Neocosmospora lechatii (*Nectriaceae*) a new species from French Guiana

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Abstract: A description of *Neocosmospora lechatii* sp. nov. is presented, based on two collections on dead wood of unknown origin collected in French Guiana. The specimens were obtained in culture and six loci were amplified, sequenced, and compared with the currently known phylogenetic breadth of *Neocosmospora*. The new species is described, illustrated, and morphological comparisons are made to its closest relatives.
Keywords: *Ascomycota*, fusarioid, *Hypocreales*, new species, taxonomy.

Résumé : une description de *Neocosmospora lechatii* sp. nov. est présentée, à partir de deux récoltes sur bois mort d'origine inconnue, effectuées en Guyane française. Les spécimens ont été obtenus en culture et six loci ont été amplifiés, séquencés et comparés à l'étendue phylogénétique connue des *Neocosmospora*. La nouvelle espèce est décrite, illustrée et des comparaisons morphologiques sont effectuées avec les plus proches parents.
Mots-clés : *Ascomycota*, fusarioïde, *Hypocreales*, nouvelle espèce, taxinomie.

Introduction

The genus *Neocosmospora* E.F. Sm. (*Nectriaceae*), which is allied to *Fusarium* Link (Lombard *et al.*, 2015; Crous *et al.*, 2021) is the second largest hypocrealean genus of fusarioid fungi, presently encompassing more than 100 accepted species (www.fusarium.org; Crous *et al.*, 2021). *Neocosmospora* spp. colonise a vast diversity of substrates and geographical ranges. They are associated with many different ecological niches, including devastating plant pathogens and opportunistic human pathogenic species, also including endophytes, saprophytes, and mycotoxin producers (Sandoval-Denis *et al.*, 2019).

Species of *Neocosmospora* are characterised by conspicuous dark orange to red perithecia, with two-layered, often coarsely warted perithecial walls that change colour in both 3% KOH and lactic acid; and ornamented, commonly striated, (0–)1-septate, yellow-brown ascospores (Rossman *et al.*, 1999; Sandoval-Denis *et al.*, 2019). The asexual morphs of *Neocosmospora* are commonly encountered in nature, often being characterised by robust fusarioid conidia, formed either on sporodochia or on tall, solitary aerial conidiophores, the latter typically showing long, tapered phialidic conidiogenous cells.

During a survey of microfungi in French Guiana an interesting fusarioid fungus was found that morphologically resembled *Neocosmospora*, producing typical red, warted perithecia, and large 1-sepate, coarsely striate ascospores. The fungus was isolated and preliminarily identified as a *Neocosmospora* sp. Based on its morphological characters, and molecular phylogenetic analyses, the specimens are determined to represent a novel species, described here as *Neocosmospora lechatii* in honour of its collector.

Materials and methods

The specimens were examined and single-spore cultures established using methods described elsewhere (Lechat & Fournier, 2015). Living cultures were sent to the Westerdijk Fungal Biodiversity Institute (Utrecht, The Netherlands) for confirmation of its identity and permanent storage. Fungal cultures were maintained in Oatmeal Agar (OA, recipe in Crous *et al.*, 2019) plates and slants. Fungal growth rates and pigment production were studied on Potato Dextrose Agar (PDA, recipe in Crous *et al.*, 2019), additional colony features were recorded on OA and Synthetic Nutrient-poor Agar (SNA; Nirenberg, 1976). Colour notations follow those of Rayner (1970). Micro-morphological features were studied as outlined in Crous *et al.* (2021) from 7–10-d-old cultures grown on SNA and Carnation Leaf Agar (CLA; Fisher *et al.*, 1982), incubated at 24 °C, under a 12 h near-UV light/dark cycle. Unless otherwise defined, measurements and photomicrographs were recorded using sterile water as mounting medium with a Nikon Eclipse 80i compound microscope with Differential Interference Contrast (DIC) optics and a Nikon AZ100 dissecting microscope, both equipped with a Nikon DS-Ri2 high-definition colour digital camera and the Nikon software NIS-elements D v. 5.11.02. Additional images of the fungus growing on its natural substrate were obtained from the records of the late C. Lechat and incorporated on the morphological analyses and photo plates.

For DNA isolation isolates were grown for 7 d on Malt Extract Agar (MEA, recipe in Crous *et al.*, 2019), incubated as described above. Mycelium was scrapped from the surface of the colony using a sterile scalpel and processed using the Wizard® Genomic DNA purification Kit (Promega Corporation, Madison, WI, USA), according to the manufacturer's instructions. Fragments of six DNA loci i.e., partial calmodulin gene (*cal*), the internal transcribed spacer regions with intervening 5.8S nrRNA gene (ITS), a fragment of the 28S large subunit of the nrDNA (LSU), partial DNA-directed RNA polymerase II gene largest subunit (*rpb1*), partial DNA-directed RNA polymerase II gene second largest subunit (*rpb2*) and partial translation elongation factor 1-alpha gene (*tef1*) were amplified using conditions and primer pairs as indicated elsewhere (Crous *et al.*, 2021; Guarnaccia *et al.*, 2021). Bidirectional sequences were generated using the same primer pairs as for PCR amplification on an Applied Biosystems 3730xl DNA analyser (Life Technologies, Carlsbad, California, USA). Sequences were assembled using Geneious Prime v. 2022.0.1 (Biomatters Ltd., Auckland, New Zealand). Gene sequence datasets of all six loci included in this study, representing the known species diversity of *Neocosmospora*, were downloaded from GenBank, and single-gene alignments were built using MAFFT v. 7.450 (Katoh *et al.*, 2013) as implemented in Geneious Prime, and manually checked using MEGA v. 6 (Tamura *et al.*, 2007). Single-gene phylogenies were carried out using Maximum Likelihood (ML) in IQ-TREE v. 2.1.2 (Minh *et al.*, 2020) and Bayesian Inference (BI) using MrBayes v. 3.2.7a (Ronquist & Huelsenbeck, 2003) as indicated in Crous *et al.* (2021). The phylogenetic results were visually compared for topological conflicts, and a 6-gene multi-locus phylogenetic analysis was carried out as specified above. Alignments, phylogenetic trees and accession data of strains included in the analyses were deposited in Figshare.com (project number 149332, doi: 10.6084/m9.figshare.21195601.v1 and 10.6084/m9.figshare.21176314.v1). The taxonomic novelty was deposited in MycoBank, and DNA sequence data generated in this study in GenBank.

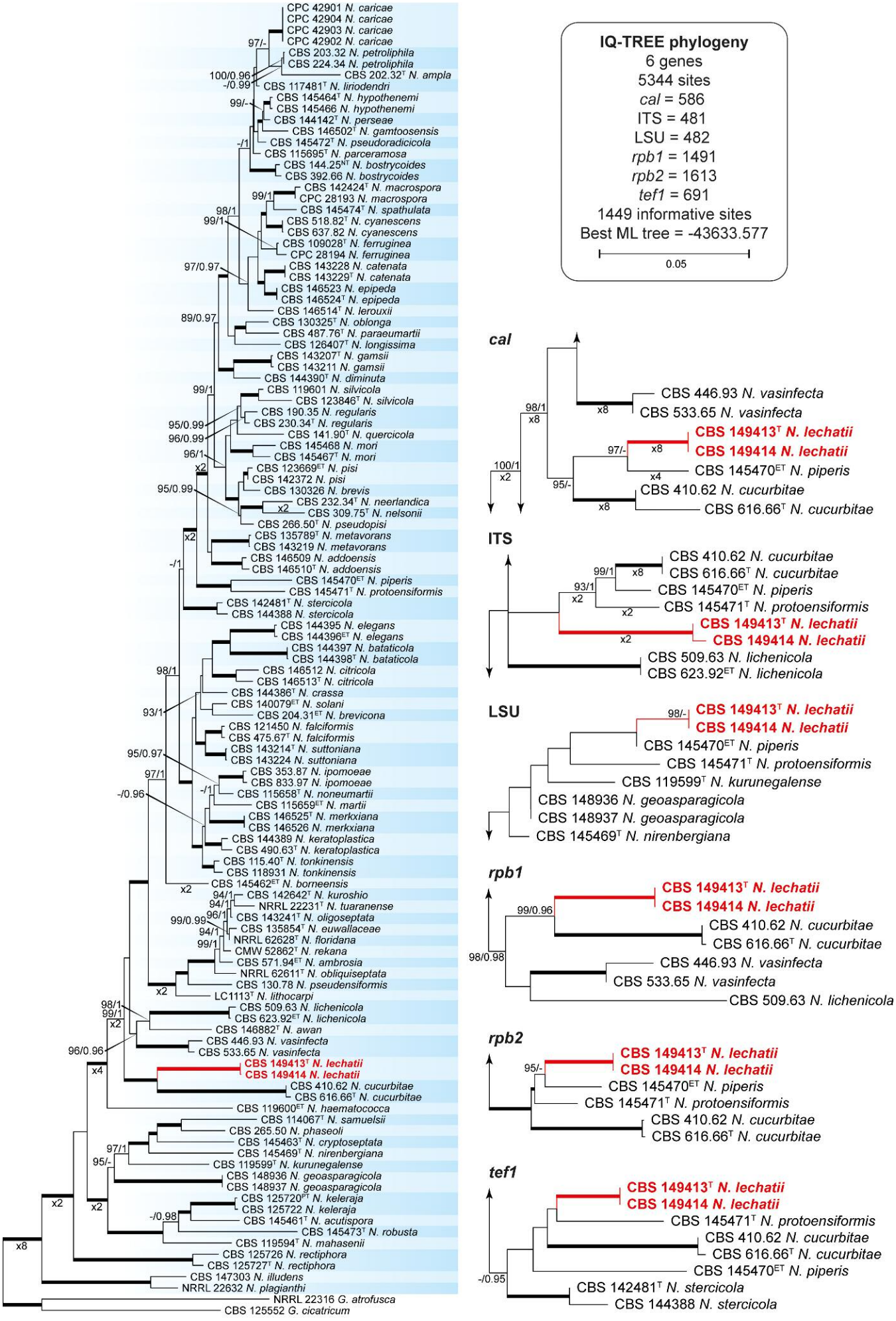
IQ-TREE phylogeny
6 genes
5344 sites
cal = 586
ITS = 481
LSU = 482
rpb1 = 1491
rpb2 = 1613
tef1 = 691
1449 informative sites
Best ML tree = -43633.577
0.05
CPC 42901 N. caricae
CPC 42904 N. caricae
CPC 42903 N. caricae
CPC 42902 N. caricae
CBS 203.32 N. petroliphila
CBS 224.34 N. petroliphila
CBS 202.32T N. ampla
CBS 117481T N. liriodendri
CBS 145464T N. hypothenemi
CBS 145466 N. hypothenemi
CBS 144142T N. perseae
CBS 146502T N. gamtoosensis
CBS 145472T N. pseudoradicicola
CBS 115695T N. parceramosa
CBS 144.25NT N. bostrycoides
CBS 392.66 N. bostrycoides
CBS 142424T N. macrospora
CPC 28193 N. macrospora
CBS 145474T N. spathulata
CBS 518.82T N. cyanescens
CBS 637.82 N. cyanescens
CBS 109028T N. ferruginea
CPC 28194 N. ferruginea
CBS 143228 N. catenata
CBS 143229T N. catenata
CBS 146523 N. epipeda
CBS 146524T N. epipeda
CBS 146514T N. lerouxii
CBS 130325T N. oblonga
CBS 487.76T N. paraeumartii
CBS 126407T N. longissima
CBS 143207T N. gamsii
CBS 143211 N. gamsii
CBS 144390T N. diminuta
CBS 119601 N. silvicola
CBS 123846T N. silvicola
CBS 190.35 N. regularis
CBS 230.34T N. regularis
CBS 141.90T N. quercicola
CBS 145468 N. mori
CBS 145467T N. mori
CBS 123669ET N. pisi
CBS 142372 N. pisi
CBS 130326 N. brevis
CBS 232.34T N. neerlandica
CBS 309.75T N. nelsonii
CBS 266.50T N. pseudopisi
CBS 135789T N. metavorans
CBS 143219 N. metavorans
CBS 146509 N. addoensis
CBS 146510T N. addoensis
CBS 145470ET N. piperis
CBS 145471T N. protoensiformis
CBS 142481T N. stercicola
CBS 144388 N. stercicola
CBS 144395 N. elegans
CBS 144396ET N. elegans
CBS 144397 N. bataticola
CBS 144398T N. bataticola
CBS 146512 N. citricola
CBS 146513T N. citricola
CBS 144386T N. crassa
CBS 140079ET N. solani
CBS 204.31ET N. brevicona
CBS 121450 N. falciformis
CBS 475.67T N. falciformis
CBS 143214T N. suttoniana
CBS 143224 N. suttoniana
CBS 353.87 N. ipomoeae
CBS 833.97 N. ipomoeae
CBS 115658T N. noneumartii
CBS 115659ET N. martii
CBS 146525T N. merkxiana
CBS 146526 N. merkxiana
CBS 144389 N. keratoplastica
CBS 490.63T N. keratoplastica
CBS 115.40T N. tonkinensis
CBS 118931 N. tonkinensis
CBS 145462ET N. borneensis
CBS 142642T N. kuroshio
NRRL 22231T N. tuaranense
CBS 143241T N. oligoseptata
CBS 135854T N. euwallaceae
NRRL 62628T N. floridana
CMW 52862T N. rekana
CBS 571.94ET N. ambrosia
NRRL 62611T N. obliquiseptata
CBS 130.78 N. pseudensiformis
LC1113T N. lithocarpi
CBS 509.63 N. lichenicola
CBS 623.92ET N. lichenicola
CBS 146882T N. awan
CBS 446.93 N. vasinfecta
CBS 533.65 N. vasinfecta
CBS 149413T N. lechatii
CBS 149414 N. lechatii
CBS 410.62 N. cucurbitae
CBS 616.66T N. cucurbitae
CBS 119600ET N. haematococca
CBS 114067T N. samuelsii
CBS 265.50 N. phaseoli
CBS 145463T N. cryptoseptata
CBS 145469T N. nirenbergiana
CBS 119599T N. kurunegalense
CBS 148936 N. geoasparagicola
CBS 148937 N. geoasparagicola
CBS 125720PT N. keleraja
CBS 125722 N. keleraja
CBS 145461T N. acutispora
CBS 145473T N. robusta
CBS 119594T N. mahasenii
CBS 125726 N. rectiphora
CBS 125727T N. rectiphora
CBS 147303 N. illudens
NRRL 22632 N. plagianthi
NRRL 22316 G. atrofusca
CBS 125552 G. cicatricum
cal
CBS 446.93 N. vasinfecta
CBS 533.65 N. vasinfecta
CBS 149413T N. lechatii
CBS 149414 N. lechatii
CBS 145470ET N. piperis
CBS 410.62 N. cucurbitae
CBS 616.66T N. cucurbitae
ITS
CBS 410.62 N. cucurbitae
CBS 616.66T N. cucurbitae
CBS 145470ET N. piperis
CBS 145471T N. protoensiformis
CBS 149413T N. lechatii
CBS 149414 N. lechatii
CBS 509.63 N. lichenicola
CBS 623.92ET N. lichenicola
LSU
CBS 149413T N. lechatii
CBS 149414 N. lechatii
CBS 145470ET N. piperis
CBS 145471T N. protoensiformis
CBS 119599T N. kurunegalense
CBS 148936 N. geoasparagicola
CBS 148937 N. geoasparagicola
CBS 145469T N. nirenbergiana
rpb1
CBS 149413T N. lechatii
CBS 149414 N. lechatii
CBS 410.62 N. cucurbitae
CBS 616.66T N. cucurbitae
CBS 446.93 N. vasinfecta
CBS 533.65 N. vasinfecta
CBS 509.63 N. lichenicola
rpb2
CBS 149413T N. lechatii
CBS 149414 N. lechatii
CBS 145470ET N. piperis
CBS 145471T N. protoensiformis
CBS 410.62 N. cucurbitae
CBS 616.66T N. cucurbitae
tef1
CBS 149413T N. lechatii
CBS 149414 N. lechatii
CBS 145471T N. protoensiformis
CBS 410.62 N. cucurbitae
CBS 616.66T N. cucurbitae
CBS 145470ET N. piperis
CBS 142481T N. stercicola
CBS 144388 N. stercicola

Fig. 1 (previous page) – Left: IQ-TREE phylogram obtained from the combined *cal*, ITS, LSU, *rpb1*, *rpb2* and *tef1* partial sequences of representative *Neocosmospora* spp.; species clades are indicated with colour boxes. Alignment basic statistics and tree scale are indicated inside the box. Right: partial view of relevant clades obtained by the single locus phylogenies (full trees available at Figshare.com under project number 149332 (doi: 10.6084/m9.figshare.21195601.v1 and 10.6084/m9.figshare.21176314.v1). Numbers at the nodes correspond to IQ-TREE bootstrap (ML-BS) values ≥ 95 % followed by Bayesian posterior probabilities (BI-PP) ≥ 0.95. Bold branches indicate full support (ML-BS = 100, BI-PP = 1). The trees are rooted to *Geejayessia atrofusca* NRRL 22316 and *G. cicatricum* CBS 125552. The scale bar indicates the expected number of nucleotide substitutions per site. The new species proposed here is indicated in red font. Ex-epitype, ex-neotype, ex-paratype and, and ex-type strains are indicated with superscript ET, NT, PT and T, respectively.

Results

The phylogenetic analysis included 5344 sites from six loci (*cal* 586, ITS 481, LSU 482, *rpb1* 1491, *rpb2* 1613, and *tef1* 691) of which 3478 were invariable (*cal* 350, ITS 312, LSU 419, *rpb1* 980, *rpb2* 1046, and *tef1* 371), and 1449 were informative (*cal* 180, ITS 128, LSU 37, *rpb1* 402, *rpb2* 459, and *tef1* 243). Evolutionary models for each data partition as calculated for ML were TNe+I+G4 for *cal* and LSU, TIM2e+R3 for ITS, TIM3e+I+G4 for *rpb1* and *rpb2*, and SYM+R4 for *tef1*; while GTR+I+G was selected for all loci under BI. The ML best tree (log-likelihood -43633.557) was found after 176 iterations. The BI lasted for 3.27 M generations and recovered 6542 trees from which 4908 were included in the final analyses. The phylogeny included sequences from 117 strains, representing 79 known *Neocosmospora* spp., two novel isolates (CBS 149413 and CBS 149414) obtained in culture from specimens collected in French Guiana, and two outgroup taxa (*Geejayessia atrofusca* NRRL 22316 and *G. cicatricum* CBS 125552). The results from ML and BI were identical, hence only the ML topology is shown in Fig. 1, with both ML bootstrap (ML-BS) and BI posterior probability (BI-PP) values added at the nodes.

The combined phylogeny resolved 80 species-level clades in *Neocosmospora* (known species published with two or less loci, and phylogenetic species yet not formally described were excluded from the analyses). Isolates CBS 149413 and CBS 149414 were resolved as a well-delimited, fully supported (ML-BS = 100, BI-PP = 1) clade, related but phylogenetically distinct to *Neocosmospora cucurbitae* (p-distances: 0.05 for the combined dataset, *rpb2*, and *tef1*; ITS 0.09, *cal* 0.07, *rpb1* 0.04, and LSU 0.03). Single-gene phylogenies confirmed the previous results; strains CBS 149413 and CBS 149414 were resolved as a distinct, partially (LSU) to fully supported (*cal*, ITS, *rpb1*, *rpb2* and *tef1*) clade with every locus tested. This novel clade is therefore described below as the novel species, *Neocosmospora lechatii*.

Taxonomy

Neocosmospora lechatii Sand.-Den. & Crous, *sp. nov*. Figs. 2–4. MycoBank: MB 845723

Diagnosis: Differs from all known *Neocosmospora* spp. by forming two types of sporodochia; and from *N. acutispora* and *N. samuelsii* by the presence of microconidia and a sexual morph. Differs from *N. cucurbitae* and *N. mori* by its homothallic mating behaviour, shorter, falcate aerial macroconidia, and its wider, robust, predominantly 7-septate sporodochial macroconidia.

Holotype: French Guiana, Saül, Gros Arbres trail, on unidentified dead wood, 26 March 2021, *leg.* C. Lechat (holotype designated here CBS H-25085), ex-type culture CBS 149413 = CLLG21062 = CPC 42648. GenBank accession numbers: *cal* = OP481878, ITS = OP497971, LSU = OP497975, *rpb1* = OP481880, *rpb2* = OP481882, and *tef1* = OP481884.

Etymology: In honour of the late French mycologist Christian Lechat (17 March 1952 – 7 Jan. 2022), who made a significant contribution to the systematics of hypocrealean fungi.

Perithecia superficial, non-stromatic, solitary or in small groups, dark orange to red, globose to broadly subglobose, 363–644 µm diam., warted, dark red in 3% KOH, yellow in 100% lactic acid. **Perithecial wall** of two regions: outer region pigmented, composed of thick-walled subglobose to angular cells; inner region hyaline, composed of flattened cells, compacted, and oriented parallel to surface of perithecial wall; apex composed of vertically elongated, thin-walled cells. **Asci** cylindrical to clavate, (104–)116–146(–153) × 11–12.5(–13.5) µm (av. 131 × 12.2 µm), apex simple, 8-spored, ascospores uniseriate. **Ascospores** ellipsoid, (13–)14–17(–20) × (6–)7.5–10 µm (av. 15.6 × 8.3 µm), 1-septate, hyaline, becoming golden-brown at maturity, coarsely striate. **Conidiophores** abundantly formed on aerial mycelium or in sporodochia. Aerial conidiophores erect or prostrate, borne on the agar substrate and aerial mycelium, 42–165 µm tall, often simple, or branched laterally and sympodially, bearing terminal single phialides; aerial conidiogenous cells monophialidic, subulate to subcylindrical, smooth- and thin-walled, 18.5–71 × 2.5–5 µm, with short, flared apical collarettes, and often conspicuous periclinal thickening. **Aerial conidia** of two types: i) microconidia ovoid to ellipsoid, smooth- and thin-walled, often with a narrow, flattened base, 0(–1)-septate, 6–13.5(–25.5) × (3–)4–6 µm (av. 10 × 4.2 µm); ii) macroconidia falcate to fusoid, gently dorsiventrally curved or almost straight, robust, apical cell blunt, basal cell obtuse, poorly- to well-developed foot-shaped, 2–4(–5)-septate, predominantly 3-septate, 2-septate conidia: (24.5–)27.5–39 × (4.5–)5–6 µm (av. 32.7 × 5.6 µm); 3-septate conidia: (26–)27.5–38(–40) × (4.5–)5.5–6 µm (av. 32.9 × 5.5 µm); 4-septate conidia: (42.5–)43–48.5(–50.5) × 4.5–6 µm (av. 46.7 × 5.4 µm); 5-septate conidia: 50.1 × 5.9 µm (only one element observed); overall: (24–)28.5–45(–50) × 4.5–6 µm (av. 36.5 × 5.5 µm), borne at the tip of monophialides and accumulating on false-heads. **Sporodochia** produced abundantly on the surface of carnation leaves and less commonly on the agar surface, of two types: i) microsporodochia pale luteous to pale green. Microsporodochial conidiophores 32–77 µm tall, laterally, and verticillately branched bearing terminal phialides; microsporodochial conidiogenous cells monophialidic, subulate to subcylindrical, (11–)17–27.5(–33) × 2.5–4 µm, smooth and thin-walled, with conspicuous periclinal thickening and a short apical collarette. Microsporodochial conidia morphologically indistinguishable from aerial microconidia. ii) macrosporodochia pale luteous to amber. Macrosporodochial conidiophores 30–54 µm tall, laterally, verticillately, and irregularly branched bearing terminal single or paired phialides; macrosporodochial conidiogenous cells monophialidic, doliiform to subcylindrical, (11.5–)14–20(–24) × 3.5–5.5 µm, smooth and thin-walled, often proliferating percurrently, periclinal thickening absent or conspicuous, short, flared collarette often visible. Macrosporodochial conidia falcate, gently dorsiventrally curved, robust, apical cell blunt to slightly papillate and curved, basal cell well-developed, foot-shaped, 5–9-septate, predominantly 7-septate, hyaline, smooth- and thick-walled; 5-septate conidia: (46.5–)55–73.5 × 5.5–6.5 µm (av. 64.1 × 5.9 µm); 6-septate conidia: (65–)67.5–76(–81.5) × 5.5–7 µm (av. 71.7 × 6.2 µm); 7-septate conidia: (68.5–)73–82.5(–88) × 6–7 µm (av. 77.6 × 6.3 µm); 8-septate conidia: (70–)72–84.5(–92) × 6–7 µm (av. 78 × 6.3 µm); 9-septate conidia: (83–)84–91(–95) × 6–7 µm (av. 87.5 × 6.6 µm); overall: (46.5–)69–84(–95) × 5.5–7 µm (av. 76.6 × 6.3 µm). **Chlamydospores** subspherical to spherical, smooth- and thin-walled, 5–10.5 µm diam, hyaline, formed intercalary or terminally on hyphae and conidia, single or in groups.

Cultural characteristics: Colonies at 25 °C for 7 days covering an entire 9-cm-diam. Petri dish on all media tested: On PDA, luteous to

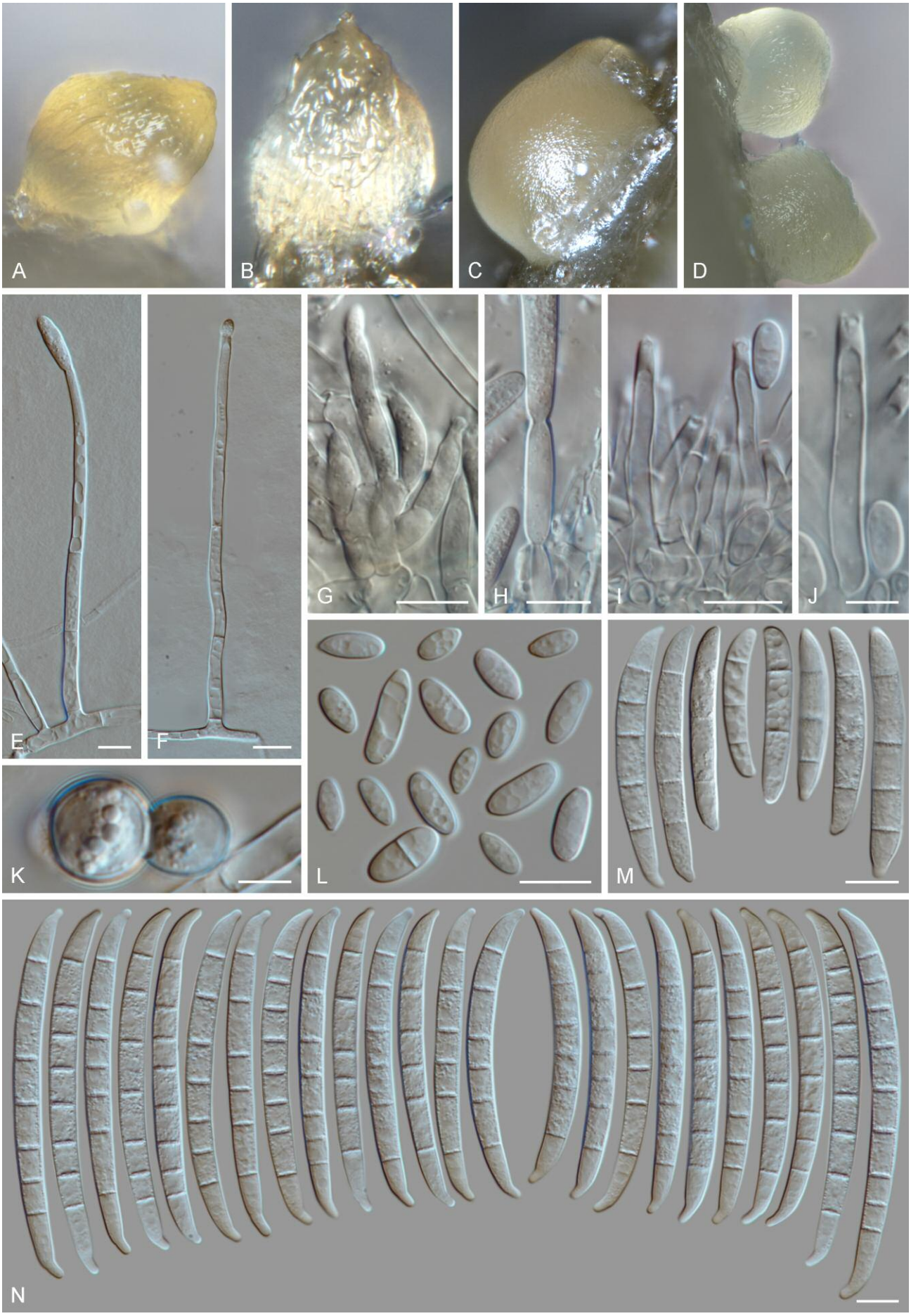

Fig. 2 – A–N: *Neocosmospora lechatii* sp. nov. (CBS 149413 ex-type), asexual morphology *in vitro*. A–D: sporodochia produced on the surface of carnation leaves; A, B: macrosporodochia; C, D: microsporodochia; E, F: aerial conidiophores and conidiogenous cells; G, H: macrosporodochial conidiophores and conidiogenous cells; I, J: microsporodochial conidiophores and conidiogenous cells; K: chlamydospores; L: microconidia; M: aerial macroconidia; N: sporodochial macroconidia. Scale bars: J, K = 5 µm, all others = 10 µm.

umber with white concentric patches of aerial mycelium, umber at centre, flat, felty to cottony, margin entire to slightly filamentous; reverse umber, ochreous to umber at centre, without diffusible pigments. On OA, luteous to umber with white concentric patches of aerial mycelium, umber at centre, flat, felty to cottony, margin entire to slightly filamentous; reverse umber, ochreous to umber at centre, without diffusible pigments. On SNA, white to pale buff with white concentric rings of short aerial mycelium, flat, felty to cottony; reverse white, without diffusible pigments.

Additional specimen examined: French Guiana, Saül, Gros Arbres trail, on unidentified dead wood, 27 March 2021, *leg*. C. Lechat, CBS H-25086, cultures CBS 149414 = CLLG21075 = CPC 42649. GenBank accession numbers: *cal* = OP481879, ITS = OP497970, LSU = OP497974, *rpb1* = OP481881, *rpb2* = OP481883, and *tef1* = OP481885.

Known distribution: French Guiana.

Discussion: The novel species *Neocosmospora lechatii* was originally assigned to this genus by its collector (C. Lechat) based on its morphological features, characterised by the production of abundant, typically warted, bright red perithecia, coarsely striated 1-septate ascospores and a fusarioid asexual morph producing micro- and macroconidia on long aerial conidiophores. These initial observations were here confirmed, and proved these specimens to belong to an undescribed, novel South American species of *Neocosmospora*.

Morphological variation of asexual characters is known to occur in *Neocosmospora*, e.g., the asymmetrically clavate macroconidia shown by insect symbiont species of the Ambrosia clade of *Neocosmospora* (Freeman *et al.*, 2013), the cylindrical conidia of *N. tonkinensis* (Bugnicourt, 1939; Sandoval-Denis *et al.*, 2019); and the reduced, acre-

Fig. 3 – A–L: *Neocosmospora lechatii* sp. nov. (CBS 149413), sexual morphology *in vitro*. A–C: perithecia; D–F: detail of perithecial wall (D in water, E in lactic acid, and F in 3% KOH); G, H: asci; I–L: ascospores. Scale bars = 10 µm.

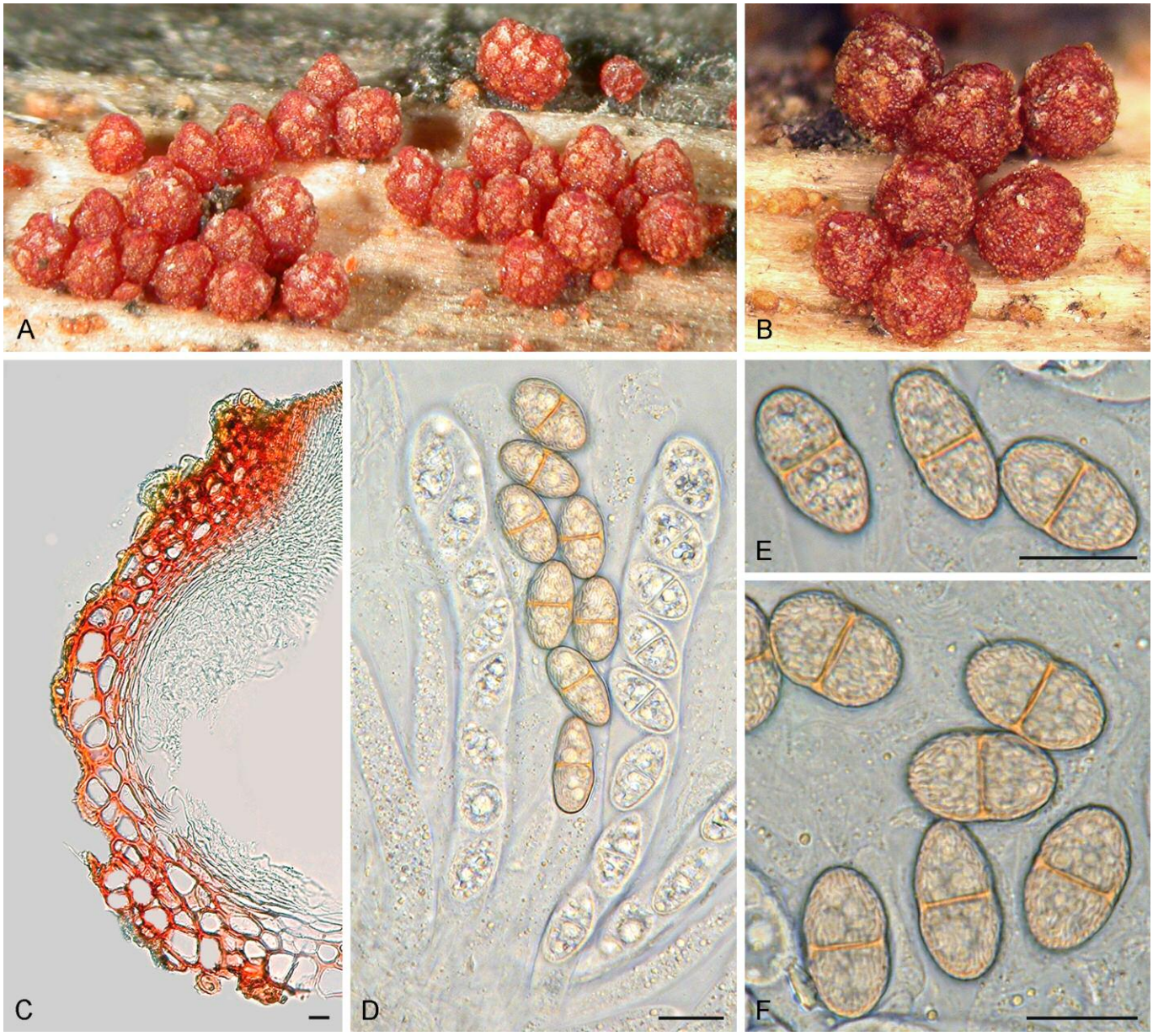

Fig. 4 – A–F: *Neocosmospora lechatii* sp. nov. (CLLG21075), sexual morphology on natural host. A, B: perithecia; C: detail of perithecial wall; D: asci; E, F: ascospores. Scale bars C = 20 µm, all others = 10 µm. All images in this figure by Christian Lechat.

monium-like conidial structures often found in *N. falciformis*, and common in *N. vasinfecta* (Smith, 1899; Summerbell & Schroers, 2002; Sandoval-Denis *et al.*, 2019). Similarly, species of *Neocosmospora* have been described forming a combination of sporodochial macroconidia mixed with reduced sporodochial conidial forms in the same sporodochium (Aoki *et al.*, 2005, 2012). *Neocosmospora lechatii* is unique from all currently known species of *Neocosmospora* by the presence of two distinct sporodochial types, here termed micro- and macrosporodochia. Typical falcate, multiseptate macroconidia were observed from the latter; microsporodochia on the other hand, although it retains the basic sporodochial organization known in fusarioid fungi, was seen to produce only microconidia from short subulate phialides, more reminiscent of the conidiogenous cells typically observed in tall aerial conidiophores.

Macroconidial dimensions of the novel species are in the size and septation range reported for *Neocosmospora cucurbitae*, its closest phylogenetic and morphological relative, being also similar to those of *N. acutispora*, *N. mori* and *N. samuelsii* (Sandoval-Denis *et al.*, 2019). However, compared with the phylogeny, all the above-mentioned species are clearly separated genealogically. Additionally, every locus commonly used for identification of fusarioid fungi (*cal*, ITS, LSU, *rpb1*, *rpb2*, and *tef1*) showed enough resolution to identify *N. lechatii*, even by using rDNA sequences alone. Morphologically, *N. lechatii* can be distinguished from *N. acutispora* and *N. samuelsii* by the absence of microconidia, and larger, more robust aerial macroconidia in the latter two species. *Neocosmospora lechatii* and *N. mori* have similar sized sporodochial conidia; however, those of *N. lechatii* are predominantly 7-septate (vs. 5-septate in *N. mori*) and besides being more commonly septate, macroconidia of *N. lechatii* have a more pronounced dorsal curvature and are overall wider and more robust than those of *N. mori*. Although morphologically very similar to *N. cucurbitae*, apart from the presence of two distinct sporodochial types, a number of other features differentiate *N. lechatii* from the former taxon, including the shorter and less septate aerial microconidia (0(–1)-septate and up to 25.5 µm long in *N. lechatii* vs. up to 3-septate and 42 µm long in *N. cucurbitae*). Furthermore, its short falcate aerial macroconidia (vs. often cylindrical in *N. cucurbitae*) and the predominantly 7-septate, wider, robust, sporodochial macroconidia with well-developed foot-cells (vs. predominantly 5-septate in *N. cucurbitae*) also distinguish these taxa.

Both *N. cucurbitae* and *N. mori* have been recorded producing sexual morphs. The first under the names *Fusarium* (*Hypomyces*) *solani* f. sp. *cucurbitae* race 1, Mating Population (MP) I, or *Nectria haematococca* MPI (Matuo & Snyder, 1973; Mehl & Epstein, 2007), and the second taxon also reported as *Fusarium* (*Hypomyces*) *solani* f. sp. *mori* MPIII, or *Nectria haematococca* MPIII (Matuo & Snyder, 1973;

O'Donnell, 2000). However, sexual morphs of these two species could not be obtained in culture for further comparisons with *N. lechatii*. Nevertheless, significant differences in mating behaviour are already evident between these taxa. While both *N. cucurbitae* and *N. mori* are heterothallic species, which prevented obtaining the sexual morphs for comparison here (Matuo & Snyder, 1973), *N. lechatii* is clearly homothallic, producing abundant perithecia with mature ascospores based on single spore cultures.

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References

Aoki T., O'Donnell K. & Scandiani M.M. 2005. — Sudden death syndrome of soybean in South America is caused by four species of *Fusarium*: *Fusarium brasiliense* sp. nov., *F. cuneirostrum* sp. nov., *F. tucumaniae*, and *F. virguliforme*. *Mycoscience*, 46: 162–183. doi: 10.1007/S10267-005-0235-Y

Aoki T., Tanaka F., Suga H., Hyakumachi M., Scandiani M.M. & O'Donnell K. 2012. — *Fusarium azukicola* sp. nov., an exotic azuki bean root-rot pathogen in Hokkaido, Japan. *Mycologia*, 104: 1068–1084. doi: 10.3852/11-303

Bugnicourt F. 1939. — *Les Fusarium et Cylindrocarpon de l'Indochine*. Encyclopédie Mycologique, 11. Paris, Lechevallier, 206 pp.

Crous P.W., Lombard L., Sandoval-Denis M., *et al.* 2021. — *Fusarium*: more than a node or a foot-shaped basal cell. *Studies in Mycology*, 98: 1–184. doi: 10.1016/j.simyco.2021.100116

Crous P.W., Verkley G.J.M., Groenewald J.Z. & Houbraken J. 2019. — *Fungal Biodiversity*. Westerdijk Laboratory Manual Series, 1. Utrecht, Westerdijk Fungal Biodiversity Institute, 425 pp.

Fisher N.L., Burgess L.W., Toussoun T.A. & Nelson P.E. 1982. — Carnation leaves as a substrate and for preserving cultures of *Fusarium* species. *Phytopathology*, 72: 151–153.

Freeman S., Sharon M., Maymon M., Mendel Z., Protasov A., Aoki T., Eskalen A. & O'Donnell K. 2013. — *Fusarium euwallaceae* sp. nov. – a symbiotic fungus of *Euwallacea* sp., an invasive ambrosia beetle in Israel and California. *Mycologia*, 105: 1595–1606. doi: 10.3852/13-066

Guarnaccia V., Van Niekerk J., Crous P.W. & Sandoval-Denis M. 2021. — *Neocosmospora* spp. associated with dry root rot of citrus in South Africa. *Phytopathologia Mediterranea*, 60: 79–100. doi: 10.36253/phyto-12183

Katoh K. & Standley M. 2013 — MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution*, 30: 772–780. doi: 10.1093/molbev/mst010

Lechat C. & Fournier C. 2015. — *Protocreopsis korfii* (*Hypocreales*, *Bionectriaceae*), a new species from Martinique (French West Indies). *Ascomycete.org*, 7: 307–310. doi: 10.25664/art-0152

Lombard L., van der Merwe N.A., Groenewald J.Z. & Crous P.W. 2015 — Generic concepts in *Nectriaceae*. *Studies in Mycology*, 80: 189–245. doi: 10.1016/j.simyco.2014.12.002

Matuo T. & Snyder W. 1973. — Use of morphology and mating populations in the identification of formae speciales in *Fusarium solani*. *Phytopathology*, 63: 562–565. doi: 10.1094/Phyto-63-562

Mehl H.L. & Epstein L. 2007. — Identification of *Fusarium solani* f. sp. *cucurbitae* race 1 and race 2 with PCR and production of disease-free pumpkin seeds. *Plant Disease*, 91: 1288–1292. doi: 10.1094/pdis-91-10-1288

Minh Q., Schmidt H.A., Chernomor O., Schrempf D., Woodhams M.D., Haeseler A. (von) & Lanfear R. 2020. — IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. *Molecular Biology and Evolution*, 37: 1530–1534. doi: 10.1093/molbev/msaa015

Nirenberg H.I. 1976. — Untersuchungen über die morphologische und biologische Differenzierung in der *Fusarium*-Sektion *Liseola*. *Mitteilungen der Biologischen Bundesanstalt für Land- und Forstwirtschaft Berlin-Dahlem*, 169: 1–117.

O'Donnell K. 2000. — Molecular phylogeny of the *Nectria haematococca-Fusarium solani* species complex. *Mycologia*, 92: 919–938. doi: 10.1080/00275514.2000.12061237

Rayner R.W. 1970. — *A mycological colour chart*. CMI and British Mycological Society, Kew, Surrey, 34 pp.

Ronquist F. & Huelsenbeck J.P. 2003. — MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics*, 19: 1572–1574. doi: 10.1093/bioinformatics/btg180

Rossman A.Y., Samuels G.J., Rogerson C.T. & Lowen R. 1999. — Genera of *Bionectriaceae*, *Hypocreaceae* and *Nectriaceae* (*Hypocreales*, Ascomycetes). *Studies in Mycology*, 42: 1–248.

Sandoval-Denis M., Lombard L. & Crous P.W. 2019. — Back to the roots: a reappraisal of *Neocosmospora*. *Persoonia*, 43: 90–185. doi: 10.3767/persoonia.2019.43.04

Smith E.F. 1899. — Wilt disease of cotton, watermelon and cowpea (*Neocosmospora* nov. gen.). *Bulletin, Division of Vegetable Physiology and Pathology, US Department of Agriculture*, 17: 1–73.

Summerbell R.C. & Schroers H.J. 2002. — Analysis of phylogenetic relationship of *Cylindrocarpon lichenicola* and *Acremonium falciforme* to the *Fusarium solani* species complex and a review of similarities in the spectrum of opportunistic infections caused by these fungi. *Journal of Clinical Microbiology*, 40: 2866–2875. doi: 10.1128/JCM.40.8.2866-2875.2002

Tamura K., Stecher G., Peterson D., Filipski A. & Kumar S. 2013. — MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution*, 30: 2725–2729. doi: 10.1093/molbev/mst197

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