Collariella hilkhuysenii
Collariella hilkhuijsenii X. Wei Wang, sp. nov.

Etymology. Named for Joost Hilkhuijsen, who collected this specimen. This species was discovered during a Citizen Science project in the Netherlands, 'Wereldfaam, een schimmel met je eigen naam', describing novel fungal species isolated from Dutch soils.

Classification — Chaetomiaceae, Sordariaceae, Sordariomycetes.

Ascomata superficial, pale mouse grey in reflected light owing to ascomatal hairs, obovate to turbinate or ellipsoidal, 250–350 μm high (including the collar), 190–300 μm diam, with a wide ostiole around a darkened collar, 25–50 μm high and 110–180 μm wide. Ascomatal wall brown, textura globulosa to angularis in surface view, and often with cells arranged in a petaloid pattern around the bases of lateral hairs. Terminal hairs arising from the apical collar, conspicuously rough, dark brown, septe, erect in the lower part, 3–5.5 μm near the base, spirally coiled in the upper part. Lateral hairs seta-like, tapering and fading towards the tips. Asci fasciculate, clavate or fusiform, spore-bearing part 20–29 × 7–10.5 μm, stalks 12–25 μm long, with 8 irregularly-arranged ascospores, evanescent. Ascospores oliveaceous when mature, limoniform, bilaterally flattened, (5.5–)6–6.5(–7) × 5–6 × 4–4.5(–5) μm, with an apical germ pore. Asexual morph unknown.

Culture characteristics — Colonies on OA with an entire edge, about 32–38 mm diam in 7 d at 25 °C, forming pale mouse grey ascomata, without aerial hypha, without coloured exudates, reverse uncoloured. Colonies on CMA similar to those on OA, but forming denser ascomata, and some ascomata developed slower. Colonies on MEA with an entire edge, membranous, about 35–41 mm diam in 7 d at 25 °C, forming dense and pale mouse grey to mouse grey ascomata and radiating furrows in the central part, with seven or more concentric rings around the mass of ascomata which are formed by immersed hyphae, without aerial hyphae; without coloured exudates, reverse uncoloured. Colonies on PCA transparent due to very spare mycelia, with an entire edge, about 31–37 mm diam in 7 d at 25 °C, forming relatively sparse pale mouse grey asco-

Consensus phylogram resulting from a Bayesian analysis of partial sequences of rpb2 region from representative strains of Collariella species. The sequences were aligned using MAFFT v. 7 (Katoh & Standley 2013) and included 852 nucleotides. GTR+I+G was used as the best nucleotide substitution model and the phylogenetic tree was generated under MrBayes v. 3.2.1 (Ronquist & Huelsenbeck 2003). Chaetomium globosum (Chaetomiaceae, Sordariaceae) was used as the outgroup taxon.