New hyphomycetes from Restionaceae in fynbos: *Parasarcopodium ceratocaryi* gen. et sp. nov., and *Rhexodenticula elegiae* sp. nov.

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Two new hyphomycetous anamorphs were isolated from plant hosts of the Restionaceae in the fynbos of the Cape Floral Kingdom of South Africa. *Parasarcopodium ceratocaryi* gen. et sp. nov. on *Ceratocaryum decipiens* produces aseptate, cylindrical conidia with amorphous mucoid appendages at both ends in rows or whorls of phialides on verruculose, mononematous conidiophores. *Rhexodenticula elegiae* sp. nov. on *Elegia capensis* produces pale brown, fusiform or broadly fusiform, 3-septate conidia on denticles located in the upper part of smooth, geniculate conidiophores. The morphological characteristics of both taxa are described, illustrated, and contrasted to other morphologically similar fungi. To elucidate the phylogenetic relationships of *Parasarcopodium,* partial large subunit rRNA (28S) gene sequence was generated from the ex-type strain, which revealed it to be a member of the Bionectriaceae (Hypocreales).

Taxonomical novelties: *Parasarcopodium* Melnik, S. Lee & Crous; *P. ceratocaryi* Melnik, S. Lee & Crous; *Rhexodenticula elegiae* Melnik, S. Lee & Crous.

The Restionaceae (restios) is a family of perennial, evergreen, grass-like plants found on all the southern continents, and includes ca. 480 species. Because of their distribution, it has led to the hypothesis that the family is ancient, dating to the end of the Cretaceous period more than sixty million years ago when the southern continents still formed the supercontinent Gondwana (HAAKSMA & LINDER 2000). Fynbos is the dominant vegetation in the Cape Floral Kingdom (CFK), which is located in the south-western part of South Africa including the Cape Peninsula and part of the west- and the south coast, and is consisting of various plant groups. Restios are the unique distinguishing part of fynbos in their ubiquitous presence whereas other plants can be absent from a particular habitat (HAAKSMA & LINDER 2000). The majority of African species are found exclusively in the Cape region of South Africa except for a few species found in other parts of Africa. Despite the unique ecological attributes of restios, no focused research has thus far been directed towards understanding the fungal mycota associated with them. Therefore, we were interested to determine if their saprobic fungi were also unique. Since 2000, we have been collecting and studying culm litter of restios. Preliminary findings have revealed a mycota that includes several known, but also many unknown species of coelomycetous anamorphs and ascomycetes (LEE & CROUS 2003a, b), with many more awaiting description.

During this study, two hyphomycete species were isolated that could not be identified. One species was isolated from *Ceratocaryum decipiens* (N.E. Br.) Linder, a plant that grows on well-drained slopes to deeper soils in the CFK at an altitude of 500–1400 m, and reaches 0.6–1.5 m in height on a spreading rhizome with 6–12 mm diam unbranched culms (LINDER 2001). The other fungal species was isolated from *Elegia capensis* (Burm. f.) Schelpe, which is particularly common in seepages and along streams, grows 1–3 m tall on a spreading rhizome with 10–15 mm diam branched culms whorled at each node, and is distributed in the CFK at an altitude of 1–1600 m where some ground water is available (LINDER 2001). The fungus isolated from *Ceratocaryum* resembled species of *Sarcopodium* Ehrenb., *Atrosetaphiale* Matsush., *Chaetopsina* Rambelli, *Vermiculariopsiella* Bender and *Myrothecium* Tode in either conidiophores, conidia or colony morphology, but could not be accommodated in any of them. The species isolated from *Elegia* was similar to taxa of *Pyricularia* Sacc. and *Rhexodenticula* W.A. Baker & Morgan-Jones, but closer to the latter in conidial shape and conidiophores. Since none of previously described taxa could accommodate these two species, they were described, illustrated, and contrasted to other similar fungi.

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Material and methods

Isolates and morphology

Dead culms were collected from the soil surface or from standing plants in the nature reserves in the Western Cape province of South Africa. The samples were either inspected immediately for fungal structures, or air-dried for later study. Air-dried samples were incubated in moisture chambers for 2–3 d before examination. Cultural characteristics were studied in triplicates of single spore culture plates of 2 % cornmeal agar (CMA, BBL™, Maryland, USA), oatmeal agar (OA, Difco, Detroit, USA), potato dextrose agar (PDA, Biolab, Gauteng, South Africa), and banana leaf agar (BLA, leaves of *Musa ventricosa* Welw. on 2 % CMA) after 7–10 d of incubation at 25 °C in the dark and in the alternation of 12 h near UV light and 12 h dark. Colours were determined according to RAYNER (1970). Microscopic observations, measurements and photography of characteristic structures were made from specimens mounted in clear lactophenol, or as otherwise specified. Mucilaginous appendages were stained in Leifson's solution (PUNITHALINGHAM & WOODHAMS 1984) or observed in water. The 95 % confidence intervals were derived from 30 observations wherever possible to determine the size of structures, with the extremes given in parentheses. Photographic images were captured with a Nikon Digital Camera DXM 1200 on a Nikon Eclipse E600 light microscope or a Nikon SMZ800 dissecting microscope. The line drawings were prepared by V. Mel'nik. Herbarium specimens are deposited at PREM (National Collection of Fungi, Pretoria, Republic of South Africa), LE (Komarov Botanical Institute, St. Petersburg, Russia) and herb. CBS (Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands) and reference cultures are maintained in the culture collection of the Department of Plant Pathology, University of Stellenbosch (STE-U) and the CBS.

DNA isolation, amplification and phylogeny

Genomic DNA was isolated from mycelia of STE-U 5494 following the method described by CROUS et al. (2000). The 5' end of the large subunit rRNA (LSU) gene was amplified using primers LR0R (REHNER & SAMUELS 1994) and LR7 (VILGALYS & HESTER 1990). PCR amplifications were conducted in a GeneAmp® PCR System 2700 thermocycler (Applied Biosystems, Foster City, California, USA) and the reaction mixture contained 5 µL of diluted gDNA, 1 x buffer, 4 mM $MgCl_2$, 500 µM of each of the dNTPs, 2.5 U (Bioline, Luckenwalde, Germany) Taq polymerase and 10 pmoles of each primer and made up to a total volume of 25 µL with sterile water. The primers NS1 and NS4 (WHITE et al. 1990) were used to amplify approximately 1000 bp of the 5' end of the small subunit rDNA (SSU) gene using the same conditions as described here but with 1.5 mM $MgCl_2$. The primers ITS1 and ITS4 (WHITE et al. 1990) were used to amplify part of the nuclear rRNA operon spanning the 3' end of the 18S rRNA gene, the first internal transcribed spacer (ITS1), the 5.8S rRNA gene, the second ITS (ITS2) region and part of the 5'end of the 28S rRNA gene. The cycling conditions comprised of denaturing at 96 °C for 5 min, followed by 30 cycles of denaturation at 96 °C (30 s), annealing 50 °C (30 s) and elongation at 72 °C (90 s). A final elongation step at 72 °C for 7 min was included. PCR products were separated by electrophoresis at 75 V for 1 h in a 0.8 % (w/v) agarose gel in 0.5 TAE buffer (0.4 M Tris, 0.05 M NaAc, and 0.01 M EDTA, pH 7.85) and visualised under UV light using a GeneGenius Gel Documentation and Analysis System (Syngene, Cambridge, UK) following ethidium bromide staining. The amplification products were purified according to the manufacturer's instructions using a commercial kit (GFX PCR DNA and Gel Band Purification Kit, Amersham Pharmacia Biotech Europe GmbH, Germany). Sequencing reactions were carried out using the PCR primers in ABI PRISM Big Dye Terminator Cycle v3.0 Sequencing Ready Reaction Kit (Applied Biosystems) according to the manufacturer's recommendations. The reaction was analysed on an ABI Prism 3100 Genetic Analyser (Applied Biosystems).

Sequence data were analysed using EditView 1.0.1 (http://www.appliedbiosystems.com). BLAST searches (ALTSCHUL et al. 1997) were performed with the analysed sequences in order to identify similar sequences for phylogenetic analysis. Thirty sequences were added from GenBank and aligned by hand with the LSU sequence of STE-U 5494 by inserting gaps using Sequence Alignment Editor v2.0 (RAMBAUT 2002). Thirty-five sequences were added from GenBank and manually aligned with the SSU sequence of STE-U 5494.

Phylogenetic analysis consisted of neighbor joining (NJ) analysis (with the Kimura 2-parameter substitution model) using PAUP* version 4.0b10 (SWOFFORD 2000). Alignment gaps were treated as missing data and all characters were unordered and of equal weight. Any ties were broken randomly when encountered. The robustness of the trees was evaluated by 1000 bootstrap replications (HILLIS & BULL 1993). Resulting trees were printed with TreeView Version 1.6.6 (PAGE 1996).

Results

Sequence and phylogenetic analyses

The large subunit sequence of CBS 110664 (= STE-U 5494) was deposited in GenBank (AY425026) and the alignment in TreeBASE (Study accession number = S933). After the introduction of gaps, the alignment included 561 nucleotide positions that were used in the phylogenetic analysis. The NJ tree that was obtained from the LSU sequence alignment and rooted to the members of Hypocreaceae (Hypocreales), *Hypocrea* and *Gliocladium,* is shown in Fig. 1. Three hypo-

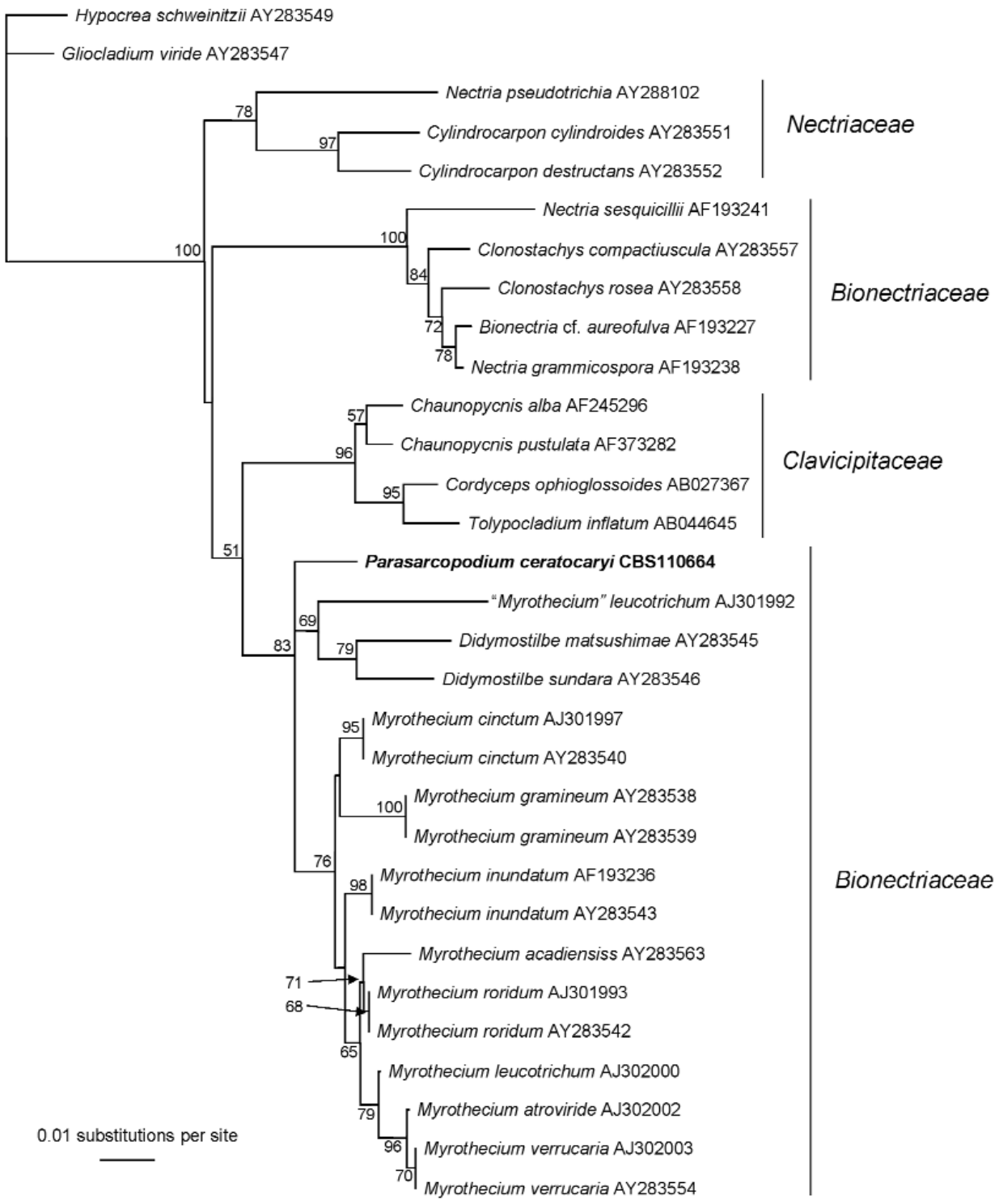


Fig. 1: Neighbor-joining tree obtained from LSU sequence data. Bootstrap supports from 1000 replicates are shown at the nodes. The tree was rooted to *Hypocrea schweinitzii* AY283549 and *Gliocladium viride* AY283547

crelean families are formed into four clades, namely Nectriaceae, Clavicipitaceae, Bionectriaceae-*Myrothecium and* Bionectriaceae-*Clonostachys.* CBS 110664 is placed in a Bionectriacea-*Myrothecium* clade as a sister taxon to subclades of *Myrothecium* and *Didymostilbe* Henn., with 83 % bootstrap support (Fig. 1).

To confirm the taxonomic placement of this isolate, the SSU and ITS sequences were also determined. The sequences were deposited in GenBank (AY344478, AY344479) and the small subunit sequence alignment in TreeBASE (Study accession number = S933). The sequence data set contained 36 sequences, including the two outgroups. After the intro-

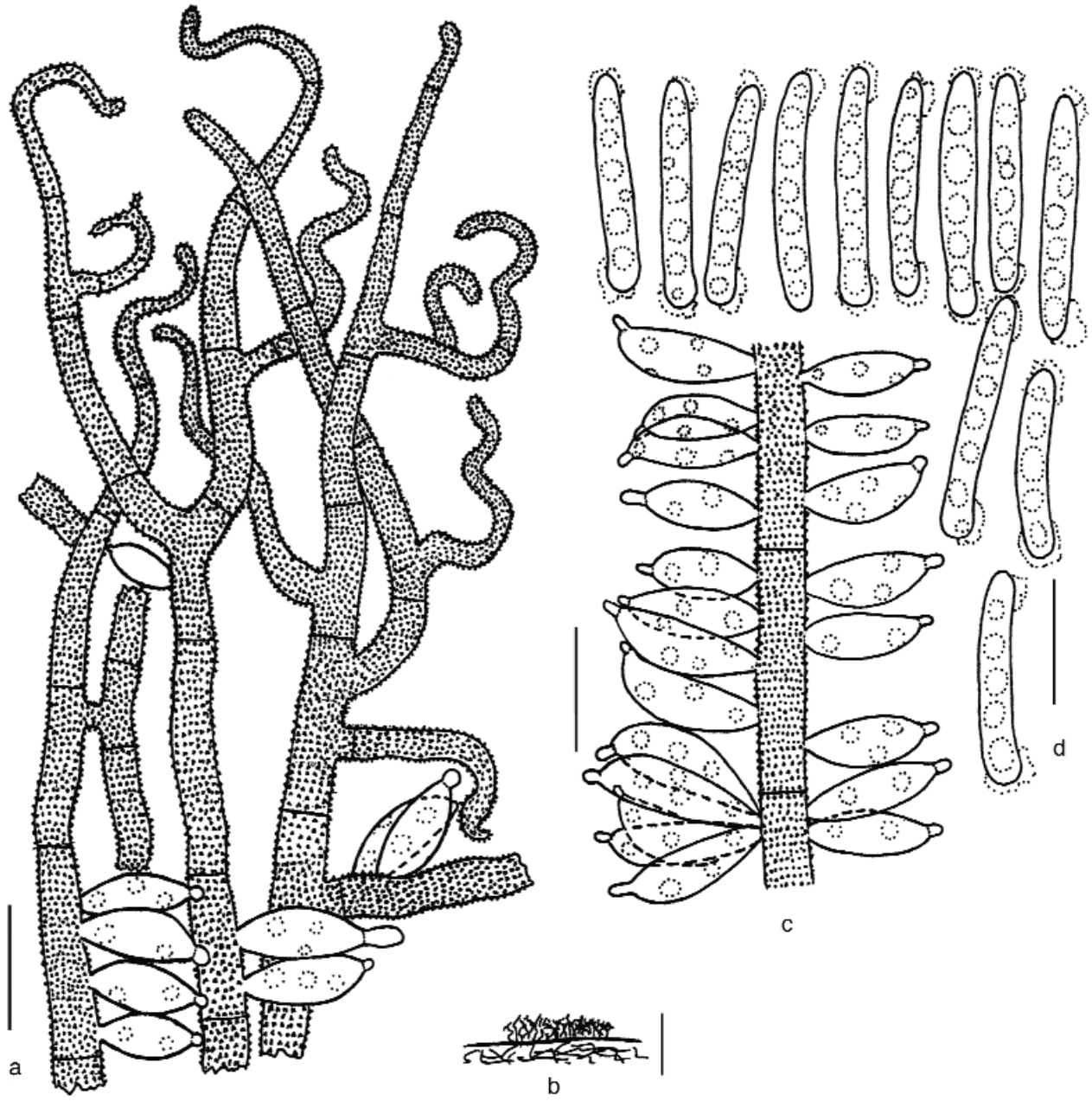


Fig. 2: *Parasarcopodium ceratocaryi* (holotype, PREM 57603). **a**. Conidiophore; **b**. Colony on the host surface: **c**. Phialides; **d**. Conidia. Bars: a, c, d = 10 μm; b = 10 mm

duction of gaps, the alignment included 794 nucleotide positions of which 98 characters were parsimony-informative. Of the remaining 696 characters, 591 characters were constant and 105 were parsimony-uninformative. Parsimony analysis of the alignment yielded only three equally parsimonious trees (TL = 357 steps, CI = 0.714, RI = 0.814, RC = 0.581) and placed CBS 110664 in the Hypocreales with 70 % bootstrap support.

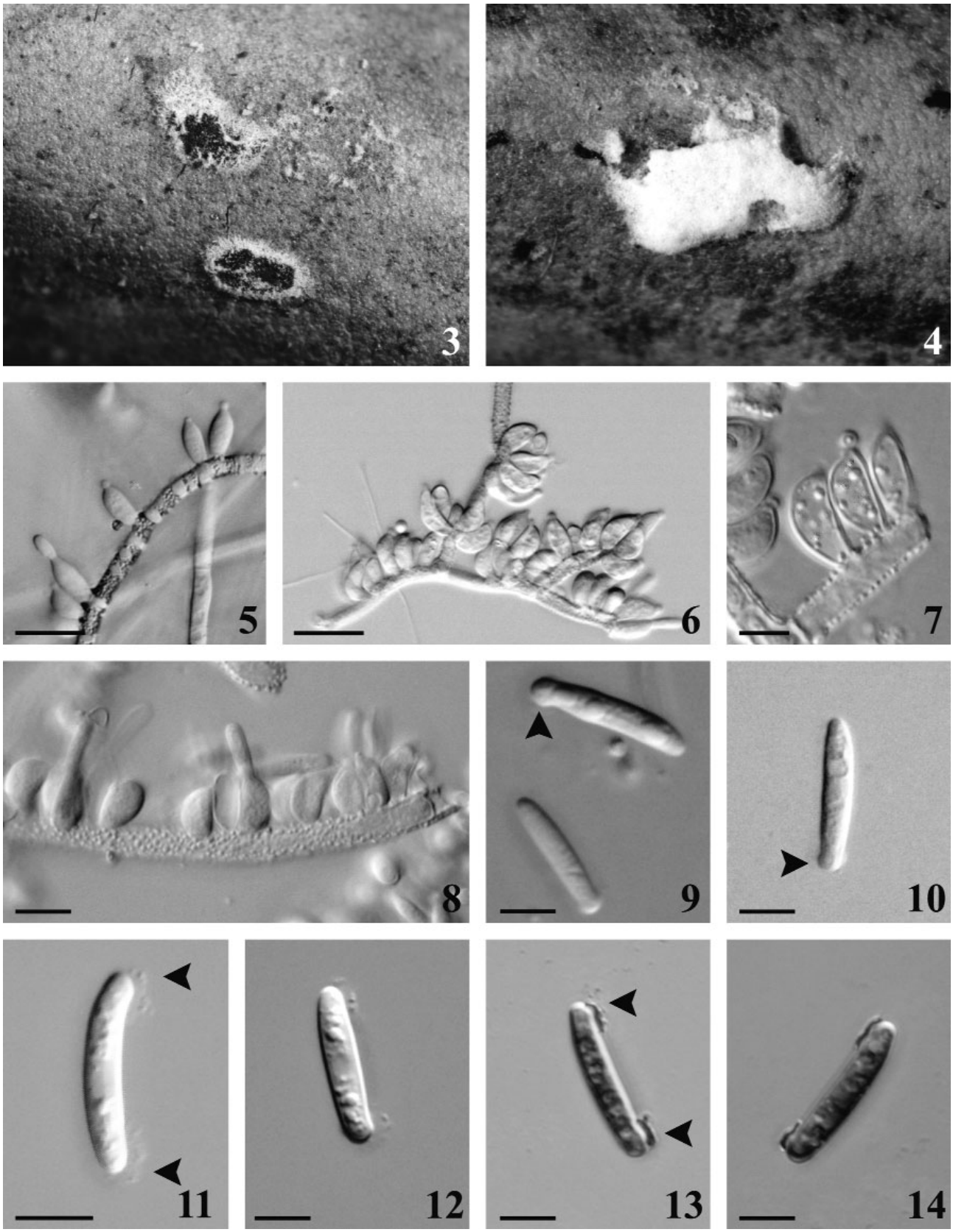
Taxonomic part

Parasarcopodium Melnik, S. Lee & Crous, **gen. nov.**

Coloniae in substrato effusae, sparsae, pilosae. Conidiophora macronematosa, simplicia, erecta, recta vel flexuosa, verruculosa, hyalina vel subhyalina, frequenter ramosa in parte superiore, in filamenta spiralia vel contorta exeuntia. Cellulae conidiogenae monophialidicae, plerumque e mediis conidiophoris oriundae, seriatae vel verticillatae, cylindrico-lageniformes vel oblonge ampulliformes. Conidia cylindrica, continua, appendicibus mucidis praedita, levia, hyalina vel dilute viridula.

Etymology: named for its resemblance to the genus *Sarcopodium*.

Typus: *Parasarcopodium ceratocaryi* Melnik, S. Lee & Crous.



Figs. 3–14: *Parasarcopodium ceratocaryi* (holotype, PREM 57603). **3**, **4**. Colony on the host surface. **5–8**. Phialides attached to conidiophores. **9**, **10**. Conidia with swollen bases (arrowheads). **11**, **12**. Conidia with H-type mucous appendages in water (arrowheads). **13**, **14**. Conidia with mucous appendages in Leifson's solution (arrowheads). Bars: 5, 6 = 10 µm; 7–14 = 5 µm

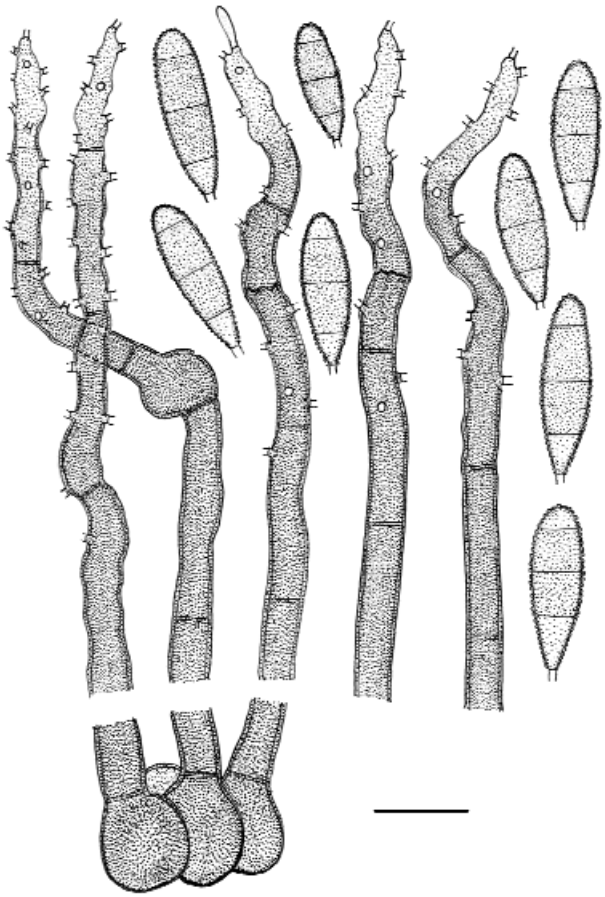


Fig. 15: *Rhexodenticula elegiae* (holotype, LE 212480). Conidiophores with denticulate conidiogenous cells and conidia. Bar = 10 µm

Colonies on the substratum effuse, scattered, hairy, white when young, at maturity with dark-green (black) conidial masses at the apex of, or just below the canopy of spiral hyphae. Mycelium superficial, partly immersed, composed of very pale brown, branched, septate, smooth hyphae. Conidiophores macronematous, mononematous, erect, straight or sometimes flexuous, verruculose, becoming warty with age, hyaline or subhyaline, septate, often branched in the upper region, with spiralling or twisted, gradually narrowing ends, sometimes with anastomoses in the lower region of conidiophores. Conidiogenous cells usually in the middle region of conidiophores or their branches; in rows or whorls, monophialidic, discrete, determinate, cylindro-lageniform or oblong-ampulliform, having no clearly visible collarette, usually slightly bent, smooth, guttulate, hyaline. Conidia cylindrical, aseptate, straight or slightly bent, with obtuse apical end and sometimes slightly swollen basal end, with amorphous mucoid appendages (type H; NAG RAJ 1993) at both ends, smooth, hyaline or with a faint greenish tinge, becoming dark green in mass.

Parasarcopodium ceratocaryi Melnik, S. Lee & Crous, **sp. nov.** Figs. 2-14

Coloniae in substrato 0.5–2 mm diam. Conidiophora ad 300 µm longa, ad basim 3–4 µm lata, ad 1–1.5 µm angustata prope apicem ramosissimum, nonnumque in parte inferiore anastomosantia. Cellulae conidiogenae phialides, 8–10 x 3.5–4 µm, apex latus 0.3–0.5 µm, ad 15 seriatae vel ad 8 verticillatae. Conidia cylindrica, continua, recta vel modice curvata, parte distali obtusa, ad basim nonnumquam modice inflata, utrinque appendice amorpho mucido praedita, (12) 14–18 (19.5) x (2) 2.5–3 µm.

Etymology: named after its host, *Ceratocaryum*.

Typus: Lectus in Africa meridionali, in Provincia Capensi occidentali, Jonkershoek Reservatum naturale, 33°57' S, 18°58' E, 500 m asl., in culmis emortuis *Ceratocaryi decipientis*, 15 Jul. 2001, S. Lee SL731, holotypus PREM 57603, isotypi LE 212441 et herb. CBS 6590, cultura ex-typo STE-U 5494, CBS 110664.

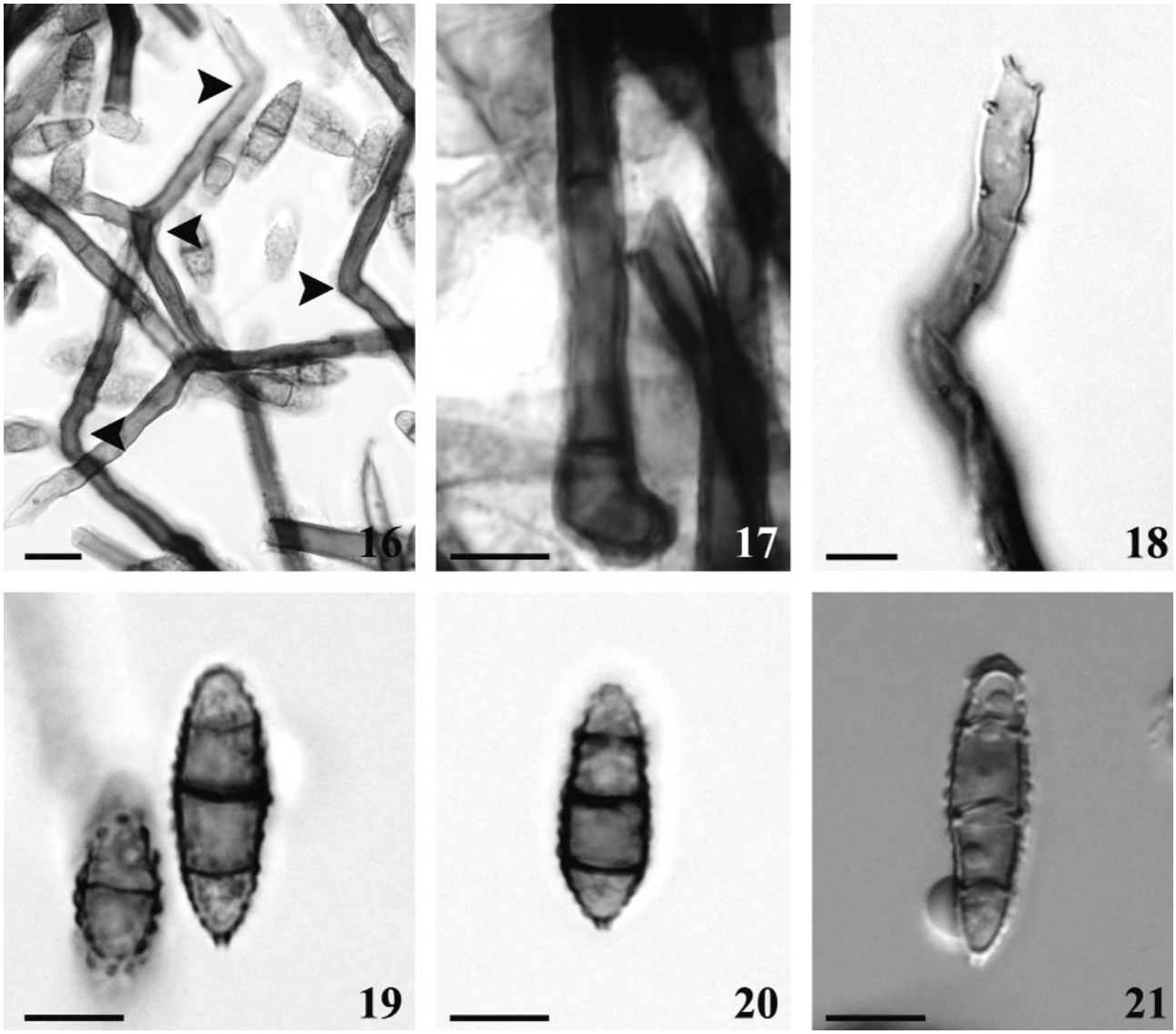
Colonies on the substratum 0.5–2 mm diam (Figs. 2-4). Conidiophores up to 300 µm long, 3–4 µm wide at the base, narrowing to 1–1.5 µm near the richly branched apex, sometimes with anastomoses in the lower part of the conidiophores (Fig. 2). Conidiogenous cells phialidic, 8–10 x 3.5–4 µm, 0.3–0.5 µm wide at the top, in rows (up to 15), or in whorls (up to 8) (Figs. 2, 5-8). Conidia cylindrical, aseptate, straight or slightly bent, with an obtuse apical end, and sometimes slightly swollen basal end, with amorphous mucoid appendages at both ends, (12) 14–18 (19.5) x (2) 2.5–3 µm (Figs. 2, 9-14). The amorphous mucoid appendages are more clearly visible in water than in Leifson's solution, in which they shrink and become suppressed.

Cultural characteristics: Colonies fertile on BLA after 10 d in the dark and on OA 10 d under alternate light. Colonies sterile after 10 d on OA in the dark and on CMA, PDA and BLA under alternate light. Colonies on all the media circular with entire margins, flat, with different coloration. Aerial mycelium superficial, sparse to moderately so. Colonies on CMA and BLA 50–53 mm diam in 7 d, hyaline, same in reverse. Colonies on PDA 54–59 mm diam in 7 d, under alternate light rosy buff (13''f) centre with a wide white periphery, primrose (23''b) in reverse, with zonation and in the dark primrose (23''b), same in reverse, without zonation. Colonies on OA under alternate light rosy vinaceous (7''d), rosy buff (13''f) in reverse and in the dark white, same in reverse.

Rhexodenticula elegiae Melnik, S. Lee & Crous, **sp. nov.** Figs. 15-21

Coloniae effusae, brunneae vel fuscae, pilosae. Conidiophora macronematosa, simplicia, singula vel fasciculata, nonnumquam sursum semel vel bis percurrenter proliferentia, erecta, levia, brunnea, ad 190 µm longa, 3–4 µm lata, 7–8 µm lata ad basim. Cellulae conidiogenae integratae, terminales, polyblasticae, denticulatae, denticuli cylindrici, 1 x 0.5 µm. Conidia solitaria, sicca, fusiformia, 3-septata, verrucosa, pallide brunnea, duabus cellulis centralibus fuscioribus, sursum rotundata, (14) 16–19 (21) x (4) 5 µm, ad basim margine 1 µm protrudente praedita.

Etymology: named after its host, *Elegia*.



Figs. 16–21: *Rhexodenticula elegiae* (holotype, LE 212480). **16**. Conidiophores showing strong geniculation (arrowheads). **17**. Swollen base of conidiophore. **18**. Denticulate conidiogenous cells. **19–21**. Fusiform conidia. Bars: 16, 17 = 10 µm; 18-21 = 5 µm

Typus: Lectus in Africa meridionali, in Provincia Capensi Occidentali, Helderberg Reservatum naturale, 34°1' S, 18°43' E, 800 m asl., in culmo emortuo *Elegiae capensis*, 13 Apr. 2002, una cum *Trichocladio macrosporo* P.M. Kirk, *Pseudospirope simplice* (Kunze : Fr.) M.B. Ellis, holotypus LE 212480, isotypus PREM 57604.

Colonies effuse, brown to dark brown, hairy. Mycelium partly immersed to superficial, composed of pale brown to brown, septate, branched hyphae. Conidiophores macronematous, mononematous, solitary or in more or less fasciculate groups, simple, sometimes with 1–2 percurrent proliferations in the upper part, erect, cylindrical, sometimes with nodose swellings towards the middle, straight or flexuous, with the upper part sometimes becoming strongly geniculate, septate, smooth, thick-walled, brown, somewhat paler and thin-walled towards the apex, up to 190 µm long, 3–4 µm wide, gradually narrowing up to 2 µm wide at the apical point, moderately swollen and 7–8 µm wide at the base, arising from a cluster of tightly-packed more or less globose, 8–12 (14) µm wide cells (Figs. 15-17). Conidiogenous cells integrated, terminal, polyblastic, denticulate, denticles numerous, located in the upper part of conidiophores, to 50 (90) µm from the apex; cylindrical, approx. 1 µm long, approx. 0.5 µm wide, thin-walled, cut off by a septum to form a separating cell, which fractures at the middle in a circumscissile fashion and remains as a persistent, peg-like extension (Figs 15, 18). Conidia solitary, dry, acropleurogenous, fusiform or broadly fusiform, 3-septate, densely covered with minute warts, pale brown, with the two middle cells slightly darker and longer than the polar cells (especially the apical one), rounded at the apex, basal cells pointed, bearing a narrow basal marginal frill approx. 1 µm

long derived from the upper portion of the rhexolytically split separating cells, (14) 16–19 (21) x (4) 5 µm (Figs 15, 19-21).

Discussion

Parasarcopodium ceratocaryi

Parasarcopodium resembles species of *Sarcopodium* in having effuse, hairy colonies with long, setiform, often flexuous, verruculose conidiophores (SUTTON 1981). *Sarcopodium* produces similar structures in sporodochial conidiomata, which are verruculose, straight or circinate and irregularly to verticillately or penicillately branched. These structures are, however, not conidiophores but setae (SUTTON 1981). *Atrosetaphiale flagelliformis* Matsush. (MATSUSHIMA 1995) and *Chaetopsina intermedia* R.F. Castañeda & W.B. Kendr. (CASTAÑEDA & KENDRICK 1991, MATSUSHIMA 1995) are similar to *Parasarcopodium* in having pigmented, phialidic conidiogenous cells that are lageniform or oblong-ampulliform, located on setiform, pigmented conidiophores. However, *A. flagelliformis* differs from *Parasarcopodium ceratocaryi* having filiform, aseptate conidia and *C. intermedia* by having scolecosporous, falcate or fusiform, 0(1)-septate conidia. *Chaetopsina mellitolunae* Crous & Seifert also has ampulliform phialides, but these are formed singly or in pairs on branches of slightly pigmented, setiform conidiophores with cylindrical conidia (CROUS, SEIFERT & CASTAÑEDA 1996). Conidia of *P. ceratocaryi* sometimes exhibit a swollen base, which is similar to that of *Vermiculariopsiella immersa* (Desm.) Bender (NAWAWI, KITHUBUTHEEN & SUTTON 1990). However, in the latter fungus, the conidial bases are obtuse to rounded, with a pointed to subacute protuberance on one side. Moreover, conidia of *P. ceratocaryi* have amorphous, mucoid appendages at both ends, whereas conidia of *V. immersa* and other species of *Vermiculariopsiella* lack appendages.

A teleomorphic connection of *Parasarcopodium* to the Bionectriaceae (Hypocreales) was established by phylogenetic analysis based on the LSU sequence data (Fig. 1) and confirmed by the SSU and ITS sequence data (data deposited in TreeBASE). The components of the Bionectriaceae-*Myrothecium* clade, *Parasarcopodium, Myrothecium* and *Didymostibe,* are linked by their green coloured conidial masses, which is a characteristic of anamorphic Bionectriaceae differentiating it from Nectriaceae (SCHROERS 2001). In the clade, *Parasarcopodium* is distinctly separated from both *Myrothecium* and *Didymostilbe* and related to them as a sister taxon. *Didymostilbe* which is the only genus in the clade having a known teleomorph, *Peethambara* Subram. & D.J. Bhat., differs from *Parasarcopodium* in having 2-septate, hyaline conidia produced on phialides in synnematous, penicilliate conidiophores (CARMICHAEL et al. 1980). TULLOCH (1972) circumscribed *Myrothecium* as having phialidic conidiogenous cells, repeatedly branched conidiophores and the presence of marginal hyphae, setae and different conidiomatal forms. With the introduction of a new species, *M. acadiense* Seifert & G. Sampson, which has percurrently proliferating conidiogenous cells sometimes resulting in dense annellations, SEIFERT, LOUIS-SEIZE & SAMPSON (2003) not only allowed some flexibility in accommodating heterogeneous conidiogenesis but also justified the inclusion of various conidiomatal forms in the genus *Myrothecium.* Aside from molecular evidence, a number of morphological characteristics differentiate *Parasarcopodium* from *Myrothecium*: stroma-like aggregation of cells is absent in *Parasarcopodium*, but always present in *Myrothecium*, slimy conidial appendages are present at both ends of conidia of *Parasarcopodium* whereas only one apical appendage or none are observed in *Myrothecium*, and a hymenium-like arrangement of conidiogenous cells and penicillate conidiophores is present in *Myrothecium*, but absent in *Parasarcopodium.*

Parasarcopodium can be distinguished from other known anamorphs of *Bionectria* in not-having rather well-branched conidiophores (SCHROERS 2001). However, in the sense of condiogenesis, *Parasarcopodium,* which produces conidia from well-defined phialides, fits into other anamorph genera in the Hypocreales which have conidia produced enteroblastically from phialidic conidiophores (SAMUELS & SEIFERT 1987) although few exceptions have to be considered (ROGERSON & SAMUELS 1993, SEIFERT, LOUIS-SEIZE & SAMPSON 2003).

Conidial dimensions of *P. ceratocaryi* on the artificial media were varied: conidia on BLA in the dark were (10) 13–16 (18) x 2–3 µm and on OA under alternate light were (10) 11–13 (14) x 2–3 µm.

Rhexodenticula elegiae

The second fungus newly described from restios, *Rhexodenticula elegiae*, is morphologically similar to the type species of *Rhexodenticula* W.A. Baker & Morgan-Jones, *R. cylindrospora* (R.F. Castañeda, Saikawa & Hennebert) W.A. Baker & Morgan-Jones in conidial dimensions (13–21 x 4–5 µm) (BAKER, PARTRIDGE & MORGAN-JONES 2001). The two species, however, differ in conidial shape and septation: conidia of *R. cylindrospora* are cylindrical, (1) 2–3-septate, but in *R. elegiae* conidia are fusiform to broadly fusiform, never cylindrical, and always 3-septate. Conidiophores of *R. cylindrospora* sometimes become slightly geniculate in the distal part and percurrent proliferation has not been observed, while they are strongly geniculate in *R. elegiae* and sometimes have 1–2 percurrent proliferations. Denticles of *R. cylindrospora* are located in the very upper part of conidiophores (BAKER, PARTRIDGE & MORGAN-JONES 2001), while those of *R. elegiae* are located along the length, 50 (90) µm from the apex of the conidiophores, which are up to 190 µm in length. *Pyricularia fusispora* (Matsush.) Zucconi, Onofri & Persiani (1984) (≡ *Vakrabeeja fusispora* Matsush.) is another close species to *R. elegiae* (MATSUSHIMA 1971, 1975, ZUCCONI, ONOFRI & PERSIANI 1984). However, *R. elegiae* differs from *P. fusispora* in smaller spore dimensions than those of *P. fusispora* (26–34

4.8–6 µm), having no constriction at each conidial septum as in *P. fusispora*, having a rounded apical cell in contrast to the pointed ones in *P. fusispora*, and strongly geniculate conidiophores (MATSUSHIMA 1971, 1975, MOUCHACCA 1990, ZUCCONI, ONOFRI & PERSIANI 1984).

Trichocladium macrosporum, which represents a new record for South Africa, was originally described on dead wood of an unknown tree from Devon in the UK (KIRK 1981), and subsequently recorded in New Zealand on rotten wood and decorticated branches of *Cyathodes fasciculata* (G. Forst.) Allan, *Elaeocarpus dentatus* Vahl, and *Rhipogonum scandens* Forst. (HUGHES 1989). The other hyphomycete present on this specimen, *Pseudospiropes simplex*, is rather cosmopolitan, and is commonly associated with litter of numerous hosts.

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