
Triseptosporium fallopiae

Fungal Planet 1910 MB 861174

Triseptosporium Crous & Hülsewig, ***gen. nov.***

Etymology: Named after the its 3-septate conidia.

Classification: *Nectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, unbranched. *Conidiogenous cells* terminal, hyaline, smooth, subcylindrical; apex phialidic with flared collarette. *Conidia* aggregating in mucoid mass, slightly curved, (1–)3-septate, fusoid, apex subobtuse, base truncate, widest in middle, tapering towards both ends.

Type species: *Triseptosporium fallopiae* Crous & Hülsewig

MB 861175

Triseptosporium fallopiae Crous & Hülsewig, ***sp. nov.***

Etymology: Named after the host genus it was isolated from, *Fallopia*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* solitary, erect, flexuous, subcylindrical, unbranched, up to 250 µm tall, 4–5 µm diam. *Conidiogenous cells* terminal, hyaline, smooth, subcylindrical, 90–120 × 4 µm; apex phialidic with flared collarette. *Conidia* aggregating in mucoid mass, slightly curved, (1–)3-septate, fusoid, apex subobtuse, base truncate, 3–4 µm diam., widest in middle, tapering towards both ends, (30–)34–38(–40) × (7–)8 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and folded surface, reaching 20 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse pale luteous.

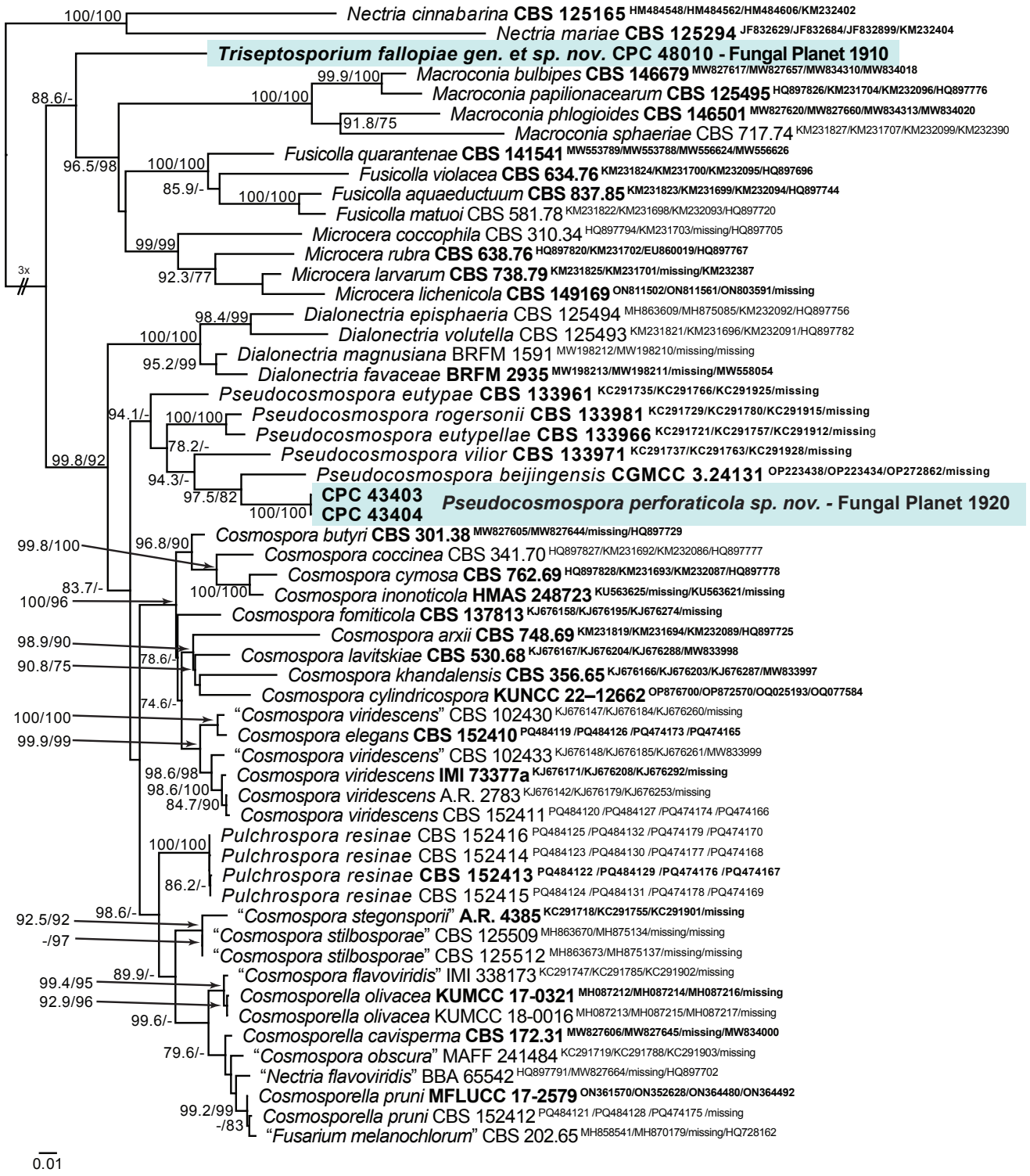
Typus: **Germany**, North Rhine-Westphalia, Witten, Recreation area Hohenstein, on rotten stems of on *Fallopia japonica* (*Polygonaceae*), 24 Feb. 2024, *T. Hülsewig*, Thorben 1195 = HPC 4416 (**holotype** CBS H-25799; culture ex-type CPC 48010 = CBS 153466; ITS, LSU, *rpb2* (first and second part), *tef1* (first part) and *tub2* sequences GenBank PX640125.1, PX640148.1, PX620759.1, PX583880.1 and PX583898.1).

Notes: The *Cosmospora* generic complex contains several nectrioid genera with acremonium-like or fusarioid asexual morphs, namely *Cosmospora*, *Cosmosporella*, *Dialonectria*, *Pseudocosmospora*, and *Pulchrospora* (Czachura & Janik 2025). *Triseptosporium* (presently only known from its asexual morph), adds yet another genus to this complex, characterised by acremonium-like conidiophores, but with fusoid, (1–)3-septate conidia having subobtuse apices and truncate bases.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cosmospora berkeleyana* [strain CBS 236.70, GenBank MH859582.1; Identities = 510/533 (96 %), eight gaps (1 %)], *Pseudocosmospora vilior* [strain CIRM-BRFM 3052, GenBank PV109356.1; Identities = 506/529 (96 %), five gaps (0 %)], and *Cosmosporella pruni* [strain MFLUCC 17-2579, GenBank NR_189388.1; Identities = 505/528 (96 %), five gaps (0 %)]. Closest hits using the **LSU** sequence are *Pulchrospora resinae* [as *Hypocreales* sp. PC-2024a; strain CBS 152415, GenBank PQ484131.1; Identities = 854/866 (99 %), no gaps], *Cosmospora berkeleyana* [strain CBS 121.70, GenBank MH871292.1; Identities = 857/870 (99 %), no gaps], and *Cosmospora coccinea* [strain CBS 342.70, GenBank MH871455.1; Identities = 857/870 (99 %), no gaps]. Closest hits using the ***rpb2*** (first part) sequence had distant similarity to *Cosmospora aquatica* [voucher MFLU 15-0072, GenBank MN194020.1; Identities = 671/777 (86 %), nine gaps (1 %)], *Cosmospora viridescens* [strain CBS 102433, GenBank HQ897712.1; Identities = 669/777 (86 %), nine gaps (1 %)], and *Cosmospora butyri* [strain IRAN 4322C, GenBank PP187011.1; Identities = 666/778 (86 %), 11 gaps (1 %)]. Closest hits using the ***rpb2*** (second part) sequence had distant similarity to *Cosmospora rishbethii* [strain CBS 496.67, GenBank HQ897714.1; Identities = 724/827 (88 %), two gaps (0 %)], *Cosmospora flavoviridis* [strain BBA 65542, GenBank HQ897702.1; Identities = 720/826 (87 %), two gaps (0 %)], and *Cosmosporella cavisperma* [strain BBA 64137, GenBank HQ897762.1; Identities = 718/826 (87 %), two gaps (0 %)]. Closest hits using the ***tef1*** (first part) sequence had distant similarity to *Cosmosporella pruni* [as *Cosmosporella* sp. RHP-2022a; voucher MFLU 17-0974, GenBank ON364467.1; Identities = 408/545 (75 %), 35 gaps (6 %)], *Fusicolla quarantenae* [strain 111JB, GenBank MW556625.1; Identities = 374/490 (76 %), 39 gaps (7 %)], and *Fusicolla violacea* [strain CBS 634.76, GenBank KM231956.1; Identities = 400/532 (75 %), 36 gaps (6 %)]. Closest hits using the ***tub2*** sequence had distant similarity to *Cosmospora lavitskiae* [strain 7976, GenBank KU563620.1; Identities = 475/549 (87 %), 21 gaps (3 %)], *Cosmospora viridescens* [strain 1802, GenBank PQ456771.1; Identities = 476/553 (86 %), 20 gaps (3 %)], and *Cosmospora cylindricospora* [voucher HKAS 125785, GenBank OQ025193.1; Identities = 505/587 (86 %), 21 gaps (3 %)].

Supplementary material: doi: 10.6084/m9.figshare.30529955 (alignment and phylogenetic tree).

Colour illustrations: Collection site in Germany. Sporulation on SNA; conidiogenous cells; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Nectriaceae* ITS-LSU-*tub2*-*rpb2* nucleotide alignment (Czachura & Janik 2025). Values > 74 % from the SH-aLRT test and bootstrap support values > 74 % from 1000 non-parametric bootstrap replicates are shown at the nodes. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript, following table in Czachura & Janik 2025) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Nectria cinnabarina* (CBS 125165; GenBank HM484548/HM484562/HM484606/KM232402) and *Nectria mariae* (CBS 125294; GenBank JF832629/JF832684/JF832899/KM232404) and the novelties described here are highlighted with coloured blocks and **bold** font. Two branches were shortened to facilitate layout. Alignment statistics: 57 strains including the outgroup; 3079 characters including alignment gaps analysed: 1356 distinct patterns, 790 parsimony-informative, 261 singleton sites, 2028 constant sites. The best-fit models identified in IQ-TREE using the TESTNEW option were: ITS (1–622): TIM2e+I+R2; LSU (623–1493): TIM+F+I+R3; *tub2* (1494–2206): TNe+I+G4; *rpb2* (2207–3079): TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site.

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