Phylogenetic lineages in the Capnodiales

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Abstract: The Capnodiales incorporates plant and human pathogens, endophytes, saprobes and epiphytes, with a wide range of nutritional modes. Several species are lichenised, or occur as parasites on fungi, or animals. The aim of the present study was to use DNA sequence data of the nuclear ribosomal small and large subunit RNA genes to test the monophyly of the Capnodiales, and resolve families within the order. We designed primers to allow the amplification and sequencing of almost the complete nuclear ribosomal small and large subunit RNA genes. Other than the Capnodiales (sooty moulds), and the Davideliaceae, which contains saprobes and plant pathogens, the order presently incorporates families of major plant pathological importance such as the Mycosphaerellaceae, Teratosphaeriaceae and Schizothyriaceae. The Piedraiaceae was not supported, but resolves in the Teratosphaeriaceae. The Dissoconium is introduced as a new family to accommodate Dissoconium and Ramichloridium. Lichenisation, as well as the ability to be saprobic or plant pathogenic evolved more than once in several families, though the taxa in the upper clades of the tree lead us to conclude that the strictly plant pathogenic, necrotrophic families evolved from saprobic ancestors (Capnodiales), which is the more primitive state.

Key words: Ascomycetes, Brunneosphaerella, Capnodiales, DNA sequence comparisons, Mycosphaerella, novel primers, systematics.

INTRODUCTION

The Dothideomycetes encompasses plant and human pathogens, endophytes, saprobes and epiphytes. The class presently contains two subclasses, namely Pleosporomycetidae and Dothideomycetidae (Schoch et al. 2006, 2009a). Although the main orders, Pleosporales and Dothiales correlate with the presence or absence of pseudoparaphyses and other centrum characteristics, many orders remain unresolved. The Dothideomycetidae include the orders Dothiales, Capnodiales and Myriangiales, which lack paraphyses, pseudoparaphyses and periphysoids. Based on a multi-gene phylogeny, and the presence of ostiolar paraphyses as possible synapomorphy, the Capnodiales were recognised as the order incorporating the Capnodiales, Davideliaceae, Mycosphaerellaceae and Piedraiaceae (Schoch et al. 2006). However, several studies (Hunter et al. 2006, Crous et al. 2007a, b) showed the Mycosphaerellaceae to be polyphyletic, and to contain additional variation at the familial level, leading to the circumscriptions of the Teratosphaeriaceae and Schizothyriaceae. Crous et al. (2009b, c) again revealed Teratosphaeriaceae to be too widely defined, including some further unresolved families.

The present study focuses on the Capnodiales, which is based on the Capnodiales, representing a group of leaf epiphytes associated with honeydew of insects, usually visible as a black growth on leaf surfaces, fruit and twigs. Members of the Capnodiales form superficial ascomata with fasciculate asci, and hyaline to dark, septate ascospores. Anamorphs are dematiaceous, and include mycelial (phragmo- to dictyoconidia), spematidal and pycnidial synanamorphs (Hughes 1976, Cheewangkoon et al. 2009).

The Mycosphaerellaceae was treated as a family in the Dothideales by Hawksworth et al. (1995), while Kirk et al. (2001) introduced a separate order, the Mycosphaerellales for this family, and Kirk et al. (2008) again placed it in the Capnodiales. The Mycosphaerellaceae is recognised by having characteristic pseudothecial ascomata that can be immersed or superficial, embedded in host tissue or erumpent, having ostiolar paraphyses, but lacking interascal tissue at maturity. Ascospores are hyaline, but in some cases slightly pigmented (Barr 1987), and predominantly 1-septate, although some taxa with 3-septate ascospores have been recorded (Crous et al. 2003). Although up to 30 anamorph genera have been linked to Mycosphaerella (Crous et al. 2000, 2001, 2007a-c, 2009a-c, Crous 2009), recent studies have shown this to be incorrect, and that the family in fact consists of numerous genera with morphologically conserved Mycosphaerella-like teleomorphs, and distinct anamorphs (Crous et al. 2007a, b, 2009b, c).

Families tentatively placed in the Capnodiales (Lumbsch & Huhndorf 2007, Kirk et al. 2008) include epiphytes (Antennulariaceae, Capnodiales, Metacapnodiales) (Hughes 1976), saprobes and plant pathogens (Davideliaceae, Dissoconium, Mycosphaerellaceae, Schizothyriaceae, Teratosphaeriaceae) (Aptroot 2006, Crous 2009), and colonisers or hair shafts of mammals (Piedraiaceae) (de Hoog et al. 2000). To address the status of the Capnodiales as an order, and the intrafamilial relationships within this order, DNA sequences of...
the 18S, 5.8S and 28S nrRNA genes were generated for a set of specifically selected taxa. A further aim was to clarify genera within these families, and resolve anamorph-teleomorph relationships for the taxa investigated.

MATERIALS AND METHODS

Isolates

Isolates were selected (Table 1 - see online Supplementary Information) that are representative of the Mycosphaerellaceae (Crous 1998, Crous et al. 2004a, c, 2006a, b, 2007a), Schizothyriaceae (Batzer et al. 2005, 2007), Teratosphaeriaceae (Crous et al. 2007a, 2008b, c, 2009a–c), Pediobasidaceae (Kruys et al. 2006), Davidiellaceae (Braun et al. 2003, Schubert et al. 2007a, b), Capnodiaeae (Schoch et al. 2006), as well as numerous other genera for which the familial relationships have remained unclear, such as the Phaeophracospora complex (Crous et al. 1997, 2007a, 2009b, c, Andjic et al. 2007), Polythricium (Simon et al. 2009), the Dissoconidium complex (Crous et al. 2004c, 2007c, 2008b, Arzanlou et al. 2008b), and several less well-known genera represented by one or two species only. For fresh material excised leaf spots bearing ascomata were soaked in water for approximately 2 h, after which they were placed in the bottom of Petri dish lids, with the top half of the dish containing 2 % malt extract agar (MEA; Crous et al. 2009d). Ascospor germination patterns were examined after 24 h, and single-ascospor and conidial cultures established as described by Crous et al. (1991). Colonies were sub-cultured onto synthetic nutrient-poor agar (SNA), potato-dextrose agar (PDA), oatmeal agar (OA), MEA (Crous et al. 2009d), and incubated at 25 °C under continuous near-ultraviolet light to promote sporulation. Other cultures were obtained from the culture collection of the Centraalbureau voor Schimmelcultures (CBS-KNAW) in Utrecht, the Netherlands or the working collection of Pedro Crous (CPC).

DNA isolation, amplification and molecular phylogeny

Genomic DNA was extracted from mycelium taken from fungal colonies on MEA using the UltraClean™ Microbial DNA Isolation Kit (Mo Bio Laboratories, Inc., Solana Beach, CA, U.S.A.). A part of the nuclear rDNA operon spanning the 3' end of the 18S rRNA gene (SSU), the first internal transcribed spacer (ITS1), the 5.8S rRNA gene, the second ITS region (ITS2) and the first 900 bp at the 5' end of the 28S rRNA gene (LSU) was amplified and sequenced using novel and previously published primers (Table 2; see below).

Novel primers were designed using a variety of complete SSU and LSU sequences obtained from the GenBank sequence database (www.ncbi.nlm.nih.gov/). The selection was not limited only to fungi belonging to the Dothideomycetes but encompassed as many as possible full sequences in order to make the primers as robust as possible. We aimed to keep the melting temperature (Tm) of the novel primers at 40–45 °C and the GC content to approximately 50 % to keep them as compatible as possible to existing published primers. Primer parameters were calculated using the OligoAnalyzer tool on the web site of Integrated DNA Technologies (http://eu.idtdna.com/analyzer/Applications/OligoAnalyzer/) with the “Oligo Conc” parameter set at 0.2 mM and the “Na+ Conc” parameter set at 16 mM. A framework of existing and novel primers was then aligned onto the sequence of Magnaporthe grisea (GenBank accession AB026819) to derive primer positions (Table 2) and evaluate coverage over the gene regions. These primers were amplified and sequenced in the following overlapping sections to cover the almost complete SSU and LSU for the selected strains (Table 2): SSU1Fd or SSU6Fm with SSU2Rd, SSU2Fd with SSU3Rd, SSU7Fm with SSU4Rd or SSU6Rm, SSU4Fd with 5.8S1Rd, V9G or LSU1Fd with LSU3Rd, LSU8Fd with LSU8Rd, LSU4Fd with LSU5Rd, and LSU5Fd with LSU7Rd. For some strains (Table 3) it was necessary to add an additional overlap for SSU4Fd with 5.8S1Rd (using SSU4Fd with SSU7Rm and SSU8Fm with 5.8S1Rd), for LSU6Fd with LSU8Rd (using LSU8Fd with LSU3Rd and LSU3Fd with LSU8Rd), and for LSU5Fd with LSU7Rd (using LSU5Fd with LSU6Rd and LSU6Fd with LSU7Rd) to complete the gaps due to large insertions.

The internal transcribed spacer regions, as well as all insertions (Table 3) were excluded from all analyses. Sequence data were deposited in GenBank (Table 1) and alignments in TreeBASE (www.treebase.org). Two separate analyses were performed: The first using only partial LSU data due to the limited number of complete LSU sequences available and the second using the almost complete SSU, 5.8S nrDNA and LSU alignment.

Maximum likelihood analyses (ML) were conducted in RAxML v. 7.0.4 (Stamatakis 2006) for the partial LSU alignment. A general time reversible model (GTR) with a discrete gamma distribution and four rate classes was applied. A tree was obtained by simultaneously running a fast bootstrap search of 1000 pseudoreplicates (Stamatakis et al. 2008) followed by a search for the most likely tree. Maximum Likelihood bootstrap value (MLBP) equal or greater than 70 % are given at the nodes (Fig. 1).

Maximum likelihood analyses (ML) were conducted in RAxML v. 7.0.4 (Stamatakis 2006) for the almost complete SSU, 5.8S nrDNA and LSU alignment. A general time reversible model (GTR) with a discrete gamma distribution and four rate classes was applied to each partition (SSU, 5.8S nrDNA and LSU). A tree was obtained by simultaneously running a fast bootstrap search of 500 pseudoreplicates (Stamatakis et al. 2008) followed by a search for the most likely tree. Maximum Likelihood bootstrap value (MLBP) equal or greater than 70 % are given at the nodes (Fig. 2).

Taxonomy

Fungal structures were mounted in lactic acid, and 30 measurements × 1000 magnification) obtained per structure type. The range obtained is presented, except for spore measurements, where the 95 % confidence intervals are given with the extremes in parentheses. Colony colours (surface and reverse) were assessed after 1–2 wk on MEA at 25 °C in the dark, using the colour charts of Rayner (1970). All cultures obtained in this study are maintained in the culture collection of the Centraalbureau voor Schimmelcultures (CBS-KNAW) in Utrecht, the Netherlands (Table 1). Nomenclatural novelties and descriptions were deposited in MycoBank (Crous et al. 2004b). Names for which the taxonomy has not been resolved, but need to be allocated to another genus, are placed in inverted commas, e.g. “Mycosphaerella” iridis.
Table 2. Details of primers used for this study and their relation to selected published primers. Primer names ending with a "d" denotes a degenerate primer whereas those ending with a "m" denotes specific primers designed based on the partial novel sequences generated. The start and end positions of the primers are derived using *Magnaporthe grisea* GenBank accession AB026819 as reference in the 5’–3’ direction.

| Name   | Sequence (5’ – 3’) | Orientation | %GC | Tm (°C) | Start | End   | Reference                        |
|--------|-------------------|-------------|-----|---------|-------|-------|----------------------------------|
| 5.8S1Fd | CTC TTG GTT CBV GCA TCG | Forward     | 57.4 | 49.8 – 54.2 – 56.8 | 2333  | 2350  | This study                       |
| 5.8S1Rd | WAA TGA CGC TCG RAC AGG CAT G | Reverse   | 52.3 | 57.6 – 58.9 – 60.2 | 2451  | 2472  | This study                       |
| F377   | AGA TGA AAA GAA CTT TGA AAA GAG AA | Forward | 26.9 | 40.3   | 3005  | 3030  | www.lutzonilab.net/primers/ page244.shtml |

**ITS1**

| Name   | Sequence (5’ – 3’) | Orientation | %GC | Tm (°C) | Start | End   | Reference                        |
|--------|-------------------|-------------|-----|---------|-------|-------|----------------------------------|
| ITS1   | TCC GTA GGA CCT TCG G  | Forward     | 63.2 | 49.5   | 2162  | 2180  | White et al. (1990)              |
| ITS1F  | CTT GGT CAT TTA GAA GTA A   | Forward | 36.4 | 39.0   | 2124  | 2145  | Gardes & Bruns (1993)            |
| ITS1Fd | CGA TTG AAT GGG TCA GTG AGG C | Forward | 54.5 | 48.0   | 2043  | 2064  | This study                       |
| ITS1Rd | GAT ATG CTT AAG TCC AGC GGG | Reverse  | 47.6 | 43.1   | 2671  | 2691  | This study                       |
| ITS4   | TCC TCC GCT TAT TGA TAT GC | Reverse  | 45.0 | 41.6   | 2685  | 2704  | White et al. (1990)              |
| ITS4S  | CCT CCG CTT ATT GAT ATG CTT AAG | Reverse | 41.7 | 42.9   | 2680  | 2703  | Kreutzer et al. (1996)           |
| ITS5   | GGA AGT AAA AGT CGT AAC AGG G | Forward | 40.9 | 40.8   | 2138  | 2159  | White et al. (1990)              |
| LR0R   | GAA CCC GCT GAA CTT AAG C | Forward     | 52.6 | 43.2   | 2668  | 2686  | Rehner & Samuels (1994)          |
| LR2    | TTT TCA AAG TCC TTC TC  | Reverse     | 23.5 | 28.5   | 3009  | 3025  | www.lutzonilab.net/primers/ page244.shtml |
| LR2R   | AAG AAC TTT GAA AAG AG  | Forward     | 29.4 | 30.4   | 3012  | 3028  | www.lutzonilab.net/primers/ page244.shtml |
| LR3    | GGT CGG TGT TTC AAG AC  | Reverse     | 52.9 | 40.5   | 3275  | 3291  | Vilgalys & Hester (1990)         |
| LR3R   | GTC TTG AAA CAC GGA CC  | Forward     | 52.9 | 40.5   | 3275  | 3291  | www.lutzonilab.net/primers/ page244.shtml |
| LR5    | TCC TGA GGG AAA CTT CG  | Reverse     | 52.9 | 41.0   | 3579  | 3595  | Vilgalys & Hester (1990)         |
| LR5R   | GAA GTT TCC CTC AGG AT  | Forward     | 47.1 | 37.8   | 3580  | 3596  | wwwbiology.duke.edu/fungi/ mycolab/primers.htm |
| LR6    | CGC CAG TTC TGC TTA CC  | Reverse     | 58.8 | 43.5   | 3756  | 3772  | Vilgalys & Hester (1990)         |
| LR7    | TAT TAC CAC CAA GAT CT  | Reverse     | 41.2 | 35.3   | 4062  | 4078  | Vilgalys & Hester (1990)         |
| LR8    | CAC CTT GGA GAC CTG CT  | Reverse     | 58.8 | 44.3   | 4473  | 4489  | www.lutzonilab.net/primers/ page244.shtml |
| LR8R   | AGC AGG TCT CCA AGG TG  | Forward     | 58.8 | 44.3   | 4473  | 4489  | www.lutzonilab.net/primers/ page244.shtml |
| LR9    | AGA GCA CTG GGC AGA AA  | Reverse     | 52.9 | 43.6   | 4799  | 4815  | www.lutzonilab.net/primers/ page244.shtml |
| LR10   | AGT CAA GCT CAA GAG CG  | Reverse     | 52.9 | 41.6   | 5015  | 5031  | www.lutzonilab.net/primers/ page244.shtml |
| LR10R  | GAC CCT GTT GAG CTT GA  | Forward     | 52.9 | 41.6   | 5013  | 5029  | www.lutzonilab.net/primers/ page244.shtml |
| LR11   | GCC AGT TAT CCC TGT GGT AA | Reverse  | 50.0 | 43.9   | 5412  | 5431  | www.lutzonilab.net/primers/ page244.shtml |
| LR12   | GAC TTA GAG GGC TCG AG  | Reverse     | 52.9 | 39.4   | 5715  | 5731  | Vilgalys & Hester (1990)         |
| LR12R  | CTG AAC GCC TCT AAG TCA G AA | Forward | 47.6 | 43.7   | 5715  | 5735  | wwwbiology.duke.edu/fungi/ mycolab/primers.htm |
| LR13   | CAT CGG AAC AAC AAT GC  | Reverse     | 47.1 | 38.8   | 5935  | 5951  | www.lutzonilab.net/primers/ page244.shtml |
| LR14   | AGC CAA ACT CCC CAC CTG | Reverse     | 61.1 | 47.6   | 5206  | 5223  | www.lutzonilab.net/primers/ page244.shtml |
| LR15   | TAA ATT ACA ACT CGG AC  | Reverse     | 35.3 | 32.5   | 2780  | 2796  | www.lutzonilab.net/primers/ page244.shtml |
| LR16   | TTC CAC CCA AAC ACT CG  | Reverse     | 52.9 | 42.1   | 3311  | 3327  | Moncalvo et al. (1993)           |
| LR17R  | TAA CCT ATT CTC AAA CTT | Forward     | 27.8 | 31.2   | 3664  | 3681  | www.lutzonilab.net/primers/ page244.shtml |
| LR20R  | GTG AGA CAG GTT AGT TTT ACC CT | Forward | 43.5 | 43.6   | 5570  | 5592  | www.lutzonilab.net/primers/ page244.shtml |
| LR21   | ACT TCA AGC GTT TCC CTT T | Reverse     | 42.1 | 41.7   | 3054  | 3072  | www.lutzonilab.net/primers/ page244.shtml |
| LR22   | CCT CAC GGT ACT TGT TCG CT | Reverse   | 55.0 | 46.8   | 2982  | 3001  | www.lutzonilab.net/primers/ page244.shtml |
| Name       | Sequence (5’ – 3’) | Orientation | %GC | Tm (°C) | Start | End | Reference                        |
|------------|-------------------|-------------|-----|---------|-------|-----|----------------------------------|
| LSU1Fd     | GRA TCA GGT AGG RAT ACC CG | Forward     | 55.0 | 41.8 – 46.4 – 46.3 | 2655  | 2674 | This study                      |
| LSU1Rd     | CTG TTG CCG CTT CAC TCG C | Reverse     | 63.2 | 49.6 | 2736  | 2754 | This study                      |
| LSU2Fd     | GAA ACA CGG ACC RAG GAG TC | Forward     | 57.5 | 45.5 – 46.5 – 47.6 | 3280  | 3299 | This study                      |
| LSU2Rd     | ATC CGA CRA CNT CAG GAT CGG TCG | Reverse     | 52.1 | 48.3 – 49.0 – 49.8 | 3379  | 3402 | This study                      |
| LSU3Fd     | GTC ATY CYA GAC AGC MGG ACG | Forward     | 57.1 | 44.7 – 47.4 – 50.2 | 3843  | 3863 | This study                      |
| LSU3Rd     | CAC ACT CCT TAG CGG ATT CGG AC | Reverse     | 56.5 | 49.1 | 3876  | 3898 | This study                      |
| LSU4Fd     | CGG CAG CAG GTC TAC AAG G | Forward     | 68.4 | 51.2 | 4469  | 4487 | This study                      |
| LSU4Rd     | CTT GTC ATR TTT GTC GAC TTC CC | Reverse     | 54.3 | 47.4 – 48.7 – 50.0 | 4523  | 4545 | This study                      |
| LSU5Fd     | GGC CTA AAG GAT CGA TAG GCC ACA | Forward     | 70.6 | 51.6 | 3357  | 5072 | This study                      |
| LSU5Rd     | GGA CTA AAG GAT CGA TAG GCC ACA | Reverse     | 52.0 | 48.3 | 5355  | 5379 | This study                      |
| LSU6Fd     | CGG AAG CAG GAT TCG GTA AGC G | Forward     | 54.5 | 48.1 | 5499  | 5520 | This study                      |
| LSU6Rd     | TCT AAA CCC ACG TCA CTT CCC C | Reverse     | 54.5 | 48.6 | 5543  | 5564 | This study                      |
| LSU7Fd     | GTC ACG ATC TRC TAA GGG TAA GCC | Reverse     | 52.1 | 46.0 – 47.4 – 48.8 | 5943  | 5966 | This study                      |
| LSU7Rd     | GCA GAT CGT ACT AAC AAG GCT ACT CTA C | Reverse     | 46.4 | 47.9 | 5927  | 5954 | This study                      |
| LSU8Fd     | CCA GAG GAA ACT CTG GTG GAG GC | Forward     | 60.9 | 51.2 | 3469  | 3491 | This study                      |
| LSU8Rd     | GTC AGA TTC CCC TTG TCC GTA CC | Reverse     | 56.5 | 48.9 | 4720  | 4742 | This study                      |
| LSU9Fm     | GTG AGC ATG CCT CGT CAT C | Forward     | 54.5 | 47.9 | 4882  | 4903 | This study                      |
| LSU9Rm     | GAT TYT GGC AAC CCC GTP CCC | Reverse     | 59.5 | 49.2 – 50.0 – 50.9 | 4979  | 4999 | This study                      |
| LSU10Fm    | GGG AAC TGG AGT GGC ATG TCT G | Forward     | 54.5 | 48.6 | 5543  | 5564 | This study                      |
| LSU10Rm    | TTC TAA GCG AAT TCT GCT TTC G | Reverse     | 54.5 | 48.1 | 5499  | 5520 | This study                      |
| LSU11Fm    | TTTG GTC AAGCA ACTG GCGCATGC | Forward     | 50.0 | 49.4 | 3753  | 3776 | This study                      |
| LSU12Fd    | GTTG GGG GCTTATGCGATTCTTTAGCC | Forward     | 52.0 | 48.3 | 5355  | 5379 | This study                      |
| NS1        | GTA GTC ATA TGC TTG TCT C | Forward     | 42.1 | 36.9 | 413   | 431  | White et al. (1990)               |
| NS1R       | GAG ACA AGT TCA GTA CTA C | Reverse     | 42.1 | 36.9 | 413   | 431  | www.lutzonlab.net/primers/page244.shtml |
| NS2        | GGC TGC TGG CAC CAG ACT TGC | Reverse     | 66.7 | 53.8 | 943   | 963  | White et al. (1990)               |
| NS3        | GCAA GCT TGCGG CAGCCAGCC | Forward     | 66.7 | 53.8 | 943   | 963  | White et al. (1990)               |
| NS4        | CTT CCG TCA ATT CCT TTA AG | Reverse     | 40.0 | 38.2 | 1525  | 1544 | White et al. (1990)               |
| NS5        | AAG GAT AAG GAA TGG ACG GAA G | Forward     | 36.4 | 40.1 | 1523  | 1544 | White et al. (1990)               |
| NS6        | GCA TCA CAG ACC TGT TAT TGC CTC | Reverse     | 50.0 | 47.5 | 1806  | 1829 | White et al. (1990)               |
| NS7        | GAG GCA ATA ACA GGT CGT TGC TGC | Forward     | 50.0 | 47.5 | 1806  | 1829 | White et al. (1990)               |
| NS8        | GCC GTA TCA CCT AGC GA | Reverse     | 60.0 | 50.4 | 2162  | 2181 | White et al. (1990)               |
| NS17       | CAT GTC TAA GTT TAA GCA A | Forward     | 31.6 | 34.2 | 447   | 465  | Gargas & Taylor (1992)            |
| NS18       | CTC ATT CCA ATT ACA AGA CC | Reverse     | 40.0 | 38.0 | 887   | 906  | Gargas & Taylor (1992)            |
| NS19       | CGG GAG AAG GAG CCT GAG AAA C | Forward     | 59.1 | 49.3 | 771   | 792  | Gargas & Taylor (1992)            |
| NS20       | CGT CCC TAT TAA TCA TTA CG | Reverse     | 40.0 | 37.3 | 1243  | 1262 | Gargas & Taylor (1992)            |
| NS21       | GAA TAA TAG AAT AGG ACG | Forward     | 33.3 | 30.5 | 1193  | 1210 | Gargas & Taylor (1992)            |
| NS22       | AAT TAA GCA GAC AAA TCA CT | Reverse     | 30.0 | 36.4 | 1687  | 1706 | Gargas & Taylor (1992)            |
| NS23       | GAC TCA ACA CGG GGA AAC TC | Forward     | 55.0 | 45.5 | 1579  | 1598 | Gargas & Taylor (1992)            |
| NS24       | AAC CTT TGT TAC GAT TTT TA | Reverse     | 30.0 | 36.2 | 2143  | 2162 | Gargas & Taylor (1992)            |
| SR1R       | GTA GCA TCA GAA ACG GCT AC | Forward     | 60.0 | 47.8 | 779   | 798  | Spatafora et al. (1995)           |
| SR3        | GAA AGT TGA TAC GGC T | Forward     | 43.8 | 34.8 | 696   | 711  | www.biology.duke.edu/fungi/mycolab/primers.htm |
**Table 2. (Continued).**

| Name             | Sequence (5' – 3') | Orientation | %GC | Tm (°C) | Start | End   | Reference      |
|------------------|--------------------|-------------|-----|---------|-------|-------|----------------|
| SSU1Fd           | CTG CCA GTA GTC ATA TGC TTG TCT C | Forward     | 48.0 | 46.5    | 407   | 431   | This study     |
| SSU1Rd           | CTT TGA GAC AAG CAT ATG AC | Reverse     | 40.0 | 48.7    | 416   | 435   | This study     |
| SSU2Fd           | GAA CAA YTR GAG GCC AAG | Forward     | 50.0 | 47.8 – 50.7 – 53.5 | 930 | 947 | This study     |
| SSU2Rd           | TAT ACG CTW YTG GAG C TG | Reverse     | 47.2 | 48.4 – 49.9 – 51.2 | 974 | 991 | This study     |
| SSU3Fd           | ATC AGC TCG YGT AGT C | Forward     | 44.7 | 48.4 – 49.5 – 50.5 | 1389 | 1407 | This study     |
| SSU3Rd           | TAY GGT TRA GAC TAC RAC GG | Reverse     | 47.5 | 49.0 – 52.5 – 56.0 | 1397 | 1416 | This study     |
| SSU4Fd           | CGG TTC TTA GTT GGT G | Forward     | 52.9 | 50.0    | 1670 | 1686 | This study     |
| SSU4Rd           | CAG ACA AAT CAC TCC ACC | Reverse     | 50.0 | 50.3    | 1682 | 1699 | This study     |
| SSU5Fd           | TAT ACG CTG CTC TGT GAC | Reverse     | 47.2 | 48.9 – 50.1 – 51.2 | 2037 | 2054 | This study     |
| SSU5Rd           | TAY GGT TRA GAC TAC RAC GG | Reverse     | 55.6 | 52.5    | 2148 | 2166 | This study     |
| SSU6Fd           | GCT TGT CTC AAA GAT TAA GCC ATG CAT GTC | Forward | 43.3 | 49.0    | 423   | 452   | This study     |
| SSU6Rm           | GCA GGT TAA GGT CTC GTT CGC TAT CCG | Reverse | 51.9 | 50.1    | 1707 | 1733 | This study     |
| SSU7Fd           | GAG TGT TCA AAG CAG GCC T N T | Forward | 55.8 | 51.0 – 52.2 – 53.3 | 1153 | 1178 | This study     |
| SSU7Rm           | CAA TGC TCK ATC CCC AGC AGC AC | Reverse | 58.7 | 49.5 – 50.8 – 52.1 | 1921 | 1943 | This study     |
| SSU8Fd           | GCA CGC GCG CTA CAC TGA C | Forward | 68.4 | 52.2    | 1842 | 1866 | This study     |
| V9G              | TTA CGT CCC TGC CCT TGT TA | Forward | 56.7 | 42.8    | 2002 | 2021 | de Hoog & Gerrits van den Ende (1998) |

**Table 3.** Isolates containing group I intron sequences. The insertion positions of these introns are derived using *Magnaporthe grisea* GenBank accession AB026819 as reference in the 5’–3’ direction.

| Isolate                   | Insertion between | 18S or 28S nrDNA | Intron size (bp) | Blast result               |
|---------------------------|-------------------|------------------|------------------|----------------------------|
| Batcheloromyces leucadendri CBS 110892 | 1559 – 1560 | 18S nrDNA 350  | No significant similarity |
|                           | 1820 – 1821 | 18S nrDNA 399  | 190/252 of AV545722 Hydrodropisphaera erubescens 18S nrDNA |
|                           | 4875 – 4876 | 28S nrDNA 328  | 211/264 of DQ246237 Teratosphaeria mexicana 28S nrDNA |
|                           | 5424 – 5425 | 28S nrDNA 538  | No significant similarity |
|                           | 5538 – 5539 | 28S nrDNA 383  | 218/283 of EU181458 Trichophyton soudanense 28S nrDNA |
| Batcheloromyces proteae CBS 110696 | 1559 – 1560 | 18S nrDNA 325  | No significant similarity |
|                           | 1820 – 1821 | 18S nrDNA 399  | 191/254 of AV545722 Hydrodropisphaera erubescens 18S nrDNA |
|                           | 4875 – 4876 | 28S nrDNA 328  | 211/263 of DQ246237 Teratosphaeria mexicana 28S nrDNA |
|                           | 5424 – 5425 | 28S nrDNA 535  | 75/90 of DQ442697 Axula adeninivorans 26S nrDNA |
|                           | 5538 – 5539 | 28S nrDNA 372  | 34/36 of GQ120133 Uncultured marine fungus 28S nrDNA |
| Catenulostroma macowanii CBS 110756 | 1559 – 1560 | 18S nrDNA 395  | 297/379 of DQ843802 Mycosphaerella latebrosa 18S nrDNA |
|                           | 5424 – 5425 | 28S nrDNA 914  | No significant similarity |
| Catenulostroma macowanii CBS 111029 | 1559 – 1560 | 18S nrDNA 395  | 303/379 of DQ843802 Mycosphaerella latebrosa 18S nrDNA |
|                           | 5424 – 5425 | 28S nrDNA 914  | No significant similarity |
| Cercospora api CBS 118712 | 1820 – 1821 | 18S nrDNA 733  | 288/363 of EU167577 Mycosphaerella milleri 18S nrDNA |
| Cercospora capsici CPC 12307 | 1820 – 1821 | 18S nrDNA 732  | 287/363 of EU167577 Mycosphaerella milleri 18S nrDNA |
| Cercospora jansseniae CBS 145.37 | 1820 – 1821 | 18S nrDNA 350  | 295/365 of EU167577 Mycosphaerella milleri 18S nrDNA |
| Devriesia staurophora CBS 375.81 | 3560 – 3561 | 28S nrDNA 309  | No significant similarity |
| Miuraea persicae CPC 10069 | 1820 – 1821 | 18S nrDNA 603  | 394/443 of DQ848342 Mycosphaerella populorum 18S nrDNA |
| Mycosphaerella latebrosa CBS 652.85 | 1559 – 1560 | 18S nrDNA 370  | 234/296 of DQ848311 Septoria betulae 18S nrDNA |
|                           | 1820 – 1821 | 18S nrDNA 933  | Matches same species |
|                           | 2168 – 2169 | 18S nrDNA 494  | 377/449 of DQ848326 Septoria aphanisia 18S nrDNA |
|                           | 4875 – 4876 | 28S nrDNA 481  | No significant similarity |
| missing 5018 – 5019 | 28S nrDNA Not present | Not present | Not present |
| Isolate | Insertion between | 18S or 28S nrDNA | Intron size (bp) | Blast result |
|---------|------------------|------------------|-----------------|--------------|
| Mycosphaerella latebrosa CBS 687.94 | 5424 – 5425 | 28S nrDNA | 680 | No significant similarity |
| Mycosphaerella latebrosa CBS 687.94 | 5538 – 5539 | 28S nrDNA | 471 | No significant similarity |
| Mycosphaerella markii CBS 110942 | 1559 – 1560 | 18S nrDNA | 341 | 332/355 of DQ848296 Mycosphaerella musae 18S nrDNA |
| Mycosphaerella markii CPC 11222 | 1559 – 1560 | 18S nrDNA | 341 | 332/355 of DQ848296 Mycosphaerella musae 18S nrDNA |
| Passalora-like genus CPC 11876 | 5538 – 5539 | 28S nrDNA | 580 | No significant similarity |
| Passalora bellynckii CBS 150.49 | 1559 – 1560 | 18S nrDNA | 409 | 147/191 of DQ848296 Mycosphaerella musae 18S nrDNA |
| Passalora dodonaea CPC 1223 | 5424 – 5425 | 28S nrDNA | 738 | No significant similarity |
| Phaeocercospora punctata CBS 113315 | 5424 – 5425 | 28S nrDNA | 723 | No significant similarity |
| Phaeocercospora punctata CPC 10532 | 5424 – 5425 | 28S nrDNA | 731 | No significant similarity |
| Ramularia coleosporii CPC 11516 | 1559 – 1560 | 18S nrDNA | 445 | No significant similarity |
| Ramularia grevilleana CPC 656 | 5538 – 5539 | 28S nrDNA | 546 | No significant similarity |
| Septoria apiicola CBS 400.54 | 5424 – 5425 | 28S nrDNA | 763 | No significant similarity |
| Septoria obesa CBS 354.58 | 1820 – 1821 | 18S nrDNA | 575 | No significant similarity |
| Septoria pyricola CBS 222.31 | 5424 – 5425 | 28S nrDNA | 723 | No significant similarity |
| Septoria quercicola CBS 663.94 | 1559 – 1560 | 18S nrDNA | 334 | 241/308 of DQ848303 Mycosphaerella latebrosa 18S nrDNA |
| Septoria rosae CBS 355.58 | 1820 – 1821 | 18S nrDNA | 442 | 379/452 of DQ848335 Mycosphaerella latebrosa 18S nrDNA |
| Sonderhenia eucalypticola CPC 11252 | 4875 – 4876 | 28S nrDNA | 345 | No significant similarity |
| Stigmina platani CBS 110755 | 5424 – 5425 | 28S nrDNA | 367 | 122/155 of DQ618980 Lipomyces spencermartinsiae 28S nrDNA |
| Stigmina synanamorph CPC 11721 | 5424 – 5425 | 28S nrDNA | 526 | No significant similarity |
| Teratosphaeria aff. rubiola CBS 114419 | 5538 – 5539 | 28S nrDNA | 580 | No significant similarity; high identity to Teratosphaeria rubiola |
| Isolate                          | Insertion between | 18S or 28S nrDNA | Intron size (bp) | Blast result                                                                 |
|---------------------------------|-------------------|------------------|------------------|------------------------------------------------------------------------------|
| Teratosphaeria aff. nubilosa CBS 116283 | 4871 – 4872      | 28S nrDNA       | 141              | No significant similarity; high identity to Teratosphaeria nubilosa          |
|                                 | 5538 – 5539      | 28S nrDNA       | 580              | No significant similarity; high identity to Teratosphaeria nubilosa          |
| Teratosphaeria juvenalis CBS 110906 | 1559 – 1560      | 18S nrDNA       | 403              | 52/61 of DQ471010 Rutstroemia firma 18S nrDNA                                |
|                                 | 4875 – 4876      | 28S nrDNA       | 345              | 224/290 of EF115309 Cordyceps bassiana 28S nrDNA                            |
|                                 | 5424 – 5425      | 28S nrDNA       | 478              | 47/50 of EF115313 Cordyceps bassiana 28S nrDNA                              |
|                                 | 5538 – 5539      | 28S nrDNA       | 402              | No significant similarity                                                   |
| Teratosphaeria juvenalis CBS 111149 | 1559 – 1560      | 18S nrDNA       | 403              | 52/61 of DQ471010 Rutstroemia firma 18S nrDNA                                |
|                                 | 4875 – 4876      | 28S nrDNA       | 345              | 224/290 of EF115309 Cordyceps bassiana 28S nrDNA                            |
|                                 | 5424 – 5425      | 28S nrDNA       | 478              | 47/50 of EF115313 Cordyceps bassiana 28S nrDNA                              |
|                                 | 5538 – 5539      | 28S nrDNA       | 402              | No significant similarity                                                   |
| Teratosphaeria mexicana CBS 110502 | 954 – 955        | 18S nrDNA       | 316              | 129/158 of DQ518890 Lipomyces spencermartinsiae 26S nrDNA                   |
|                                 | 1559 – 1560      | 18S nrDNA       | 360              | No significant similarity                                                   |
|                                 | 1820 – 1821      | 18S nrDNA       | 388              | 126/168 of AF281670 Cryptendoxyla hypophloia 18S nrDNA                       |
|                                 | 3560 – 3561      | 28S nrDNA       | 383              | 124/151 of EF647754 Thecaphora thlaspeos 28S nrDNA                          |
|                                 | 4875 – 4876      | 28S nrDNA       | 327              | 99/114 of L81104 Gaeumannomyces graminis var. tritic 28S nrDNA               |
|                                 | 5018 – 5019      | 28S nrDNA       | 315              | No significant similarity                                                   |
|                                 | 5424 – 5425      | 28S nrDNA       | 553              | No significant similarity                                                   |
| Teratosphaeria mexicana CBS 120744 | 954 – 955        | 18S nrDNA       | 318              | 130/158 of DQ518890 Lipomyces spencermartinsiae 26S nrDNA                   |
|                                 | 1559 – 1560      | 18S nrDNA       | 360              | No significant similarity                                                   |
|                                 | 1820 – 1821      | 18S nrDNA       | 388              | 126/168 of AF281670 Cryptendoxyla hypophloia 18S nrDNA                       |
|                                 | 3560 – 3561      | 28S nrDNA       | 383              | 124/151 of EF647754 Thecaphora thlaspeos 28S nrDNA                          |
|                                 | 4875 – 4876      | 28S nrDNA       | 327              | 99/114 of L81104 Gaeumannomyces graminis var. tritic 28S nrDNA               |
|                                 | 5018 – 5019      | 28S nrDNA       | 309              | No significant similarity                                                   |
|                                 | 5424 – 5425      | 28S nrDNA       | 659              | No significant similarity                                                   |
| Teratosphaeria nubilosa CBS 115669 | 4871 – 4872      | 28S nrDNA       | 141              | No significant similarity; high identity to Teratosphaeria aff. nubilosa     |
|                                 | 5538 – 5539      | 28S nrDNA       | 580              | No significant similarity; high identity to Teratosphaeria aff. nubilosa     |
| Teratosphaeria nubilosa CBS 116005 | 4871 – 4872      | 28S nrDNA       | 141              | No significant similarity; high identity to Teratosphaeria aff. nubilosa     |
|                                 | 5538 – 5539      | 28S nrDNA       | 580              | No significant similarity; high identity to Teratosphaeria aff. nubilosa     |
| Teratosphaeria ohnowa CBS 112896  | 954 – 955        | 18S nrDNA       | 325              | 28/28 of DQ848329 Botryosphaeria quercuum 18S nrDNA                          |
|                                 | 3560 – 3561      | 28S nrDNA       | 294              | 168/227 of FJ358267 Chaetothyriales sp. 28S nrDNA                            |
|                                 | 5424 – 5425      | 28S nrDNA       | 607              | 47/48 of EF115313 Cordyceps bassiana 28S nrDNA                              |
| Teratosphaeria ohnowa CBS 112973 | 954 – 955        | 18S nrDNA       | 324              | 28/28 of DQ848329 Botryosphaeria quercuum 18S nrDNA                          |
|                                 | 3560 – 3561      | 28S nrDNA       | 294              | 168/227 of FJ358267 Chaetothyriales sp. 28S nrDNA                            |
|                                 | 5424 – 5425      | 28S nrDNA       | 607              | 47/48 of EF115313 Cordyceps bassiana 28S nrDNA                              |
| Teratosphaeria pseudosuberosa CBS 118911 | 3560 – 3561      | 28S nrDNA       | 324              | 28/28 of DQ848329 Botryosphaeria quercuum 18S nrDNA                          |
|                                 | 4875 – 4876      | 28S nrDNA       | 364              | No significant similarity                                                   |
| Teratosphaeria sp. CBS 208.94    | 954 – 955        | 18S nrDNA       | 342              | No significant similarity                                                   |
|                                 | 3560 – 3561      | 28S nrDNA       | 309              | 59/70 of AF281670 Cryptendoxyla hypophloia 18S nrDNA                          |
|                                 | 4875 – 4876      | 28S nrDNA       | 296              | 44/51 of EF551317 Tremella globispora 28S nrDNA                              |
| Teratosphaeria suberosa CPC 11032 | 5424 – 5425      | 28S nrDNA       | 313              | 159/197 of AB033529 Penicillium odatum 18S nrDNA                             |
|                                 | 5538 – 5539      | 28S nrDNA       | 596              | 80/99 of AB044639 Cordyceps kanzashiana 28S nrDNA                            |
| Thedgonia-like genus CPC 12304    | 1820 – 1821      | 18S nrDNA       | 444              | 262/331 of EU167577 Mycosphaerella milleri 18S nrDNA                         |
Fig. 1. RAxML tree using only the partial LSU alignment with bootstrap values after 1 000 pseudorepetitions on the nodes. Type strains and novel species described in this study are indicated in bold.
Fig. 1. (Continued).
Fig. 2. RAxML tree using the SSU, 5.8S nrDNA and LSU alignment with bootstrap values after 500 pseudorepetitions on the nodes.
Fig. 2. (Continued).
Mycosphaerella handelii CBS 113302
Septoria quercicola CBS 663.94
Septoria lactucae CBS 352.58
Passalora eucalypti CBS 111318
Pseudocercospora angolensis CBS 149.53
Pseudocercospora angolensis CBS 112933
Pseudocercospora sphaerulinae CBS 112621
Pseudocercospora platani CBS 110755
Sgmina synanamorph CPC 11772
Pseudocercospora acmicola CPC 10283
Pseudocercospora punctata CBS 113315
Mycosphaerella pyri CBS 222.31
Pseudocercospora griseola f. griseola CBS 194.47
Pseudocercospora griseola f. griseola CBS 880.72
Mycosphaerella bixae CBS 111804
Pseudocercospora luzardii CPC 2556
Pseudocercospora humuli CPC 11358
Pseudocercospora protearum var. leucadendri CPC 1869
Pseudocercospora pseudoeucalyptorum CBS 114242
Pseudocercospora kaki CPC 10636
Pseudocercospora cruenta CBS 462.75
Pseudocercospora vitis CPC 11595
Pseudocercospora paraguanyensis CBS 111317
Pseudocercospora fijiensis X300
Pseudocercospora atromarginalis CPC 11372
Pseudocercospora pallida CPC 10776
Pseudocercospora fuligena CPC 12296
Pseudocercospora cordiana CBS 114685
Pseudocercospora cruenta CPC 10846
Pseudocercospora macrospora CBS 114696
Pseudocercospora chenguenensis CPC 10785
Passalora graminis CBS 113303
Sonderhenia eucalypticola CPC 11252
Mycosphaerella irregulariramosa CBS 111211
Mycosphaerella heimioides CBS 111190
Mycosphaerella heimi CBS 110682
Mycosphaerella holualoana CBS 110699
Mycosphaerella acaciaigena CBS 112515
Mycosphaerella acaciaigena CBS 112516
Cercospora virgaureae CBS 113304
Ramulispora sorghi CBS 110579
Ramulispora sorghi CBS 110578
Pseudocercosporella capsellae CPC 10301
Pseudocercospora sp. CPC 11592
Mycosphaerella latebrosa CBS 687.94
Mycosphaerella latebrosa CBS 652.85
Pseudocercosporella sp. CPC 11414
Miuraea persicae CPC 10069
Cercospora zebrinae CBS 102325
Septoria leucanthemi CBS 109090
Septoria apiicola CBS 400.54
Septoria obesa CBS 354.58
Septoria convolvuli CBS 102325
Septoria senecionis CBS 102366
Septoria dysentericae CPC 12328

Bootstrap support values:
- = 95 % and higher
- = 90 % to 94 %
- = 80 % to 89 %
- = 70 % to 79 %

0.1

Fig. 2. (Continued).
RESULTS

DNA amplification and phylogeny

Amplification products of approximately 1 700 bases were obtained for the standard amplification of the isolates listed in Table 1. The LSU region of these sequences was used to obtain additional sequences from GenBank that were added to the partial LSU alignment. We expected a total size of approximately 5 500 bp for the concatenated SSU, ITS1, 5.8S nrDNA, ITS2 and LSU at the start of the study; however, our alignment totalled about 12 000 bp due to numerous insertions (most likely group 1 introns) encountered for several strains (Table 3). These insertions frequently resulted in products too large to amplify or sequence effectively and sometimes required us to design additional novel primers in extra overlapping steps to complete these gaps (see Materials and Methods for details). Searching the GenBank database using these insertions had varied success (Table 3). Sequences of the 18S nrDNA are more abundant in the database whereas sequences of the second half to two-thirds of the 28S nrDNA are mostly absent. This also evident in Table 3, where insertions in the SSU more frequently found with similarity sequences in the database and insertions in the LSU (e.g. those between positions 5018–5019 and 5424–5425) frequently did not retrieve any significant similarity. Although there were some exceptions (e.g. the insertion between 1820 and 1821 in the SSU of Batcheloromyces leucadendri), most of the insertions in the SSU obtained hits with SSU sequences of species of Capnodiales in the database. In one case, between 954 and 955 for the SSU sequence of Teratosphaeria mexicana (both strains), a partial hit was obtained with an LSU sequence of Lipomyces spencermartinsiae (GenBank DQ518980). Many of the insertions in the LSU sequences did not retrieve significant hits in the database and those that did were with unrelated taxa. It is quite possible that this is an artifact of the poor representation of full-length LSU sequences in the database, especially for members of the Capnodiales. In some cases, an LSU insertion retrieved a hit with SSU sequences in the database, e.g. the insertion between 5538 and 5539 in Batcheloromyces proteae and between 3560 and 3561 and 4875 and 4876 in Teratosphaeria mexicana strain CBS 120744. In two cases (Mycosphaerella latebroa and Phaeophleospora eugeniicola), an insertion was either lost or gained between two strains of the same species. The primers designed in this study allowed us to effectively amplify and sequence the SSU and LSU for the selected isolates. Although these primers were not tested on taxa outside of the Capnodiales (except for one of the outgroups, Neofusicoccum australe), we attempted to design them as robust as possible using degeneracy if needed. We therefore expect that these primers will have wider applicability than just the Capnodiales in cases where other published primers fail to amplify or amplify poorly.

The RAxML search of the partial LSU alignment yielded a most likely tree (Fig. 1) with a log likelihood -13397.994021. The matrix had 395 distinct alignment patterns, with 6 % completely undetermined characters in the alignment. The manually adjusted alignment contained 295 sequences (including the outgroup sequence, Dothidea insculpta GenBank DQ247802) and 763 characters including alignment gaps. The RAxML search of the almost complete SSU, 5.8S nrDNA and LSU alignment yielded a most likely tree (Fig. 2) with a log likelihood -39022.88140. The matrix had 1211 alignment patterns with 0.01 % of the characters consisting of gaps or undetermined characters. The manually adjusted alignment contained 205 sequences (including the outgroup sequences, Neofusicoccum australe CPC 10899 and Magnaporth grisea GenBank AB026819) and 5110 characters including alignment gaps. The obtained phylogenies (Figs 1–2) are discussed in the Taxonomy section below.

Taxonomy

Several well-supported clades could be distinguished in the present study (Figs 1–2), correlating to families in the Capnodiales. These families, and several new genera and species, are treated below.

Treatment of phylogenetic clades

Capnodiales Woron. Ann. Mycol. 23: 177. 1925.

Data obtained from multi-gene phylogenies prompted Schoch et al. (2006) to merge Mycosphaerellales with Capnodiales. Although the present study included numerous additional isolates, the orders remain problematic. Although there is support for the Mycosphaerellales as an order, additional families such as the Schizothyriaceae and Diacoconaceae (see below) would have to also be elevated to order level, which would result in orders containing a single family, while Teratosphaeriaceae appears to comprise unresolved lineages. For this reason it was decided to retain these families within Capnodiales, but noting that as more families are added and better circumscribed, it is quite possible that the Mycosphaerellales would again be resurrected.

Mycosphaerellales Lindau, in: Engler & Prantl, Nat. Pflanzenfamilien 1(1): 421. 1897.

Type species: Mycosphaerella punctiformis (Pers.: Fr.) Starbäck, Bh. Kongl. Svenska Vetensk.-Akad. Handl. 15(3, 2): 9. 1889.

Notes: The Mycosphaerellales contains numerous genera, 20 of which are listed by Crous (2009), with many names under consideration (Crous et al. 2009b, c). From these data it is clear that genera such as Passalora, Pseudocercospora, Pseudocercosporella, Septoria, Zasmidium and Ramichloridium are paraphyletic (Hunter et al. in prep.). Well-resolved genera include Cercospora, Cercospora, Ramularia, Ramulispora, Sonderzenia and Polythrinicum. One particularly problematic clade contains Periconiella, Ramichloridium, Verrucosporidium and Zasmidium, along with “Mycosphaerella” and Rasutoria teleomorphs. Barr (1987) erected Rasutoria for species with brown ascospores occurring on Gymnospermae. Rasutoria cl RJkh clusters in a clade adjacent to “Mycosphaerella” species with hyaline ascospores, such as M. aleuritidis and Mycosphaerella daviesicola (Verrucosporidium daviesicola) (Beilharz & Pascoe 2002).

The genus Phaeophleospora (1916) clusters with Lecanosticta acicola. The genus Lecanosticta (1922) has typical Phaeophleospora-like conidia, except that its conidiomata are acervular, and not pycnidial. If the type of Lecanosticta, L. pini also clusters in this clade, the generic concept Phaeophleospora may have to be widened to include Lecanosticta, as was done with Kirramyces to include Colletogloeopsis (Cortinas et al. 2006a, b).

Considerable controversy has surrounded the coelomycetes that Crous et al. (1997) placed in Phaeophleospora. Based on DNA phylogenetic data, it has now been shown that Kirramyces anamorphs (Walker et al. 1992), including those accommodated in Colletogloeopsis (Crous & Wingfield 1996, Crous et al. 2004c, 2006c, Cortinas et al. 2006a, b), are linked to Teratosphaeria (Andijc et al. 2007, Crous et al. 2009b, c). Crous et al. (2007a)
showed *Phaeohelospora* to reside in the *Mycosphaerellaceae* and *Kirrmyces* in the *Teratosphoraceae*, respectively. However, most taxa investigated to date were collected from *Eucaulpytus*. As shown in the present study, *Phaeohelospora atkinsonii*, a pathogen of *Hebes* spp. (Wu et al. 1996, Pennycook & McKenzie 2002), clusters distant from *Phaeohelospora s. str.*, while the same is true for *Phaeohelospora concentrica*, which is a pathogen of *Protea* spp. (Taylor et al. 2001a), and *Phaeohelospora stonei*, a pathogen of *Eucaulpytus* (Crous et al. 2007c, 2009c). These taxa thus clearly represent yet another two genera in the *Phaeohelospora* complex. An older name that would potentially be available is *Scoleciasis*. However, when B. Sutton examined exsiccati of the type species, *S. aquatica*, only ascomata of a *Leptosphaeria* species were found (Crous et al. 1997). The association of *S. aquatica* with the *Leptosphaeria* was also noted in the original description, and this may indicate that *Scoleciasis* is allied to taxa in the *Phaeosphaeriopsist/Phaeoseptoria* complex (Arzaniou & Crous 2006). Both *P. atkinsonii* and *P. concentrica* have a typical *Kirrmyces* morphology, namely brown, percurrently proliferating conidiogenous cells, and brown, obclavate, verruculose, transversely euseptate conidia. Further species thus need to be included in analyses before these generic concepts can be clarified.

During the course of this study several fresh collections of *Leptosphaeria protearum* were obtained. *Leptosphaeria protearum* is a major leaf spot and blight pathogen of *Protea* spp. (Knox-Davies et al. 1987), and causes severe losses in plantations of South African *Protea* spp. in Hawaii, and has been recorded in many countries where South African *Proteas* are cultivated (Taylor & Crous 1998, Taylor et al. 2001b, Crous et al. 2004a). Cultures of this pathogen were found to cluster in the *Mycosphaerellaceae*, where they represent an undescribed genus, characterised by having bitunicate ascii without pseudoparaphyses, brown, 3-septate ascospores, and a *Coniothyrium*-like anamorph. Its close phylogenetic relationship to *Phaeohelospora concentrica* (Fig. 1) suggests that they could be congeneric, and that in future more *Phaeohelospora*-like anamorphs may be found to cluster in this clade. We propose a new genus to accommodate *Leptosphaeria protearum* below.

**Brunneosphaerella** Crous, gen. nov. MycoBank MB514694.

*Etymology:* *Brunneus* + *Sphaerella* = is after its brown ascospores and *Sphaerella*-like morphology.

*Mycosphaerellaceae* similis, sed ascosporis brunneis, 3-septatis.

*Ascomata* amphiogenous, immersed to semi-immersed, black, single, gregarious, substomatal, pyriform or globose with a papillate, periphysate ostiole. *Peridium* consisting of three strata of slightly compressed *textura angularis*, an outer stratum of dark brown, thick-walled cells, becoming paler in the central stratum, and hyaline, thin-walled in the inner stratum. *Asci* clavate to cylinodo-clavate, often curved, tapering to a pedicel, narrowing slightly to a rounded apex with an indistinct ocular chamber, 8-spored, bitunicate with fissitunicate dehiscence. *Pseudoparaphyses* absent. *Ascospores* biseriate, fusiform, broader at the apical end, initially hyaline and 1-septate, becoming yellow-brown and 3-septate at maturity, slightly constricted at median to supra-median septum.

*Type species:* *Brunneosphaerella protearum* (Syd. & P. Syd.) Crous, comb. nov.

**Brunneosphaerella jonkershoekensis** (Marinc., M.J. Wingf. & Crous) Crous, comb. nov. MycoBank MB514695. Fig. 3.

*Basionym:* *Leptosphaeria jonkershoekensis* Marinc., M.J. Wingf. & Crous, In: Marincowitz et al., *Microfungi occurring on Proteaceae in the fynbos*: 62. 2008.

*Ascomata* pseudothecial, subpedimeral, immersed, obpyriform, papillate, 180–205 × 160–235 µm. *Peridium* 20–30 µm thick, composed of relatively large cells, 11–15 × 2.5–5.5 µm; cells arranged in three strata; outer stratum consisting of 3–5 layers of dark brown, very thick-walled cells; middle stratum transient, consisting of a few layers of pale brown, thick-walled, compressed cells; inner stratum consisting of 1–2 layers of thin-walled, very compressed cells. *Pseudoparaphyses* absent. *Asci* bitunicate, inflated cylindrical to clavate, 81–95 × 13–15 µm, ocular chamber dome-shaped, indistinct. *Ascospores* pale brown, fusoid to ellipsoidal, tapering towards the base, (25–)29–34–(36) × (5–)8–7–(9) µm (av. 31.4 × 6.7 µm), apical cell the shortest, upper hemisphere slightly larger than lower, at times slightly curved, 3-septate, smooth, guttulate (adapted from Marincowitz et al. 2008).

**Host range and geographic distribution: Protea repens** (South Africa, Western Cape) (Marincowitz et al. 2008).

Specimen examined: *South Africa*, Western Cape Province, Jonkershoek Nature Reserve, leaf litter of *Protea repens*, 6 Jun. 2000, S. Marincowitz, PREM 59447 holotype.

*Notes:* Although no culture is presently available for this species, it clearly represents a species of *Brunneosphaerella*, characterised by its bitunicate ascii, and brown, 3-septate ascospores, as well as the absence of pseudoparaphyses. *Brunneosphaerella jonkershoekensis* can easily be distinguished from *B. protearum* based on its much larger ascospores (Crous et al. 2004a).

**Brunneosphaerella protearum** (Syd. & P. Syd.) Crous, comb. nov. MycoBank MB514696. Fig. 4.

*Basionym:* *Leptosphaeria protearum* Syd. & P. Syd., *Ann. Mycol.* 10: 441. 1912.

*Anamorph:* *Coniothyrium* *protearum* Joanne E. Taylor & Crous, IMI Descriptions of Fungi and Bacteria No. 1343. 1998.

*Leaf spots* circular to irregular, discrete to confluent, variable in size, under conditions favourable to disease symptoms more similar to a blight than a leaf spot, necrotic, sunken with a raised dark brown margin and with conspicuous black ascomata in the dead tissue, 4–30 mm diam. *Ascomata* pseudothecial, substomatal, amphiogenous, immersed to semi-immersed, not erumpent, black, single, gregarious, 180–320 µm diam; in section, substomatal, subpedimeral, pyriform or globose with a papillate, periphysate ostiole, immersed in a stroma consisting of deteriorated host mesophyll cells filled with fungal hyphae, (210–)230–264–(288) µm high, (180–)200–255–(300) µm diam. *Peridium* consisting of three strata of slightly compressed *textura angularis*, an outer stratum of dark brown, thick-walled cells, becoming paler in the central stratum, and hyaline, thin-walled in the inner stratum, altogether (20–)24.5–37.5(–50) µm thick. *Asci* clavate to cylinodo-clavate, often curved, tapering to a pedicel, narrowing slightly to a rounded apex with an indistinct ocular chamber, 8-spored, bitunicate with fissitunicate dehiscence, (70–)80–87.5(–105) × (13.5–)14.5–16(–21.5) µm. *Pseudoparaphyses* absent. *Ascospores* biseriate, fusiform, broader
at the apical end, initially hyaline and 1-septate, becoming yellow-brown and 3-septate at maturity, slightly constricted at median to supra-median septum, (21.5–)27.5–29.5(–37.5) × (6.3–)7.5–8(–10) µm in water mounts, (21–)25.5–27.5(–31) × (5.5–)6–7(–8) µm in lactophenol. Conidiomata barely visible and interspersed between ascomata, pycnidial, subepidermal, substomatal, separate, globose to pyriform, occasionally with well-developed papilla, dark brown, < 200 µm diam. Conidiophores reduced to conidiogenous cells. Conidiogenous cells discrete, smooth, hyaline, doliiform to ampulliform, holoblastic, proliferating 1–2 times percurrently, 4–6 × 3–4 µm. Conidia pale brown to medium brown, thick-walled on maturity, smooth to finely verruculose, eguttulate, ellipsoidal to globose, often truncate at one end, 5–10 × 3–7 µm (adapted from Crous et al. 2004a).

Host range and geographic distribution: Protea cynaroides, P. ‘Susara’ (Portugal, Madeira) (Moura & Rodrigues 2001); P. caffra, P. compacta, P. cynaroides, P. gaguedi, P. grandiceps, P. lacticolor, P. laurifolia, P. lepidocarpo dendron, P. lonifolia, P. magnifica, P. nitida, P. punctata, P. repens, P. ‘Sheila’, Protea spp. (South Africa); P. cynaroides, P. laurifolia, P. nerifolia, P. ‘Ivory Musk’, P. ‘Mink’, P. ‘Pink Ice’, P. ‘Rose Mink’, P. susannae, Protea sp. (U.S.A., Hawaii) (Taylor et al. 2001b); P. cynaroides, P. gaguedi, P. nerifolia, Protea sp. (Zimbabwe, Inyanga) (Masuka et al. 1998).

Specimens examined: South Africa. Western Cape Province, Bettys’ Bay, leaf litter of Protea magnifica, 11 Jul. 2000, S. Marincowitz, PREM 59448; Helderberg Nature Reserve, leaf litter of Protea laurifolia, 14 Aug. 2000, S. Marincowitz, PREM 59482; Helderberg Nature Reserve, leaf litter of Protea obdusiolfa, 14 Aug. 2000, S. Marincowitz, PREM 59495; Jonkershoek Nature Reserve, leaf litter of Protea nitida, 6 Jun. 2000, S. Marincowitz, PREM 59442; Jonkershoek Nature Reserve, leaf litter of Protea repens, 6 Jun. 2000, S. Marincowitz, PREM 59450; Jonkershoek Nature Reserve, S33°59’11.2” E18°57’14.7” leaves of Protea sp., 1 Apr. 2007, P.W. Crous, CBS H-20330, cultures CPC 13914–13916; Jonkershoek Nature Reserve, S33°59’26.1” E18°57’59.5” leaves of Protea repens, 1 Apr. 2007, P.W. Crous, CBS H-20331, cultures CPC 13911–13913; Jonkershoek Nature Reserve, leaves of Protea sp., 1 Apr. 2007, P.W. Crous, CBS H-20332, cultures CPC 13908–13910; Jonkershoek Nature Reserve, “Tweede Waterval”, leaves of Protea sp., 1 Apr. 2007, P.W. Crous, CBS H-20333, cultures CPC 13902–13907; Jonkershoek Nature Reserve, leaves of Protea nitida, 12 Apr. 2008, L. Mostert, CBS H-20334, cultures CPC 15231–15233; Kirstenbosch Botanical Garden, leaves of Protea sp., 13 Jan. 2009, P.W. Crous, CBS H-20335, culture CPC 16338.

Notes: Although Taylor & Crous (1998) reported a Coniothyrium-like anamorph to develop in culture, none of the cultures examined in the present study on MEA, PDA or OA could be induced to sporulate, though spermatogonia and ascomatal initials were commonly observed. The fact that cultures of Leptosphaeria protearum, which represents a well-known and serious pathogen of Proteaceae, clustered in the Mycosphaerellaceae, was totally unexpected. A further surprise was the fact that this species appears to represent a complex of several cryptic taxa. Whether these taxa can be correlated with differences in host range and geographic distribution can only be resolved once more collections have been obtained for study. Although the genus Sphaerulina, which represents Mycosphaerellaceae-like taxa with 3-septate, hyaline ascospores, is part of the Mycosphaerellaceae (Crous et al., unpubl data), the type species, S. myriadea, clusters in the Septoria clade, and is thus unavailable for the species occurring on Proteaceae. Morphologically Brunneosphaeria is also distinct in...
Fig. 4. Brunneosphaerella protearum. A–D. Leaf spots on different Protea spp. E. Close up of leaf spot showing ascomata. F. Substomatal ascomata. G–H. Vertical sections though ascomata, showing wall structure. I–K. Germinating ascospores on MEA. L–M, R. Bitunicate asci. N–Q, S. Juvenile to mature ascospores. Scale bars: G = 75 µm, H = 10 µm.
that ascospores are always brown at maturity, and anamorphs have brown, percurrently proliferating conidiogenous cells, appearing Phaeophleospora-like. The recognition of Brunneosphaerella as a distinct genus in the Mycosphaerellaceae also raises the intriguing possibility that many phytopathogenic species of the Leptosphaeria-complex with brown, 3-septate ascospores, but lacking paraphyses, actually belong to Brunneosphaerella.

**Passalora ageratinae** Crous & A.R. Wood, sp. nov. MycoBank MB514697. Fig. 5.

**Etymology:** Named after the host on which it occurs, Ageratina adenophora.

**Leaf spots** amphigenous, angular to irregular, 2–8 mm diam, medium brown, frequently with pale to grey-brown central part, and raised, dark brown border; pale to medium brown in reverse, with raised, dark brown border. **Mycelium** internal, consisting of smooth, branched, pale brown, 2–3 µm wide hyphae. **Caespituli** fasciculate, amphigenous, medium brown, arising from a brown, erumpent stroma, up to 80 µm wide, 40 µm high. **Conidiophores** subcylindrical, straight to geniculose-sinuous, unbranched, medium brown, finely verruculose, 1–3-septate, 15–40 × 3–4.5 µm. **Conidiogenous cells** terminal, pale to medium brown, finely verruculose with terminal, sympodial conidiogenous loci that are 1–2 µm diam, slightly thickened, darkened and refractive, 10–20 × 3–4 µm. **Conidia** in unbranched chains, pale brown, smooth, finely to prominently guttulate, subcylindrical to narrowly obclavate, apex obtuse, base long obconically subtruncate, (0–)1–3–(5–)septate, (20–)30–60–(80) × (3–)14–(4.5) µm; hila 1–1.5 µm wide, somewhat thickened, darkened and refractive.

**Culture characteristics:** On MEA erumpent, with uneven, folded surface, lobate margin, and moderate aerial mycelium; centre pale mouse-grey with patches of cinnamon, outer margin olivaceous-grey; reverse olivaceous-grey with patches of cinnamon; reaching 15 mm diam; on PDA spreading, with cinnamon to cream patches in centre, becoming umber towards smooth margins, with diffuse red pigment in agar; reverse olivaceous-grey, with patches of red, reaching 15 mm diam; on OA flat, spreading, up to 30 mm diam, iron-grey, with white, solitary mycelia strands, though aerial mycelium generally absent, reaching 30 mm diam.

**Host range and geographic distribution:** Ageratina adenophora, Australia, South Africa.

**Specimen examined:** South Africa, KwaZulu-Natal Province, Hilton, on leaves of Ageratina adenophora, 28 May 2008, A.R. Wood, CBS H-20336 holotype, cultures ex-type CPC 15365 = CBS 125419, CPC 15366, 15367.

**Notes:** Ageratina adenophora (crofton weed; Asteraceae), which is indigenous to Mexico, has invaded many countries as a rapidly growing weed, forming dense thickets (Morris 1989, Parsons & Cuthbertson 1992, Wagner et al. 1999, Zhu et al. 2007, Muniappan et al. 2009). It is considered a serious weed in agriculture and forestry (Bess & Haramoto 1958, Sharma & Chhetri 1977, Kluge 1991), often replacing more-desired vegetation or native species.

A leaf spot pathogen, originally misidentified as Cercospora eupatori (this species is currently known as Pseudocercospora eupatori), was found to infect plants in Australia where a stem galling fly (Procecidochares utilis; Tephritidae) was introduced from Hawaii as a biological control agent (Dodd 1961). Presumably the fungus was introduced together with the flies originally from Mexico to Hawaii and then to Australia. Subsequently this same fungus was obtained from Australia and released in South Africa after host specificity testing indicated it was restricted to A. adenophora.
(Morris 1989). The fungus causes partial defoliation of mature plants (Dodd 1961, Auld 1969), though the impact depends on environmental conditions (Dodd 1961). Seedlings are however killed rapidly (Wang et al. 1997).

This fungus, which has hitherto been known simply as "Phaeoramularia" sp., still lacks a name and proper description. The genus Phaeoramularia is treated as a synonym of Passalora (Crous & Braun 2003), and hence the species is named in the latter genus as P. ageratinae. Interestingly, this species appears to be closely related to Passalora fulva, which is a serious pathogen of tomato (Solanaceae) (Thomma et al. 2005).

Passalora armatae Crous & A.R. Wood, sp. nov. MycoBank MB514698. Fig. 6.

*Etymology:* Named after the host on which it occurs, Dalbergia armata.

Passalorae dalbergicolae similis, sed conidiophoris in synnematibus densis, conidiis ad basim obconice truncatis, apice rostrato.

*Leaf spots* amphigenous, on upper surface visible as red-brown, irregular to subcircular spots with indistinct margins, 0.5–2 mm diam; in reverse indistinct, chlorotic to medium or red-brown. Mycelium internal, consisting of smooth, branched, pale brown, 2–3 µm wide hyphae. Caespituli hypophyllous, fasciculate to synnematous, up to 200 µm high and 250 µm wide, situated on a prominently erumpent, pale brown stroma, up to 100 µm high and wide. Conidiophores subcylindrical, unbranched, flexuous, guttulate, pale to medium brown, smooth. 120–180 × 4–6 µm, 2–6-septate. Conidiogenous cells terminal, subcylindrical, guttulate, pale to medium brown, finely verruculose, becoming somewhat swollen, appearing slightly clavate, 25–70 × 6–8 µm; conidiogenous loci 4–20 per conidiogenous cell, sympodial, round, darkened, thickened, refractive, prominent, 2–3 µm wide, up to 1 µm high. Conidia (27–)30–40(–45) × 9–10(–12) µm, pale to medium brown, smooth to finely verruculose, granular to guttulate, thin-walled, ellipsoidal to obovoid, transversely 2–4-euseptate, widest in middle of basal cell, or middle of conidium, tapering to an obconically truncate base; hilum thickened, darkened and refractive; apical cell conical, elongating to an apical beak up to 20 µm long. When cultivated conidia remain attached to conidiogenous cells, giving conidiophores the appearance of small tufts which is very characteristic, and not commonly observed in Passalora.

*Culture characteristics:* On MEA slow growing, erumpent, with dense white aerial mycelium, which becomes mouse-grey, reaching 5 mm diam after 1 wk; on PDA mouse-grey (surface), iron-grey (reverse), with diffuse red pigment in agar; on OA similar to PDA, also with diffuse red pigment in agar.

*Host range and geographic distribution:* Dalbergia armata, South Africa.

Specimen examined: South Africa, KwaZulu-Natal Province, South Coast, Mpenjati Nature Reserve, between Ramsgate and Port Edward, on leaves of Dalbergia armata, 28 May 2008, A.R. Wood, CBS H-20337 holotype, cultures ex-type CPC 15419 = CBS 125420, CPC 15420, 15421.

*Notes:* Passalora dalbergiae, which occurs on Dalbergia sissoo (Fabaceae) in India, is distinct from P. armatae in having superficial mycelium and solitary conidiophores (Hernández-Gutiérrez &
Dianese (2009). The previously described *Passalora dalbergiicola* is similar to *P. armatae* in conidial dimensions (3–septate, 25–45 × 7–10 μm; Ellis 1976), but distinct in that conidiophores are not in dense synnemata, conidiogenous cells can have a single apical loci, and conidia have a less prominent basal taper, and lack the apical beaks typical of *P. armatae* (*in vivo* and *in vitro*).

**Schizothyriaceae** Höhn. ex Trotter, Sacc., D. Sacc. & Traverso, In: Saccardo, Syll. Fung. 24(2): 1254. 1928.

*Type species:* *Schizothyrium acerinum* Desm., Ann. Sci. Nat. Bot. 11: 360. 1849.

*Notes:* Members of the *Schizothyriaceae* are associated with flyspeck symptoms on apples and pear fruit. The fungi grow superficially on the epicuticular wax, thereby reducing the marketability of the fruit, but do not penetrate the cuticle (Belding et al. 2000). Batzer et al. (2005, 2007) reported a range of diverse fungi to be associated with flyspeck symptoms on apples, the most prominent being species of *Schizothyrium*.

**Dissoconiaeae** Crous & de Hoog, fam. nov. MycoBank MB514699.

Ascomata pseudothecioides, immers, globosa, uniloculares. Sine pseudoparaphysesibus. Asci fasciculati, octospori, bitunicati. Ascospores ellipsoidae-fusiformes, 1-septatae, hyalinae. Conidiophora separata, ex hyphis ortunda, subcylindrica, subulata, lageniforma vel cylindrica, apicem venus attenuata, apice obtuse rotundato vel truncate, recta vel semel geniculata, laeavia, modice brunea, 0–plerisepata, locis terminalibus vel lateralis, rhachidum cum cicatrīces leniter incrassates, fuscati. Conidia solitaria, pallide olivacea-brunnea, laevia, ellipsoidea, 0–plerisepata, locis terminalibus vel lateralis, rhachidi cum cicatricibus leniter subcylindrica, subulata, lageniformia vel cylindrica, apicem versus attenuata, apice pseudoparaphysibus. Asci fasciculati, 8-spored, bitunicati. Ascosporae ellipsoidea-brunnea, laeavia, ellipsoidea, obclavata vel globosa, 0–plerisepata, hils aliquantum fuscati. Conidia secundaria nulla vel formata ad conidia prima, pallide olivacea vel subhyalina, aseptata, pyriformia; conidiis impigres vel passive emittentibus.

*Ascomata* pseudothecioides, immers, globosa, uniloculares. Sine pseudoparaphysesibus. Asci fasciculati, octospori, bitunicati. Ascospores ellipsoidae-fusiformes, 1-septatae, hyalinae. Conidiophora separata, ex hyphis ortunda, subcylindrica, subulata, lageniforma vel cylindrica, apicem venus attenuata, apice obtuse rotundato vel truncate, recta vel semel geniculata, laeavia, modice brunea, 0–plerisepata, locis terminalibus vel lateralis, rhachidum cum cicatrīces leniter incrassates, fuscati. Conidia solitaria, pallide olivacea-brunnea, laeavia, ellipsoidea, obclavata vel globosa, 0–plerisepata, hils aliquantum fuscati. Conidia secundaria nulla vel formata ad conidia prima, pallide olivacea vel subhyalina, aseptata, pyriformia; conidiis impigres vel passive emittentibus.

*Type* species: *Dissoconium aciculare* de Hoog, Oorschot & Hijwegen, Proc. K. Ned. Akad. Wet., Ser. C, Biol. Med. Sci. 86(2): 198. 1983.

*Notes:* Since the family was established by Crous et al. (2007a) it has been shown to be too widely defined, incorporating many diverse genera (Crous et al. 2009b, c), and even families such as the *Piedraecaeae* (Fig. 1). The node as such is not well supported, suggesting that as more taxa are added, further families remain to be separated from the *Teratosphaeriaceae*. Presently it incorporates diverse elements, and even lichens such as *Cystoecoles ebeneus* and *Anisomeridium consorbinum*. The identity of the latter strain (CBS 101364) needs to be confirmed, as its position in the tree appears doubtful.

The genus *Catenulostrum*, which is associated with numerous diverse substrates and habitats (Crous et al. 2007a), is typified by *C. protearum*, for which an epitype is designated in the present study. Several strains isolated from rock surfaces (Guiedan et al. 2008, Ruibal et al. 2008, 2009, this volume) cluster with *Catenulostrum* (Fig. 1), and appear to represent undescribed species of the latter. Of interest is the fact that the type species of *Aulographina, A. pinorum* (CBS 302.71, 174.90), which has hysterothecia, clusters in a clade with *Catenulostrum microsorum*, which has a *Teratosphaeria*-like teleomorph with pseudothecia (Taylor & Crous 2000, Crous et al. 2004a, 2007a). Isolates of *A. pinorum* were found to produce a *Catenulostrum* anamorph in culture. This raises two possibilities, namely that either the incorrect fungus was originally isolated from pine needles (namely *Catenulostrum abietis*), or that this is a species complex, in which *A. pinorum* resides. If these strains are indeed confirmed to represent *A. pinorum*, then it reveals the genus *Aulographina* to be heterogeneous, as *A. eucalypti*, which is a major leaf spot pathogen of *Eucalyptus* (Crous et al. 1989, Park et al. 2000, Carnegie & Keane 2003), clusters distant from *A. pinorum*. The taxonomy of these taxa is currently being addressed, and will be reported on elsewhere (Cheewangkoon et al., in prep.). During the course of this study some new members of the *Teratosphaeriaceae* were collected, which are described below:

**Dissoconium aciculare** de Hoog, Oorschot & Hijwegen, Proc. K. Ned. Akad. Wet., Ser. C, Biol. Med. Sci. 86(2): 198. 1983.
Catenulostroma protearum (Crous & M.E. Palm) Crous & U. Braun, Stud. Mycol. 58: 17. 2007. Fig. 7.

Basionym: Trimmatostroma protearum Crous & M.E. Palm, Mycol. Res. 103: 1303. 1999.

Culture characteristics: On MEA spreading, erumpent, with folded surface, and unevenly lobed, smooth margins; aerial mycelium sparse; surface iron-grey to greenish black, reverse greenish black; reaching 15 mm diam after 2 wk; similar on PDA and OA.

Host range and geographic distribution: Protea, Leucadendron and Hakea spp., South Africa.

Specimens examined: South Africa, on leaves of Protea grandiceps, L. Schroeder, 15 Sept. 1986, holotype BPI 1107849; South Africa, Western Cape Province, Stellenbosch, Assegaibos, on leaves of Leucadendron trinatum, F. Roets, 16 Apr. 2008, epitype designated here CBS H-20338, culture ex-epitype, CPC 15369, 15370 = CBS 125421; ditto, on leaves of Hakea sericea, CBS H-20339, single ascospore culture CPC 15368.

Notes: Catenulostroma protearum was originally described from dead leaves of Protea grandiceps collected in South Africa (Crous & Palm 1999). Unfortunately the cultures died before they could be deposited, and hence the phylogenetic position of Catenulostroma remained uncertain. This proved to be problematic, as the genus was later shown to be heterogeneous (Crous et al. 2007a). The designation of the epitype in the present study clarifies the phylogenetic position of the genus, and reveals Catenulostroma s. str. to represent species that occur in extreme environments, on rocks, or on hard, leathery leaves such as Proteaceae and Gymnospermae.

Devriesia hilliana Crous & U. Braun, sp. nov. MycoBank MB514700. Fig. 8.

Etymology: Named in fond memory of Dr C.F. Hill. “Frank” collected numerous fungi over the years, and sent them to the various international colleagues he knew to be working on these groups. The present species was one of a batch of novel taxa that Frank collected and sent to us for treatment shortly before he had a relapse. Frank’s friendship and mycological expertise will be sorely missed.

Devriesiae streitziae similis, sed conidiis minoribus, (5–)7–10(–12) × (2–)2.5(–3) µm.

Colonies sporulating on MEA, Mycelium consisting of branched, septate, pale brown, smooth, 2–3 µm wide hyphae. Conidiophores solitary, erect on creeping hyphae, unbranched, medium brown, smooth, flexuous, thick-walled, 15–50 × 2–3 µm, 3–11-septate. Conidiogenous cells terminal, medium brown, subcylindrical, smooth, 5–20 × 2–3 µm; proliferating sympodially; hila flattened, unthickened, somewhat darkened, 1–1.5 µm wide. Conidia medium brown, smooth, subcylindrical to narrowly fusoid-ellipsoidal or obclavate, apical conidium with obtuse apex, additional conidia with truncate ends, somewhat darkened, 1–1.5 µm wide; conidia straight to irregularly bent, mostly in unbranched chains, (5–)7–10(–12) × (2–)2.5(–3) µm.

Culture characteristics: On MEA erumpent, spreading, with folded surface, and smooth margins with sparse aerial mycelium; surface mouse-grey, with thin, olivaceous-grey margin; reverse iron-grey, reaching 8 mm diam; on PDA similar, up to 8 mm diam, centre mouse-grey, margin and reverse iron-grey; on OA erumpent with moderate mouse-grey aerial mycelium, and iron-grey margin.

Host range and geographic distribution: Macrozamia communis, Auckland, New Zealand.

Specimen examined: New Zealand, Auckland, Auckland University Campus, Princes Street, on Macrozamia communis, C.F. Hill, 20 Apr. 2008, CBS H-20340 holotype, culture ex-type CPC 15382 = CBS 123187.
Devriesia lagerstroemiae Crous & M.J. Wingf., sp. nov. MycoBank MB514701. Fig. 9.

Etymology: Named after the host on which it occurs, Lagerstroemia.

Devriesiae strelitziae similis, sed conidiis latioribus, (5–)7–10(–12) × (2–)2.5(–3) µm.

Colonies sporulating on OA. Mycelium consisting of smooth, branched, septate, 2–3 µm wide hyphae. Conidiophores rarely micronematous, predominantly macronematous, erect on creeping hyphae, brown, cylindrical with swollen basal cell, thick-walled, smooth, flexuous, 20–90 × 3–4 µm, 5–20-septate. Conidiogenous cells terminal, cylindrical to clavate, polyblastic, pale to medium brown, 5–10 × 2–3(–4) µm; scars somewhat thickened and darkened, not refractive. Ramoconidia medium brown, smooth, subcylindrical, 9–15 × 3–5 µm, (0–)1(–2)-septate, but with clavate apex and several flattened loci that are somewhat darkened and thickened, 1 µm diam. Conidia in branched chains of up to 10, pale brown, smooth, narrowly ellipsoid, 0–1-septate, (5–)8–12(–15) × 2–3(–4) µm; apical conidium with rounded apex, the rest with flattened loci that are somewhat darkened and thickened, not refractive, 0.5–1 µm diam.

Culture characteristics: On MEA erumpent, spreading, with sparse aerial mycelium and irregular margin; surface olivaceous-grey, with patches of iron-grey; reverse iron-grey, reaching 10 mm diam; on PDA similar, but on OA iron-grey, reaching 15 mm diam.

Host range and geographic distribution: Lagerstroemia indica, U.S.A., Louisiana.

Specimen examined: U.S.A., Louisiana, Baton Rouge, Cod & Cook Centre, N30°24'50.3" W91°10'6.6", on Lagerstroemia indica, P.W. Crous & M.J. Wingfield, holotype CBS H-20341, culture ex-type CPC 14403 = CBS 125422.

Notes: Devriesia lagerstroemiae clusters close to D. hilliana. As far as we know, neither species is heat-resistant, nor forms chlamydospores, and hence the placement in Devriesia is more due to phylogenetic similarity than their ecology.

Devriesia strelitziicola Arzanlou & Crous, sp. nov. MycoBank MB514702. Fig. 10.

Etymology: Named after its host plant, Strelitzia.

Devriesiae strelitziae similis, sed conidiis majoribus, (7–)25–45(–100) × (2–)2.5(–3) µm.

Colonies sporulating on OA. Mycelium consisting of medium brown, smooth, septate, branched, 2–3 µm wide hyphae; chlamydospores not observed. Conidiophores dimorphic. Microconidiophores reduced to conidiogenous cells on hyphae,
Phylogenetic lineages in the Capnodiales

erect, cylindrical, medium brown, smooth with truncate ends, proliferating sympodially, 4–7 × 2–3 µm. Macroconidiophores erect, cylindrical, straight to geniculate-sinuous, medium brown, smooth, unbranched or branched above, 30–100 × 2.5–3 µm, 3–10-septate. Conidiogenous cells terminal or lateral on branched conidiophores, medium brown, smooth, cylindrical, proliferating sympodially, 7–15 × 2.5–3 µm; loci truncate, inconspicuous, 1–1.5 µm wide. Conidia medium brown, smooth, guttulate, subcylindrical to narrowly obclavate, apex obtuse to truncate, base truncate, occurring in branched chains, widest at the basal septum, (7–)25–45(–100) × (2–)2.5(–3) µm, (0–)3–6(–13)-septate; hila inconspicuous to somewhat darkened and thickened, not refractive, 1–1.5 µm wide.

Culture characteristics: On MEA erumpent, slow growing, with moderate aerial mycelium and smooth margins; surface mouse-grey, reverse iron-grey, reaching 8 mm diam after 2 wk; similar on PDA and OA.

Host range and geographic distribution: Strelitzia sp., South Africa.

Specimen examined: South Africa, KwaZulu-Natal, Durban, Botanical Garden near Reunion, on leaves of Strelitzia sp., 5 Feb. 2005, W. Gams & H. Glen, CBS H-20342, holotype, culture ex-type X1045 = CBS 122480.

Notes: Devriesia strelitziicola is the second Devriesia species to be described from this host (Arzanlou et al. 2008a). The genus Devriesia was originally established to accommodate a group of heat-resistant, Cladosporium-like fungi (Seifert et al. 2004), and it appears that a different generic name will have to be introduced to accommodate those taxa occurring on plants. Further collections are required, however, to clarify the generic boundaries of Devriesia (Crous et al. 2007b).

Hortaea thailandica Crous & K.D. Hyde, sp. nov. MycoBank MB514703. Fig. 11.

Etymology: Named after the country where it was collected, Thailand.

Hortaeae werneckii similis, sed conidiis brunneis, verruculosis, majoribus, (9–)10–13(–15) × (4–)5(–6) µm.

Colonies sporulating on MEA. Mycelium consisting of pale brown, smooth, septate, branched, 3–4 µm wide hyphae that become darker and thick-walled in the conidiogenous region. Conidiogenous cells integrated, intercalary on hyphae, reduced to short cylindrical loci, 2–2.5 µm wide, 1–4 µm tall; collarettes inconspicuous to minute; proliferating 1–2 times concurrently at apex. Conidia ellipsoid, aseptate, pale to medium brown, (4–)5–7(–9) × (2.5–)3 µm, verruculose, apex obtuse, base subtruncate with minute collarette; becoming swollen and elongate at maturity, with 1–4 transverse and 1–2 oblique septa; (9–)10–13(–15) × (4–)5–6(–9) µm; hila inconspicuous, up to 2 µm wide, frequently with visible marginal frill; microcyclic conidiation commonly observed on OA, MEA and PDA.
Culture characteristics: On MEA erumpent, spreading; surface irregular, folded, greenish black, with sparse olivaceous-grey aerial mycelium and smooth, lobed, margins; reverse greenish black; reaching 12 mm diam after 2 wk; similar on OA and PDA.

Host range and geographic distribution: Syzygium siamense, Thailand.

Specimen examined: Thailand, Khao Yai National Park, N14°14'42.6" E101°22'15.7", on leaves of Syzygium siamense, in lesions with a cercosporoid fungus, 27 Mar. 2009, P.W. Crous & K.D. Hyde, holotype in BBH, isotype CBS H-20343, culture ex-type CPC 16652, 16651 = CBS 125423, also in BCC.

Notes: Similar to Hortaea werneckii, which is also frequently isolated from lesions in association with plant pathogenic fungi, H. thailandica occurred in leaf spots in association with a cercosporoid fungus. It is distinct from H. werneckii by forming larger conidia that turn medium brown and verruculose with age.

Several other taxa are newly placed in the Teratosphaeriaceae in the present study that require further evaluation. Xenomeris juniperi, a bitunicate ascomycete on Juniperus with pseudothecia associated with a stroma, and pigmented, 1-septate ascospores, clusters close to Teratosphaeria species occurring on Protea and Eucalyptus, where the ascomata are also associated with stromatic tissue (Taylor & Crous 2000, Crous et al. 2006c). Fresh collections of this fungus would be required, however, to resolve its status. The occurrence of Sporidesmium species in the Teratosphaeriaceae should be interpreted with care, as the genus is polyphyletic, and further studies are required to resolve its status (Shenoy et al. 2006, Crous et al. 2008a, Yang et al., in prep.).

Fig. 10. Devriesia strelitziicola. A. Strelitzia sp. with dead leaves. B. Colony on OA. C–G. Conidiophores giving rise to conidia. H–M. Conidia. Scale bars = 10 µm.
**Davidiellaceae** C.L. Schoch, Spatafora, Crous & Shoemaker, Mycologia 98: 1048. 2006.

*Type species:* *Davidiella tassiana* (De Not.) Crous & U. Braun, Mycol. Progr. 3: 8. 2003.

*Notes:* The *Davidiellaceae* was introduced for the genus *Davidiella*, which has *Cladosporium* anamorphs. As shown in the present analysis, however, allied genera such as *Toxicocladosporium*, *Verrucocladosporium*, *Rachicladosporium* and *Graphiopsis* also belong in this family. Of interest is the position of *Melanodothis caricis* in *Cladosporium* s. str. This fungus, which infects florets of *Carex* and *Kobresia*, forms a stroma that gives rise to several immersed ascomata with bitunicate, oblong asci that are apaparaphysate, and 0–(2)-septate, hyaline, 9–14.5 × 2–4 μm ascospores. In culture, a hyaline, *Ramularia*-like anamorph developed, with sympodial proliferation, catenulate conidia, with thickened, darkened loci (Arnold 1971). Although these characteristics are atypical of the *Davidiella*/*Cladosporium* species in this clade, the position of *Melanodothis caricis* in this family cannot simply be disregarded. However, the ex-type culture of this fungus (CBS 860.72) proved to be sterile.

A further unconfirmed sequence (CBS 354.29, culture sterile, but fast growing, grey-brown, *Cladosporium*-like), is that submitted as *Sphaerulina polyspora* (623723 = Type!) has pseudothecia with apaparaphysate, bitunicate asci, and ascospores that are hyaline, 3–5-septate, 20–24 × 6–7 μm. On the host it was linked to a *Phoma*-like anamorph, which also grew similar in culture (yeast-like budding), and has hyaline conidia which are ellipsoidial, 7–8 × 3.8–4 μm.

Colonies were reported as slow-growing, grey, appressed, with germinating ascospores forming yeast-like budding cells, and rarely having hyphae that extended from the margin of the colonies. The link between *Sphaerulina*-like species, with *Selenophoma* and *Aureobasidium* synanamorphs was recently illustrated by Cheewangkoon *et al.* (2009). Although members of the *Dothideomycetes*, these taxa do not cluster in the *Davidiellaceae*, and hence it seems a fair assumption that CBS 354.29 is not representative of *Sphaerulina polyspora*.

**Rachicladosporium cboliae** Crous, sp. nov. MycoBank MB514704. Fig. 12.

*Etymology:* Named after the Consortium for the Barcode of Life, CBOL, who organised a Fungal Barcoding Symposium, during which this fungus was collected.

**Rachicladosporio americanae similis, sed conidiophoris dense fasciculatis et conidiis minoribus.**
Colonies sporulating on OA. Mycelium consisting of branched, septate hyphae, pale brown, smooth, 1.5–3 µm wide, frequently constricted at septa, forming hyphal coils, but characteristically also forming intercalary and terminal clusters of chlamydospores that are brown, thick-walled, up to 6 µm diam. Conidiophores forming laterally on creeping hyphae, erect, visible as densely branched tufts on agar surface; conidiophores medium brown, smooth, thick-walled with bulbous base, lacking rhizoids, cylindrical, unbranched, flexuous, up to 250 µm long, 4–6 µm wide, 10–20-septate. Conidiogenous cells terminal, medium brown, smooth, polyblastic, subcylindrical, 10–20 × 3–4 µm; loci terminal, thickened, darkened, refractive, 1 µm diam. Ramoconidia 0(-1)-septate, subcylindrical, medium brown, smooth, 7–12 × 3–4 µm. Conidia 0(-1)-septate, in branched chains of up to 10, ellipsoid, pale brown, smooth, (6–)7–8(–10) × (2–)2.5(–3) µm; hila thickened, darkened and refractive, up to 1 µm diam.

Culture characteristics: On MEA spreading with sparse aerial mycelium and smooth margins; surface olivaceous-grey, margin mouse-grey, reverse olivaceous-grey; reaching 30 mm diam; on OA spreading, folded with moderate aerial mycelium; surface pale mouse-grey (centre) to olivaceous-grey at margin, reaching 20 mm diam.

Host range and geographic distribution: Twig litter, Virginia, U.S.A.

Specimen examined: U.S.A., Virginia, Front Royal, N38°53'35" W78°10'50", on twig debris, 14 May 2007, P.W. Crous, holotype CBS H-20344, cultures ex-type CPC 14034 = CBS 125424, CPC 14035, 14036.

Notes: Rachicladosporium cboliae is a cryptic species close to R. americanum, which was collected at the same site. They can be distinguished on the litter in that R. cboliae has conidiophores with densely branched tufts of conidia, in contrast to the more sparsely branched conidiophores of R. americanum. Furthermore, R. cboliae also forms prominent chains of chlamydospores in culture, which lacks in R. americanum. Finally, R. cboliae has smaller ramoconidia and conidia than those found in R. americanum (ramoconidia 13–23 × 3–4 µm; conidia 10–18 × 3–4 µm; Cheewangkoon et al. 2009).
DISCUSSION

The class Dothideomycetes incorporates fungal taxa exhibiting a wide range of nutritional modes, and results in these fungi being found in many diverse niches (Fig. 13). The two largest orders Pleosporales (Zhang et al. 2009; this volume) and Capnodiales encapsulate this diversity. Here we continue to expand sampling within the Capnodiales in order to provide a well founded phylogenetic scaffold for taxonomic classification, informative genomic sampling, ecological studies and evolutionary evaluations.

Capnodiales

The Capnodiales currently contain nine families (Lumbsch & Huhndorf 2007, Kirk et al. 2008), a selection of which are included in this study, namely Capnodiaceae, Davidiellaceae, Mycosphaerellaceae, Piedraiaeae, and Teratosphaeriaceae. Unfortunately, no cultures were available of the Antennulariellaceae and Metacapnodiaceae, while Coccodiniaceae was again shown to cluster outside the order, in Chaetothyriales (Crous et al. 2007a). Families supported within Capnodiales (Fig. 1) include Capnodiaceae, Davidiellaceae, Teratosphaeriaceae, Dissoconiaceae, Schizothyriaceae and Mycosphaerellaceae. No support was obtained for Piedraiaeae, which appeared to cluster within Teratosphaeriaceae.

One of the main aims of the present study was to resolve the status of the Capnodiales and Mycosphaerellales. Although we were able to distinguish a clear, well resolved node for the Mycosphaerellales (incl. Mycosphaerellaceae), this node was not well supported, and elevating it to ordinal level would mean that additional orders need to be introduced to accommodate several families outside the Capnodiales s. str. This finding led us to conclude that it is best to retain all families within a single, diverse order, namely the Capnodiales.

Evolution of nutritional modes and ecological growth habits

The ancestral state of the present assemblage of taxa is likely to be saprobic, as Phaeotheca (Sigler et al. 1981, de Hoog et al. 1997, Tsuneda et al. 2004), and Comminutispora (Ramaley 1996) represent the earliest diverging lineages. This was similarly found for a majority of lineages in the larger context of Ascomycota (Schoch et al. 2009a, b). These taxa were not only all isolated from dead materials or substrates, but they also share the same unique mode of conidiogenesis, namely endocondia, and a “black-yeast” appearance in culture. Phaeotheca, which is strongly halophilic (Zalar et al. 1999) is closely related to the lichen Racodium rupestre, which forms an association with Trentepohlia algae, in which the filamentous algae is enclosed by melanised hyphae of the fungus. This feature is also shared by another lichen, namely Cystocoleus ebeneus (Teratosphaeriaceae) (Muggia et al. 2008). The Capnodiaceae (sooty molds) that also cluster in a basal position in the tree are endophytes, growing on insect exudates (honey dew). The Capnodiaceae are related to the Davidiellaceae, which represent Cladosporium and allied genera. This family contains a wide range of ecological adaptations, from primary plant pathogens, such as Graphiopsis chlorocephala on Paeonia (Schubert et al. 2007a, Braun et al. 2008), *Mycosphaerella* iridis on Iris (David 1997), to taxa opportunistic on humans, *Cladosporium brunneum* (Schubert et al. 2007b), to halotolerant taxa, *Cladosporium sphaerospermum* (Zalar et al. 2007, Dugan et al. 2008), to saprobes, *C. herbarum, C. cladosporiotides* (Schubert et al. 2007b).

The Teratosphaeriaceae contains several disjunct elements, many of which may still eventually be removed from the family as more taxa and additional sequence data are added, providing a better resolution to some of these clades. In its widest sense, the family contains lichens (Anisomeridium, Cystocoleus), saprobes (Catenulostronia spp.), and halophilic, hyperhydrotic or lipophilic species that have been reported from humans (Piedraia, Hortaee, Penidiella, Stenella) (de Hoog et al. 2000, Bonifaz et al. 2008, Plemenitas et al. 2008), with the most derived clades tending to contain plant pathogens (Readeriella, Teratosphaeria).

Dissoconiaceae is an early diverging lineage to the Mycosphaerellales and Schizothyriaceae. Whereas most members of Dissoconiaceae appear to be commensalists, there is evidence that some species could be plant pathogenic (Jackson et al. 2004), while the Schizothyriaceae contains endophytes (Batzer et al. 2007). The Mycosphaerellaceae contains species that are biotrophic (Polythrinicum; Simon et al. 2009), necrotrophic plant pathogens (Brunneosphaerella, Cercospora, Dothistroma, Pseudocercospora, Pseudocercosporella, Ramularia, and Septoria), as well as some species that are saprobic (Passalora, Pseudocercospora, Ramichloridium and Zasidium; Arzaniou et al. 2007), or endophytic (Pseudocercosporella endophytica; Crous 1998).

Within the Capnodiales, the positioning of saprobes such as Phaeotheca and Comminutispora and the sooty moulds (Capnodiales) may represent the more primitive state, from where transitions occurred to more lichenised, saprobic, biotrophic and necrotrophic, plant pathogenic members of the order (Fig. 13). This appears to mirror the other large and diverse order in the class, the Pleosporales (Zhang et al. 2009; this volume). Lichenisation, as well as the ability to be saprobic or plant pathogenic evolved more than once, though the taxa in the later diverging clades of the tree tend to be strictly necrotrophic plant pathogens. This should be interpreted with care, however, as Polythrinicum is presently the only biotrophic member included in this analysis, and other biotrophic members of the Capnodiales may end up clustering here, among the presently dominant necrotrophic plant pathogens. One important and recent addition to Capnodiales diversity is the rock-inhabiting fungi (Ruibal et al. 2008, 2009; this volume). Although so far mainly isolated from sources in Antarctica and the Mediterranean area, it is clear that they are a ubiquitous group of fungi likely found throughout the globe. Their genetic diversity is underscored by the fact that rock inhabiting fungi of convergent morphology are also placed in other ascomycotan classes and orders (Gueidan et al. 2008). The fact that many of these species have reduced morphologies and are slow growers make their taxonomy challenging, but their phylogenetic placement within Teratosphaeriaceae and several other lineages within Capnodiales makes their inclusion in subsequent phylogenetic assessments of this order essential.

For this study, we designed novel primers to supplement primers presently available in literature. Although primers are usually designed for the genus or family of interest, they frequently tend to have a wider application. Therefore, we attempted to design our primers using a wide range of sequences from the GenBank sequence database, in the hope that these primers will eventually find application outside of the Capnodiales as well. Although this remains to be tested, we expect it to be the case. Our sequencing of the complete SSU and LSU for the selected members of the Capnodiales had a surprisingly large number of insertions present.
Fig. 13. Members of Capnodiales exhibiting different ecological growth habits. A–C. Mycosphaerella marnii (plant pathogen). A. Leaf spot on Eucalyptus. B. Homothallic colony on MEA. C. Asci. D. Conidiophore of Cladosporium sphaerospermum (saprobe). E–G. Ascomata and asci of Davidiella macrocarpa (saprobe). H–J. Dissoconium dekkeri (plant pathogen, commensalist). H. Colony sporulating on MEA, with discharged conidia at the margin. I. Asci. J. Primary and secondary conidia attached to conidiophore. K–L. Dissoconium proteae (commensalist). K. Sporulation on MEA with microsclerotia. L. Two conidial types attached to conidiophore (arrow). M–Q. Conidioxyphium gardeniorum (sooty mold). M. Sporulation on MEA. N–P. Elongated, branched conidiomata with apical ostiolar hyphae. Q. Conidia. R–T. Leaf spot, ascus and verruculose ascospores of Teratosphaeria fibrillosa (plant pathogen). U–X. Schizothyrium pomi (epiphyte). U. Thyrothecia occurring on a Rhus stem. V. Ascomatal initials forming on OA. W. Asci. X. Conidiophore and conidia in vitro. Scale bars: E = 200 µm, M–O = 50 µm, all others = 10 µm.
for numerous strains. Although some of these insertions were anticipated based on data already present in GenBank’s database, the insertions in the LSU were not expected based on the sequences used for primer design. However, this could be a result of the fewer complete LSU sequences available in the database rather than a deviation on the part of members of the Capnodiaceae. More complete LSU sequences are needed from diverse orders to test whether this is the case or not. Some of the taxa sequenced during this study had insertions present at almost all of the possible insertion positions, e.g. Mycosphaerella latebrosa, Septoria quercicola and Teratosphaeria mexicana. These taxa are distributed throughout the tree, and do not only cluster in a basal position, and therefore it is difficult to predict why so many insertions were present. If these insertions were all present in a basal position, it would have been possible to argue that the higher number of insertions represents the ancestral condition, and that these insertions are lost during evolution. However, this proved not to be the case, and it could be that these taxa accumulated these insertions.

Although the present study adds significantly to our knowledge of the Capnodiaceae, the Capnodiaceae are still underrepresented, and probably consist of numerous diverse lineages that can be elevated to family level once our phylogenies become more resolved. Regardless of this fact, the Mycosphaerellaceae clade appears to be quite robust. It seems likely that further sampling of the diverse Teratosphaeriaceae will necessitate further taxonomic changes. The fact that the saprobic and plant pathogenic and endophytic modes have evolved several times in different families, suggest that many taxa can still easily adapt to changing environments. A focus on adding more lichenicolous taxa, and taxa occurring on non-plant substrates is crucial to provide further insight into the ecological adaptations occurring in the Capnodiaceae.

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**SUPPLEMENTARY INFORMATION**

Table 1. Details of the isolates for which novel sequences were generated. Samples without an 18S rDNA accession number were only used in the 28S rDNA analysis; sequences of CBS 723.79 and CBS 123.26 were used in both analyses. The accession number for 5.8S nrDNA also includes the flanking spacer regions.

| Species                             | Accession number† | Host                | Country          | Collector | GenBank Accession numbers 18S nrDNA, 5.8S nrDNA, 28S nrDNA |
|-------------------------------------|-------------------|---------------------|------------------|-----------|-------------------------------------------------------------|
| Aulographina pinorum                | CBS 302.71; ETH 7129; UAMH 4037 | *Pinus maritima*    | France           | E. Müller | —, GU214622, GU214393                                       |
| Batcheloromyces leucadendri         | CBS 110892; CPC 1837 | *Leucadendron sp.*  | South Africa     | L. Swart  | GU214515, AY260100, EU019246                                 |
| Batcheloromyces proteae             | CBS 110696; CPC 1518 | *Protea cynaroides* | South Africa     | L. Viljoen| AY251102, AY260099, EU019247                                 |
| Brunneosphaerella protearum         | CPC 13905          | *Protea sp.*        | South Africa     | P.W. Crous| —, GU214623, GU214394                                       |
| Capnobotrya renispora              | CBS 214.90; IAM 13014; JCM 6932; TNS F-198506 | *Capnobotrys neessii* | Japan            | J. Sugiyama| AY220612, AY220612, GU214398                                |
| Capnodium coffeae                   | CBS 147.52         | *Coffea robusta*    | Zaire            | —         | DO247808, AJ244239, GU214400                                |
| Catenulostroma chromoblastomycosum | CBS 597.97         | Man, chromoblastomycosis | Zaire            | V. de Brouwere | GU214516, AJ244260, EU019251 |
| Catenulostroma elginense            | CBS 111030; CPC 1958 | *Protea grandiceps* | South Africa     | J.E. Taylor| GU214517, AY260093, EU019252                                |
| Catenulostroma germanicum           | CBS 539.88         | Stone               | Germany          | —         | GU214516, EU019253, EU019253                                |
| Catenulostroma microsporum          | CBS 110890; CPC 1832 | *Protea cynaroides* | South Africa     | L. Swart  | GU214520, AY260097, EU019255                                |
| Catenulostroma protearum            | CPC 15368          | *Leucadendron tinctum* | South Africa     | F. Roets  | —, GU214627, GU214401                                       |
| Cladosporium uredinicola            | CBS 118712         | Glycine soja        | South Korea      | H.D. Shin  | GU214655, GU214655, GU214655                                |
| Cercosporella asiatica              | CPC 12322          | *Allium porrum*     | New Zealand      | A.C. Jamieson | EU167558, EU167558, GU214410 |
| Cercosporella sp.                    | CPC 12333          | *Glycine soja*      | South Korea      | H.D. Shin  | GU214655, GU214655, GU214655                                |
| Cladosporium brunnei                | CBS 118789; CPC 5955 | *Trifolium protense* | Canada           | K. Seifert  | AY251104, AY260078, GU214406                                |
| Cercosporella papillosa              | CPC 12333          | *Glycine soja*      | South Korea      | H.D. Shin  | GU214655, GU214655, GU214655                                |
| Cercosporella sp.                    | CPC 118790; CPC 5955 | *Trifolium protense* | Australia        | M.J. Barbetti | GU214656, GU214656, GU214656 |
| Cercosporella virgaurea             | CBS 113304         | Erigeron annuus     | South Korea      | H.D. Shin  | GU214658, GU214658, GU214658                                |
| Cercosporella sp.                    | CPC 12333          | *Glycine soja*      | South Korea      | H.D. Shin  | GU214655, GU214655, GU214655                                |
| Cladosporium cladosporioides        | CBS 109.21; CPC 5955 | *Triticum aestivum* | Netherlands      | N.J. Fokkema | AY251091, AY251074, GU214409 |
| Cercosporella sp.                    | CBS 118789; CPC 5955 | *Trifolium protense* | Australia        | M.J. Barbetti | GU214656, GU214656, GU214656 |
| Cladosporium herbarum               | CBS 723.79         | *Allium porrum*     | New Zealand      | A.C. Jamieson | EU167558, EU167558, GU214410 |
| Cladosporium sp.                    | CPC 15513          | *Rubus fruticosus*  | Italy            | P.W. Crous  | —, GU214630, GU214411                                       |
| Cladosporium sp.                    | CPC 15516          | *Pyrus communis*    | Ukraine          | A. Akulov  | —, GU214631, GU214412                                       |
| Cladosporium sp.                    | ATCC 46649; CPC 5390 | *Quercus nigra*     | U.S.A.           | G. Morgan-Jones | AY251097, AY251071, EU019264 |
| Cladosporium sp.                    | CBS 330.51         | *Leaf spot in Rosa sp.* | Netherlands      | —         | —, GU214632, GU214413                                       |
Table 1. (Continued).

| Species                   | Accession number | Host                  | Country     | Collector       | GenBank Accession numbers |
|---------------------------|------------------|-----------------------|-------------|----------------|---------------------------|
| *Devriesia hilliana*      | CBS 123187; CPC 15382 | Macrozamia communis  | New Zealand | C.F. Hill       | —, GU214633, GU214414     |
| *Devriesia lagerstroemiae*| CBS 125422; CPC 14403 | Lagerstroemia indica | U.S.A.      | P.W. Crous & M.J. Wingfield | —, GU214634, GU214415     |
| *Devriesia staunophora*   | CBS 375.81; ATCC 200934; CPC 3687 | Párano soil       | Colombia    | H. Valencia    | EF137359, AF393723, GU214416 |
| *Devriesia streilziciola* | CBS 122480; X1045  | Streitizia sp.       | South Africa | W. Gams & H. Glen | GU214635, GU214417         |
| *Dissoconium aciculare*   | CBS 201.89        | Brassica sp.         | Netherlands | T. Hijwegen    | GU214522, AY725519, GU214418 |
| *Dissoconium commune*     | CBS 204.89        | Astragalius sp.      | Germany     | T. Hijwegen    | GU214523, AY725520, GU214419 |
| *Dissoconium dekkeri*     | CBS 342.82; CPC 1534 | Erysiphe, on Medicago lupulina | Germany     | T. Hijwegen    | GU214524, AF173308, EU019266 |
| *Dissoconium dekkeri*     | CBS 110747; CPC 831 | Eucalyptus nitens    | South Africa | P.W. Crous | GU214525, AY725535, GU214420 |
| *Dissoconium commune*     | CBS 114238; CPC 10440 | Eucalyptus globulus | Spain       | J.P.M. Vazquez | GU214526, AY725541, EU019267 |
| *Dissoconium dekkeri*     | CBS 114239; CPC 10492 | Eucalyptus globulus | New Zealand | W. Gams       | GU214527, AY725542, GU214421 |
| *Dissoconium dekkeri*     | CBS 110748; CMW 14906; CPC 825 | Eucalyptus grandis | South Africa | G. Kemp      | GU214528, AF309625, GU214422 |
| *Dissoconium dekkeri*     | CBS 111169; CMW 5164; CPC 1232 | Eucalyptus globulus | Zambia      | —            | GU214529, AY725550, GU214423 |
| *Dissoconium dekkeri*     | CBS 111272; CPC 1188 | Eucalyptus nitens    | South Africa | M.J. Wingfield | GU214530, AY725551, GU214424 |
| *Dissoconium dekkeri*     | CBS 111282; CPC 1233 | Eucalyptus globulus | Zambia      | —            | GU214531, AY73305, GU214425 |
| *Graphiopsis chlorocephala* | CBS 567.89; CPC 1535 | Juniperus chinensis  | Netherlands | T. Hijwegen    | AY251101, AY73309, EU019268 |
| *Dothistroma pini*        | CBS 116497; CMW 10951 | Pinus nigra          | U.S.A.      | G. Adams       | GU214532, AY08302, GU214426 |
| *Dothistroma septosporum* | CBS 112498; CPC 3779 | Pinus radiata        | Ecuador     | —            | GU214533, AY293062, GU214427 |
| *Graphiopsis chlorocephala* | CBS 121523; CPC 11969 | Paonia officinalis   | Germany     | K. Schubert    | GU214534, EU009458, EU009458 |
| *Hortaea acidophila*      | CBS 113389        | Lignite, pH 1        | Germany     | U. Höker      | —, GU214636, GU214428     |
| *Hortaea thailandica*     | CBS 125423; CPC 16651 | Syzygium siamense   | Thailand    | P.W. Crous & K.D. Hyde | —, GU214637, GU214429     |
| *Lecanosticta acicola*    | CBS 871.95; MPFN 314 | Pinus radiata        | France      | M. Morelet     | GU214663, GU214663, GU214433 |
| *Leptoxyphium fumago*     | CBS 123.26; ATCC 11925; IMI 089363; LSHB X13 | Hibiscus tiliaceus  | Indonesia   | —            | GU214535, —, GU214430     |
| *Melanodothis carici*     | CBS 860.72; ATCC 24309; DAOM 11643 | Carex stichensis   | Canada      | —            | —, GU214638, GU214431     |
| *Miuraea persicae*        | CPC 10099         | Prunus persica       | South Korea | H.D. Shin     | GU214660, GU214660, GU214690 |
| *Mycosphaerella acaciigena* | CBS 112515; CPC 3837 | Acacia mangium      | Venezuela   | M.J. Wingfield | AY251116, AY752143, GU214432 |
| *Mycosphaerella africana* | CBS 116154; CMW 4945; CPC 794 | Eucalyptus viminalis | South Africa | P.W. Crous | GU214536, AF173314, GU214433 |
| *Mycosphaerella biaxae*   | CBS 111804; CPC 2554 | Bixa orellana       | Brazil      | P.W. Crous & R.L. Benchimol | GU214557, AF362056, GU214455 |
| *Mycosphaerella ellipsoidae* | CBS 110843; CPC 850 | Eucalyptus cladocalyx | South Africa | P.W. Crous | GU214537, AY725545, GU214434 |
| *Mycosphaerella endophytica* | CBS 114662; CPC 1193 | Eucalyptus sp.      | South Africa | P.W. Crous | GU214538, DQ302953, GU214435 |
| *Mycosphaerella graminicola* | CBS 100335; IPO 69001.61 | Triticum aestivum  | —           | G.H.J. Kema   | GU214539, EU019297, EU019298 |
| *Mycosphaerella handelii* | CBS 111074; CPC 658 | Triticum sp.        | South Africa | P.W. Crous | AY251117, AF362068, EU019298 |
| *Mycosphaerella heimioides* | CBS 115943; IPO 323 | Triticum aestivum   | Netherlands | R. Daamen     | GU214540, AF181692, GU214436 |
| *Mycosphaerella kalliantha* | CBS 113302        | Rhododendron sp.    | Netherlands | P.W. Crous & U. Braun | EU167581, EU167581, GU214437 |
| *Mycosphaerella keimii*   | CBS 110682; CMW 4942; CPC 760 | Eucalyptus sp.     | Madagascar  | P.W. Crous     | GU214541, AF309606, GU214438 |
| *Mycosphaerella heimioides* | CBS 111190; CMW 3046; CPC 1312 | Eucalyptus sp.     | Indonesia   | M.J. Wingfield | GU214542, AF309609, GU214439 |
| *Mycosphaerella holualaoana* | CBS 110699; CPC 2155 | Leucaspernum sp.    | U.S.A.: Hawaii | P.W. Crous | GU214543, AY260084, GU214440 |
| Species                        | Accession number | Host                  | Country      | Collector | GenBank Accession numbers |
|-------------------------------|------------------|-----------------------|--------------|-----------|---------------------------|
| *Mycosphaerella irregularismosa* | CBS 111211; CPC 1362 | *Eucalyptus saligna*  | South Africa | M.J. Wingfield | GU214544, AF209608, GU214441 |
| *Mycosphaerella keniensis*    | CBS 11001; CMW 5147; CPC 1084 | *Eucalyptus grandis*  | Kenya        | M.J. Wingfield | GU214545, AF173300, GU214442 |
| *Mycosphaerella latebrosa*    | CBS 652.85       | *Acer pseudoplatanus* | Netherlands  | H.A. van der Aa | —                        |
| *Mycosphaerella lupini*       | CPC 1661         | *Lupinus sp.*         | U.S.A.       | W. Kaiser   | GU214547, AF362050, FJ839661 |
| *Mycosphaerella marasasi*     | CBS 110790; CPC 348 | *Syzygium cordatum*   | South Africa | M.J. Wingfield | GU214548, AF309691, GU214445 |
| *Mycosphaerella markii*       | CBS 110942; CPC 982 | *Eucalyptus botryoides* | Australia   | A.J. Carnegie | GU214549, AF309589, GU214446 |
| *Mycosphaerella latebrosa*    | CPC 11222        | *Acer pseudoplatanus* | Netherlands  | G. Verkley  | GU214546, AF152553, GU214444 |
| *Mycosphaerella parkii*       | CBS 387.92; CMW 14775; CPC 353 | *Eucalyptus grandis*  | Brazil       | M.J. Wingfield | GU214551, AF309590, GU214447 |
| *Mycosphaerella sp.*          | CBS 111166; CPC 1224 | *Eucalyptus cladocalyx* | South Africa | A.R. Wood   | GU214552, AF173302, GU214442 |
| *Mycosphaerella sp.*          | CBS 111167; CPC 1225 | *Eucalyptus cladocalyx* | South Africa | A.R. Wood   | GU214553, AF309693, GU214450 |
| *Mycosphaerella sphaerulinae* | CBS 110261; CPC 4314 | *Eucalyptus sp.*     | Chile        | —           | GU214554, AF293066, GU214451 |
| *Mycosphaerella stromatosa*   | CBS 101953; CPC 1731 | *Protea sp.*         | South Africa | S. Denman  | GU214555, AF310107, GU214452 |
| *Mycosphaerella tasmaniensis* | CBS 111687; CMW 14780; CPC 1555 | *Eucalyptus nitens* | —           | —           | GU214555, AF310107, GU214452 |
| *Passalora ageratinae*        | CBS 125419; CPC 15385 | *Ageratina adenophora* | South Africa | A.R. Wood   | GU214563, GU214453 |
| *Passalora bellynckii*        | CBS 150.49; CPC 3635 | *Cynanchum vincetoxicum* | Switzerland | S. Blumer | GU214556, AF222831, GU214454 |
| *Passalora brachycarpa*       | CBS 115124       | —                     | —           | C.F. Hill   | GU214664, GU214664, GU214664 |
| *Passalora armatae*           | CBS 125420; CPC 15419 | *Dalbergia armata*   | South Africa | A.R. Wood   | —, GU214640, GU214456 |
| *Passalora dicosoreae*        | CPC 1085         | *Diocorea tokora*    | South Korea  | H.D. Shin   | GU214665, GU214665, GU214685 |
| *Passalora dodonaea*          | CPC 1223         | *Dodonaea sp.*       | —           | P.W. Crous  | GU214558, AF309617, GU214458 |
| *Passalora eucalypti*         | CBS 111318; CPC 1457 | *Eucalyptus saligna*  | Brazil       | P.W. Crous  | GU214558, AF309617, GU214458 |
| *Passalora fulva*             | CBS 119.46; CPC 3688 | *Lycoopersicon esculentum* | —           | —           | GU214559, AF293066, GU214451 |
| *Passalora graminis*          | CBS 113303       | *Alotepecurus aequilis var. amurensis* | South Korea | H.D. Shin   | GU214666, GU214666, GU214666 |
| *Passalora perplexa*          | CBS 116364; CPC 11150 | *Acacia crasscarpa*  | Indonesia    | M.J. Wingfield | GU214559, AF752163, GU214459 |
| *Passalora sequoiae*          | CPC 11258        | *Juniperus virginiana* | U.S.A.      | C.S. Hodges | GU214667, GU214667, GU214667 |
| *Passalora sp.*               | CBS 115525; CPC 3051 | *Tilia americana*    | Canada       | K. Seifert  | GU214560, AF293064, GU214460 |
| *Passalora vaginae*           | CBS 140.34; DSM 1148; IMI 303641 | *Saccharum officinarum* | Taiwan      | —           | GU215461, AF222832, GU214461 |
| *Passalora zambae*            | CBS 112970; CPC 1228 | *Eucalyptus globulus* | Zambia       | T. Coutinho | GU214562, AF752522, EU019272 |
| *Passalora-like genus*        | CPC 11876        | *Aviceinia sp.*      | South Africa | W. Gams    | GU214564, GU214642, GQ852262 |
| *Peniophora columbiana*       | CBS 486.80       | *Paepalanthus colombianus* | Colombia    | W. Gams    | GU214565, AJ244261, EU019274 |
| *Phaeococcum paspali*         | CBS 113093; RoKI 1144 | *Setaria palmicola*  | Taiwan       | R. Kirschnr & C.-J. Chen | GU214669, GU214669, GU214469 |
| *Phaeophleospora atkinsoni*   | CBS 124565; ICM 17860 | *Leaf of Hebe sp.*  | New Zealand  | —           | GU214643, GU21462 |
| *Phaeophleospora eugenicola*  | CPC 2557         | *Eugenia sp.*       | Brazil       | —           | GU214566, FJ493190, FJ493208 |
| *Phloeoospora maculans*       | CBS 115123       | —                     | —           | C.F. Hill   | GU214670, GU214670, GU214670 |
| *Piedraea hortae var. hortae* | CBS 374.71       | *Man*                | French Guiana| —           | GU214645, GU214646 |
| *Piedraea hortae*             | CBS 375.71       | *Man*                | Brazil       | —           | GU214645, GU214645 |

Table 1. (Continued).
| Species                                | Accession number | Host                  | Country      | Collector            | GenBank Accession numbers |
|----------------------------------------|------------------|-----------------------|--------------|----------------------|---------------------------|
| *Piedraia hortae var. paraguayensis*   | CBS 367.48; IMI   | Plant, root hairs    | Brazil       | —                    | GU214678, GU214676       |
| *Piedraia quintanilhae*                | CBS 242.75; IMI   | —                     | Brazil       | —                    | GU214679                 |
| *Polychaeton citri*                    | CBS 327.63; IMI   | A. maldcitrioides     | Central Africa| R. Zare              | GU214680, GU214681       |
| *Pseudocercospora angolensis*          | CBS 112933; CPC   | *Citrus* sp.          | Zimbabwe     | —                    | GU214682, GU214683       |
| *Piedraia hortae var. paraguayensis*   | CBS 367.48; IMI   | Plant, root hairs    | Brazil       | —                    | GU214678, GU214676       |
| *Piedraia quintanilhae*                | CBS 242.75; IMI   | —                     | Brazil       | —                    | GU214679                 |
| *Polychaeton citri*                    | CBS 327.63; IMI   | A. maldcitrioides     | Central Africa| R. Zare              | GU214680, GU214681       |
| *Pseudocercospora angolensis*          | CBS 112933; CPC   | *Citrus* sp.          | Zimbabwe     | —                    | GU214682, GU214683       |

Table 1. (Continued).
| Species | Accession number | Host | Country | Collector | GenBank Accession numbers |
|---------|------------------|------|---------|----------|--------------------------|
| Pseudotaeniolina globosa | CBS 109888 | Rubus oldhamii | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Rachiocladosporium cobleiae | CBS 125424; CPC 14034 | Vicetia amurense | South Korea | H.D. Shin | GU214683, GU214683, GU214683 |
| Ramichloridium apiculatum | CPC 12310 | Vicetia amurense | South Korea | H.D. Shin | GU214687, GU214687, GU214687 |
| Ramichloridium cerosiphilum | CBS 103.59; MUCL 10034 | Sasa sp. | South Korea | H.D. Shin | GU214683, GU214683, GU214683 |
| Ramichloridium cerophilum | CBS 12310 | Vicia amurense | South Korea | H.D. Shin | GU214687, GU214687, GU214687 |
| Ramichloridium musae | CPC 11414 | Rubus oldhamii | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Ramichloridium-like genus | CPC 11294 | Vicia amurense | South Korea | H.D. Shin | GU214687, GU214687, GU214687 |
| Ramularia acroptili | CBS 120252 | Acropthlon repens | Turkey | R. Sobhian | GU214689, GU214689, GU214689 |
| Ramularia brunnea | CPC 4903 | — | — | — | GU214691, GU214691, GU214691 |
| Ramularia coleoporini | CPC 11516 | Plectranthus excisus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Ramularia endophylla | CPC 120253 | Centaurea solstitialis | Greece | D. Berner | GU214579, EU019257, EU019257 |
| Ramularia pratensis var. pratensis | CPC 324.87 | leaf spot on Brassica sp., in Mycosphaerella sp. | Netherlands | — | GU214581, EU019284, EU019284 |
| Ramularia pratensis | CPC 11294 | Rumex crispus | South Korea | H.D. Shin | GU214580, EU019284, EU019284 |
| Ramularia uredinicola | CPC 11297 | Stellaria aquatica | South Korea | H.D. Shin | GU214580, EU019284, EU019284 |
| Ramularia sp. | CBS 110578; CPC 905 | Eucalyptus nitens | Australia | W. Gams | EU754110, EF725529, EU001291 |
| Ramularia sp. | CBS 110579; CPC 906 | Sorghum sp. | South Africa | D. Nowell | GU214580, EU019284, EU019284 |
| Ramularia sp. | CBS 1117 | — | — | — | GU214581, EU019284, EU019284 |
| Ramularia sp. | CBS 112043; CPC 12636 | Eucalyptus nitens | Australia | — | GU214521, EF398485, EU001298 |
| Ramularia sp. | CBS 112630; CPC 10506 | Eucalyptus fastigata | New Zealand | W. Gams | EU754110, EF725529, EU001291 |
| Schizothyrium pomi | CBS 11297 | Stellaria aquatica | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 11297 | Stellaria aquatica | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 11297 | Stellaria aquatica | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Schizothyrium pomi | CBS 406.61 | Rubus idaeus | South Korea | H.D. Shin | GU214685, GU214685, GU214685 |
| Species                        | Accession number | Host                        | Country      | Collector | GenBank Accession numbers |
|-------------------------------|------------------|-----------------------------|--------------|-----------|--------------------------|
| Stenella araguata             | CBS 105.75; ATCC 24788; FMC 245 | Man                         | Venezuela    | —         | GU214596, EU019250, EU019250 |
| Sigmoidina platani            | CBS 110755; IMI 136770; CPC 4299 | Platanus occidentalis       | South Korea  | H.D. Shin | GU214700, GU214700, GU214700 |
| Sigmoidina synanamorph        | CPC 11721        | Betula sp.                  | Sweden       | K. & L. Holm | GU214701, GU214701, GU214701 |
| Stomiopeltis betulae          | CBS 114420       | Eucalyptus globulus         | Spain        | W. Gams   | GU214600, AY215573, GU214503 |
| Teratosphaeria aff. nubilosa  | CBS 114419; CPC 10497 | Eucalyptus tesseliana       | Australia    | J.L. Alcorn | GU214514, AF362061, EU019245 |
| Teratosphaeria alcornii       | CBS 313.76; CPC 3632 | Angophora floribunda       | Australia    | A.J. Carnegie — | GU214652, GU214504 |
| Teratosphaeria bellula        | CBS 111700; CPC 1821; JT 196 | Protea eximia              | South Africa | J.E. Taylor | GU214601, EU019301, EU019301 |
| Teratosphaeria cryptica       | CBS 110975; CMW 3279; CPC 936 | Eucalyptus globulus         | Australia    | A.J. Carnegie | GU214602, AF309623, GU214505 |
| Teratosphaeria destructans    | CBS 111369; CPC 1366 | Eucalyptus grandis          | Indonesia    | M.J. Wingfield | GU214603, DQ267595, EU019287 |
| Teratosphaeria fibrillosa     | CBS 111370; CPC 1368 | Eucalyptus sp.              | Indonesia    | P.W. Crous | GU214702, GU214702, GU214702 |
| Teratosphaeria juvenalis      | CBS 110906; CMW 13347; CPC 40 | Eucalyptus cladocalyx       | South Africa | P.W. Crous | AY720715, AY725513, FJ493217 |
| Teratosphaeria macowanii      | CBS 110756; CPC 1872 | Protea nitida               | South Africa | J.E. Taylor | EU019282, EU019282, GU214506 |
| Teratosphaeria molleniana     | CBS 111164; CMW 4940; CPC 1214 | Eucalyptus globulus         | Portugal     | M.J. Wingfield | GU214606, AF309620, EU019292 |
| Teratosphaeria nubilosa       | CBS 113679; CPC 1366 | Eucalyptus globulus         | Australia    | —         | GU214604, AY725585, GU214507 |
| Teratosphaeria ohnowa         | CBS 110905; CMW 120744; CPC 12349 | Eucalyptus sp.            | U.S.A.: Hawaii | W. Gams | GU214605, EU019302, EU019302 |
| Teratosphaeria pseudosuberosa | CBS 118911; CPC 12085 | Eucalyptus sp.              | Uruguay      | M.J. Wingfield | GU214611, DQ303011, EU019256 |
| Teratosphaeria suberosa       | CBS 116508; CPC 504 | Eucalyptus grandis          | Brazil       | A.C. Alfenas | GU214612, DQ303018, EU019306 |
| Teratosphaeria sp.            | CBS 208.94; CPC 727 | Eucalyptus grandis          | Indonesia    | A.C. Alfenas | GU214613, AY826682, EU019307 |
| Teratosphaeria stelliferboschiana | CBS 116428; CPC 10886 | Eucalyptus sp.            | South Africa | P.W. Crous | GU214583, AY725518, EU019296 |
| Teratosphaeria suberosa       | CPC 11032        | Eucalyptus sp.              | Colombia     | M.J. Wingfield | GU214614, DQ303044, GU214512 |
| Teratosphaeria suttonii       | CPC 11279        | Eucalyptus terecicorinis    | Bolivia      | M.J. Wingfield | GU214615, DQ303055, FJ932222 |
| Teratosphaeria toledana       | CBS 113313; CMW 14457 | Eucalyptus sp.            | Spain        | P.W. Crous & G. Bills | GU214617, AY725580, GU214513 |
| Teratosphaeria verrucosa      | CPC 18           | Eucalyptus cladocalyx       | South Africa | P.W. Crous | AY720713, AY725517, EU019293 |
| Thedgonia-like genus          | CPC 12304        | Optinium undulatifolius     | South Korea  | H.D. Shin | GU214703, GU214703, GU214703 |
| Species                        | Accession number | Host          | Country      | Collector          | GenBank Accession numbers                        |
|-------------------------------|------------------|---------------|--------------|--------------------|-------------------------------------------------|
| *Toxicocladosporium irritans* | CBS 185.58       | Mouldy paint  | Suriname     | M.B. Schol-Schwarz | GU214619, EU040243, EU040243                      |
| *Verrucispora daviesiae*      | CBS 116002; VPRI 31767 | *Daviesia latifolia* | Australia | V. Beiharz        | GU214620, FJ839633, FJ839669                     |
| *Verrucispora proteacearum*   | CBS 116003; VPRI 31812 | *Grevillea sp.* | Australia   | J.L. Alcorn       | GU214621, FJ839635, FJ839671                     |
| *Zasmidium anthuriicola*      | CBS 118742       | *Anthurium sp.* | Thailand     | C.F. Hill          | GU214595, FJ839626, FJ839662                     |
| *Zasmidium citri*             | CBS 116366; CMW 11730; CPC 10522 | *Acacia mangium* | Thailand | K. Pongpanich     | GU214597, AY752145, GU214502                     |

1ATCC: American Type Culture Collection, Virginia, U.S.A.; BBA: Biologische Bundesanstalt für Land- und Forstwirtschaft, Berlin-Dahlem, Germany; CBS: Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands; CMW: Culture Collection of the Forestry and Agricultural Biotechnology Institute (FABI) of the University of Pretoria, Pretoria, South Africa; CPC: Culture collection of Pedro Crous, housed at CBS; DAOM: Plant Research Institute, Department of Agriculture (Mycology), Ottawa, Canada; DAR: Plant Pathology Herbarium, Orange Agricultural Institute, Forest Road, Orange. NSW 2800, Australia; DSM: Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany; ETH: Swiss Federal Institute of Technology Culture Collection, Zurich, Switzerland; FMC: Venezuelan School of Medicine; IAM: IAM Culture Collection, Institute of Molecular and Cellular Biosciences, The University of Tokyo, Japan; ICMP: International Collection of Micro-organisms from Plants, Landcare Research, Private Bag 92170, Auckland, New Zealand; IFO: Institute for Fermentation, Osaka, Japan; IHEM: Collection of the Laboratory voor Microbiologie en Microbiële Genetica, Rijksuniversiteit Leiden, Leeghwaterstraat 10, 3584 CH Leiden, The Netherlands; IMI: International Mycological Institute, CABI-Bioscience, Egham, Surrey, U.K.; IPO: Plant Protection Service, Wageningen, The Netherlands; JCM: Japan Collection of Microorganism, RIKEN BioResource Center, Japan; JT: Working collection of Joanne E. Taylor; LSHB: London School of Hygiene & Tropical Medicine, London, U.K.; MPFN: Culture collection at the Laboratoire de Pathologie Forestière, INRA, Centre de Recherches de Nancy, 54280 Champenoux, France; MUCL: Université Catholique de Louvain, Louvain-la-Neuve, Belgium; PD: Plant Protection Service, Wageningen, The Netherlands; RoK: Private culture collection Roland Kirschner; TNS: Herbarium of the National Museum of Nature and Science of Japan, Tokyo, Japan; IAMH: University of Alberta Microfungus Collection and Herbarium, Edmonton, Alberta, Canada; VKM: All-Russian Collection of Microorganisms, Russian Academy of Sciences, Institute of Biochemistry and Physiology of Microorganisms, 142292 Pushchino, Moscow Region, Russia; VPRI: Victorian Department of Primary Industries, Knoxfield, Australia; WAC: Department of Agriculture Western Australia Plant Pathogen Collection, Perth, Australia; X: Working collection of Mahdi Arzanlou.