Conidiophores unbranched or once simple monochastral or monoverticillate. Phialides cylindrical, slightly tapering towards tip, hyaline. Conidial mass buff-colored. On SNA, conidiophores simple, unbranched, acremonium-like. Phialides cylindrical, slightly tapering towards tip, collarettes not flared, periclinal thickening conspicuous, hyaline, length 27–81 μm (mean=55; SD 11.8; n=81), width at base 2.2–4.2 μm (mean=3.3; SD 0.4; n=81), width at tip 1.5–2.8 μm (mean=2.1; SD 0.3; n=81). Conidia ellipsoidal, ovoidal with a truncate base, non-septate, smooth-walled, hyaline, 13–26(–28.4)×7–13 μm (mean=19×10; SD 2.5, 1.1; n=270).

Habitat: On bark and roots of decaying or living (diseased) tropical trees, and also isolated from soil.

Distribution: Brazil, Colombia, Costa Rica, French Guiana, Nicaragua, Panama, Venezuela (Samuels 1973; Samuels & Dumont 1982; Rossman et al. 1999), DR Congo, Gabon, Guadeloupe, Ivory Coast, Jamaica, Liberia.

Holotype of *Corallomyces elegans*: Suriname, on bark, Holotype ex herb. Schw. in herb. Berkeley (K; Neotype of *Corallomycetella heinsenii* designated in Rossman et al. 1999).


Additional type specimens examined: Brazil, Rio Grande do Sul, Saó Leopoldo, on bark, Oct. 1907, S.J. Rick (exsiccati no. 1813; NY, Isotype of *Nectria coccinea* var. *platyspora*); Estado de Amazonas, Rio Jurua, Miry, on *Mauritia flexuosa*, July 1901 (E. Ule Herbarium Brasiliense no. 2837, Holotype of *Corallomyces mauritiicola*);
Cameroon, on bark, J.R. Jungner (FH, Holotype of Corallomyces elegans var. camerunensis).


Notes: Corallomyctella elegans and C. repens are indistinguishable morphologically, except for the synnemata produced in PDA. The synnemata of C. elegans can attain a height of up to 2,500μm as described by Seifert (1985). The synnemata of C. repens only reaches 600μm and are cushion-shaped. Corallomyctella elegans is apparently restricted to the tropical Western Hemisphere and Africa.

Corallomyctella repens (Berk. & Broome) Rossman & Samuels, Stud. Mycol. 42: 113. 1999. Fig. 7

Fig. 7 Corallomycetella repens. A: Perithecia/synnemata on natural substrata; B: Perithecia on natural substrata; C: Synnemata on natural substrata; D: Perithecium in 3% KOH; E: Ascospore (surface view); F: Ascus; G: Conidial masses; H, I: Synnema in 3% KOH; J, K: Conidiophores/phialides of synnema; L: Conidia produced by synnema; M: Mononematous anamorph; N: Colony after 2 wks at 25°C on PDA; O, P: Colony reverse; Q: Colony of sterile isolate after 2 wks at 25°C on PDA; R: Colony reverse of sterile isolate. Scale bars: A, G: 500μm; B, D: 100μm; C, H, I: 200μm; E, L: 10μm; F, J, K: 20μm; N–R: 10mm.
≡Rhizostilbella rubra van der Wolk, Mycol. Centralbl. 4: 237. 1914.
=Stilbum incarnatum Wakker, Ziekten van het Suikerriet op Java, Leiden, p. 197. 1898.

Anamorph: synnematous Rhizostilbella.

Teleomorph: Perithecia solitary to gregarious, associated with reddish rhizomorphs and/or synnemata, obpyriform, scarlet, KOH+ blood-red, LA+ yellow, covered with scurf, 386–659×264–367μm (mean=548×318; SD 112, 34; n=6). Ascii narrowly clavate, apex with a ring, with eight-ascospores arranged uniseriately, 194–228×16–20μm (mean=213×18; SD 12.9, 1.4; n=10). Ascospores ellipsoid, smooth, one-septate, constricted at septum, thick walled, outer wall sometimes sinuous, appearing rough (optical section), finely striated (surface view), yellow-brown, 15–21.5×6.7–8.8μm (mean=18×7.8; SD 2.2, 0.7; n=20).

Culture and anamorph: Colonies 42–61mm diam. (mean=52; SD 6.5; n=12) after 14d at 25°C on PDA. Colony surface with white aerial mycelium, cottony to velvety; conidial masses buff colored, slimy, pionnotal produced by synnemata near the inoculum; agar discoloring yellow-green; reverse isabelline with conspicuous isabelline dichotomously branching rhizomorphs immersed in agar. Surface of sterile colonies with white aerial mycelium, cottony, reverse saffron. In culture, synnemata cushion-shaped, orange to salmon, KOH+ livid red, 403–523×520–594μm (mean=450×552; SD 64, 38; n=3). Hyphae of synnemata, septate, echinate. Conidiophores unbranched or once simple monochasial or monoverticillate. Phialides monophialidic, cylindrical, hyaline. On SNA, conidiophores simple, unbranched, acremonium-like. Phialides cylindrical, collarettes not flared, periclinal thickening conspicuous, hyaline, length 39–79μm (mean=53; SD 12.9; n=10), width at base 2.5–3.8μm (mean=3.1; SD 0.5; n=10), width at tip 1.8–2.7μm (mean=2.3; SD 0.2; n=10). Conidia ellipsoidal to ovoidal with a truncate base, non-septate, smooth-walled, hyaline, 13–19×7–11μm (mean=16×9; SD 1.5, 0.9; n=30).

Habitat: On bark and roots of decaying or living (disease) tropical trees, and also isolated from soil.

Distribution: China, India, Indonesia, and Sri Lanka.

Holotype of Sphaerostibe repens: Sri Lanka (Ceylon), Peradeniya, on decaying wood of Artocarpus integrifolia, August, Holotype Herb. Berkeley (K), no. 1005.


Notes: Corallomyctecetella repens is only known from South to Southeast Asia. Morphologically, it is nearly indistinguishable from C. elegans, except for
its short, cushion-shaped, synnemata in PDA. The observed synnema are from a single culture (CBS 118.84), which was isolated in 1963. One could question whether conidiomata development has changed from a stipitate synnema to the cushion-shaped synnema over the years. Fresh collections from Asia are needed to select an epitype in order to stabilize the name and determine the extent of morphological variation.

**Corallonectria** C. Herrera & P. Chaverri, gen. nov.

MycoBank No. MB803108

Generic type: **Corallonectria jatrophae** (A. Møller) C. Herrera & P. Chaverri

Etymology: From Greek *korallion* = coral. Referring to the short, red stalk on which the perithecia develop and making reference to the genus *Corallomycetella*.

Perithecia seated on a short red stalk, in caespitose clusters of 2 to several, ovoid to obpyriform, collapsing laterally or not collapsing when dry, scarlet, KOH+ blood-red, LA+ yellow, with a white to yellow furfuraceous coating of hyphae below apex; furfuraceous coating missing in age; apex acute, smooth, uniloculate. Perithecial surface cells forming *textura angularis*. Perithecial wall of one region of cells forming *textura angularis*, becoming narrow, compressed towards the centrum, 30–40μm thick. Ascii clavate, apex simple, with eight ascospores arranged biseriately. Ascospores fusiform-ellipsoid, sometimes reniform, 1-septate, often constricted slightly at septum, pale brown when discharged, smooth-walled. Anamorph synnematus, fusarium-like.

Habitat: On bark of decaying or living (diseased) tropical trees.

Distribution: Tropical America and Greater Antilles.

Notes: *Corallonectria* is similar to *Corallomycetella* in that it produces rhizomorphs on PDA. However, the anamorphic states are different. *Corallomycetella* has a synnematous Rhizostilbella anamorph, while *Corallonectria* has a synnematous fusarium-like anamorph. *Corallonectria* is also characterized by a white to yellow furfuraceous coating below the apex of the perithecia, and relatively large, pale-brown, and smooth ascospores.

**Corallonectria jatrophae** (A. Møller) C. Herrera & P. Chaverri, comb. nov.

MycoBank No. MB803109


≡ *Nectria madeirensis* Henn., Hedwigia 43: 244. 1904.

≡ [*Corallomyces caricae* Henn., Hedwigia 43: 245. 1904, genus illeg., Art. 53].


Anamorph: synnematus, fusarium-like.

Teleomorph: Perithecia seated on a short red stalk, in caespitose clusters of 2 to several, ovoid to obpyriform, 729–1,308×447–748μm (mean=932×575; SD 171, 83; n=17), not collapsing or collapsing by lateral pinching, orange-red to scarlet, with a white to yellow furfuraceous coating below apex; apex acute, smooth, scarlet. Asci clavate, apex simple, with eight ascospores arranged biseriately. Ascospores fusiform-ellipsoid, sometimes reniform, 1-septate, often constricted slightly at septum, pale brown when discharged, smooth, (26–)27–41.7×6.8–12.2μm (mean=32×9; SD 2.9, 0.9; n=139).
Fig. 8 *Corallonectria jatrophae*. A: Perithecia on natural substrata; B: Median section of perithecium; C: Ascus; D: Perithecium in 3% KOH; E: Ascospores (optical section); F: Ascospore (surface view); G: Colony after 2 wks at 25°C on PDA; H, I: Colony reverse; J: Synnemata after 2 wks at 25°C on PDA; K: Synnema after 8 wks at 25°C on PDA; L: Phialides of synnema; M: Conidia produced by synnema. Scale bars: A, D: 200 μm; B: 100 μm; C: 20 μm; E, F, L, M: 10 μm; G–I: 10 mm; J: 700 μm; K: 1,000 μm.
Culture and anamorph: Colonies 42–57mm diam (mean=48; SD 9.7; n=4) after 14d. at 25°C on PDA. Colony surface with white aerial mycelium, cottony to velvety; agar discoloring amber; synnemata produced near inoculum; agar discoloring amber; reverse saffron, with saffron dichotomously branching rhizomorphs immersed in agar. Synnemata cylindrical, slender to robust, straight or curved, rarely branching, appearing furfuraceous with loose, white hyphae, with a terminal cupulate capitulum (several with age), pale-luteous, KOH+ apricot to scarlet, 1,178–2,464×225–359μm (mean=1,698×286; SD 425, 43; n=10; taller with age). Conidiophores unbranched or once simple monochasial or monoverticillate. Phialides cylindrical, hyaline, length 9–34μm (mean=22; SD 10.5; n=7), width at base 2.9–3.9μm (mean=3.3; SD 0.3; n=7), width at tip 1.9–2.7μm (mean=2.2; SD 0.3; n=7). Conidial mass forming inside cupulate capitula, flame-shaped, luteous. Conidia fusarium-like, long-fusiform, slightly curving at the apical and basal ends, apical cell acute, basal cell pedicellate, hyaline, forming on PDA, not observed on SNA, 3–4(–5)-septate: 3-septate (68–)71–84×5.2–7.7μm (mean=77×6.5; SD 3.8, 0.6; n=30), 4-septate 73–90×5.0–7.5μm (mean=80×6.6; SD 3.9, 0.6; n=30), 5-septate (75–)92–100×5.0–7.2μm (mean=91×6.0; SD 8.4, 0.7; n=6).

Habitat: On bark of decaying or living (diseased) tropical trees.

Distribution: South and Central America (Belize, Brazil, Colombia, Costa Rica, French Guiana, Nicaragua, Panama, Puerto Rico, Venezuela; Rossman et al., 1999; Samuels, 1973; Samuels & Dumont, 1982).


Additional type specimens examined: Brazil, Manaus, on bark of unidentified plant, Batista, 20 Feb. 1961 (URM 22, Holotype of Macbridella amazonensis); Rio Jurua, Cacoeria, on dead stems of Carica sp., May 1901, Ule 2822 (FH, Isotype of Corallomyces caricae). Marmellos, Rio Madeira, on decaying bark, Mar. 1902, Ule 3115, Mycotheca Brasiliensis no. 69 (The Botanical Museum, University of Copenhagen, Isotype of Nectria madeirensis).


Brazil, Estado do Pará, Belterra, Maguai, Floresta Nacional do Tapajós, elev. 28m., S2°46’59.6”, W55°01’38.9”, on bark, 7 May 2011, O. Liparini Pereira & P. Chaverri (PC 1300), BPI 884209.

French Guiana, Route de Belizon, track to Montage Tortue, 15km from road N2, 52°20’, 4°25’, on bark of newly killed tree, 18 Feb. 1988, A.Y. Rossman & C. Feuillet (3222), BPI 1107291; ibid., A.Y. Rossman & C. Feuillet (3230B), BPI 1107295.


Illustrations: Samuels (1973, Figs 10-13, as N. amazonensis); Wollenweber (1930, No. 684, as C. jatrophae).

Notes: Corallonectria jatrophae is the only species in the genus Corallonectria. It can be easily identified by furfuraceous perithecia on a short red stalk. On PDA, this species produces a luteous colony with rhizomorphs. Ideally an epitype from the same collecting region as the type would be designated, which it would make our isolate from Brazil (PC 1300) ideal. However, the isolate did not survive –80°C storage. Our phylogeny demonstrated that isolates from Puerto Rico (CBS 913.96) and Brazil (PC 1300) are conspecific, suggesting a broad biogeographic range. Based on the teleomorph, they are indistinguishable. Thus, the specimen from Puerto Rico is designated as epitype.

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