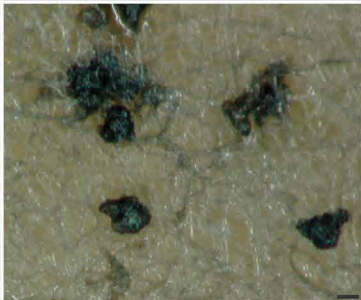


Stagonosporopsis vannaccii



Fungal Planet 1033 – 18 December 2019

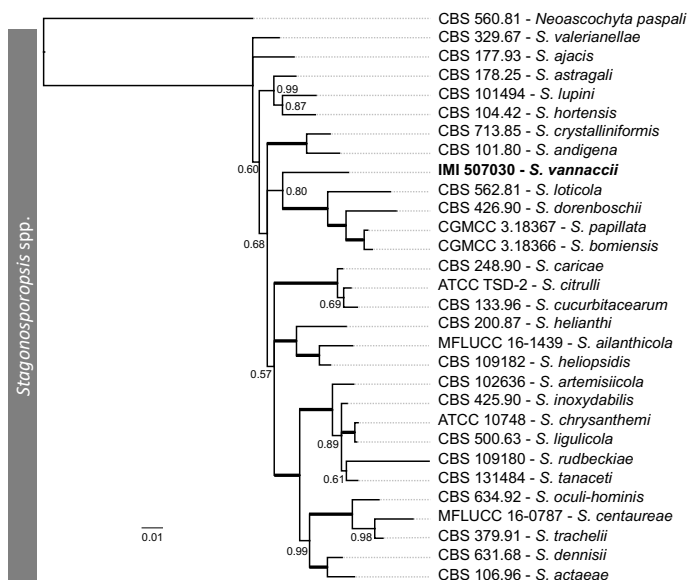
***Stagonosporopsis vannaccii* Baroncelli, Cafà, Castro, Bouffleur & Massola, sp. nov.**

Etymology. Named in honour of the Italian mycologist Giovanni Vannacci, for his important contributions to the study of fungi.

Classification — *Didymellaceae*, *Pleosporales*, *Dothideo-myces*.

Hyphae hyaline, smooth, thin-walled, septate, 1.3–4 µm wide onto potato-dextrose-agar (PDA). **Conidiomata** pycnidial, black, unilocular, globose to subglobose, solitary or confluent, glabrous, superficial in the culture medium, 152.1–198.7 µm diam. **Ostiole** single and central, slightly papillate to papillate and occasionally rostrate. **Pycnidial wall** pseudoparenchymatous. **Conidiogenous cells** phialidic, hyaline, smooth, ampulliform, 6.7–13.3 × 2–2.7 µm. **Conidia** hyaline, ellipsoidal to cylindrical with rounded ends, aseptate, with two polar guttules after ageing, 3.4–6.4 × 2–2.7 µm. **Appressoria** sepia, obovoid to ovoid, truncate, entire or undulate edges, 2.9–6.6 × 3.2–9.1 µm. **Sexual morph** unknown.

Culture characteristics — On PDA: colonies circular, flattened, reaching 64–66 mm diam after 6 d under 12 h photoperiod and 25 °C, margin entire, aerial mycelium sparse. Colonies surface with concentric circles fusco-black, violet-slate, vinaceous-grey and pale vinaceous-grey (from centre to edge), reverse fusco-black according to Rayner's colour chart (Rayner 1970). On synthetic nutrient-poor agar (SNA): colonies circular, flattened, reaching 65–67 mm diam after 6 d under 12 h photoperiod and 25 °C, margin entire, aerial mycelium sparse, surface grey-sepia in the centre and pale mouse grey at the edge, reverse grey-sepia. No pycnidia were observed on SNA.



Colour illustrations. Piracicaba, Brazil, soybean plants. Colony on PDA and SNA after 6 d at 25 ± 1 °C; conidiomata pycnidia under the dissecting microscope; conidiogenous cells; conidia and appressoria. Scale bars = 10 µm.

Typus. BRAZIL, S13°18'46.7" W56°02'33.4" (Sinop, MT), from pod of soybean (*Glycine max*), cultivar M8766RR, 2016, F. Rogério (holotype IMI 507030, cultures ex-type LFN0148 = IMI 507030, ITS, LSU, *tub2*, *tef1*, *act*, *rpb2* sequences GenBank MK519453, MK519452, MK519454, MK519455, MN534890 and MN534891, MycoBank MB831973).

Notes — *Stagonosporopsis vannaccii* was isolated from anthracnose symptoms on pods of soybean in central Brazil in 2017. Pathogenicity was proved through seed inoculation in accordance with Costa et al. (2003) on different soybean cultivars. Inoculated seeds of BMX Bónus 8579 IPRO and M6210 IPRO cultivars had the germination reduced by 50 % and 70 %, respectively, and gave rise to plantlets with damping-off symptoms. Based on the similarity of symptoms, it is very likely that the disease caused by *S. vannaccii* in soybean is being confused with damping-off caused by *Colletotrichum* spp. in the field. Further studies should show the real importance of this disease to the soybean crop. *Stagonosporopsis* spp. has been reported causing diseases in other cultures in Brazil, such as *S. caricae* in *Carica papaya* (Aveskamp et al. 2010, Vivas et al. 2014) and *S. cucurbitacearum* in *Luffa cylindrica* (Silva et al. 2013b), and also in other countries, such as *S. tanacetii*, *S. chrysanthemi* and *S. inoxydabilis* in *Asteraceae* in Australia (Vaghefi et al. 2012), *S. cucurbitacearum* in *Cucumis melo* in Thailand (Nuangmek et al. 2018) and *S. cucurbitacearum*, *S. citrulli* and *S. caricae* in *Cucurbita* species (Stewart et al. 2015).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the **LSU** sequence is *Allophoma minor* strain CBS 315.83 (GenBank GU238106.1; Identities = 1326/1327 (99.9 %), no gaps). Closest hits using the **ITS** sequence are *Stagonosporopsis trachelii* isolate NJ1-2 and strain CBS 384.68 (GenBank MH062183.2 and GU237856.1, respectively; Identities = 471/475 (99.2 %), no gaps). The closest hits using the **tub2** sequence are *S. ligulicola* strain SWJ-6 and strain NB-5 (GenBank KJ868169.1 and KJ868168.1, respectively; Identities = 321/333 (96.44 %), 2 gaps (0.3 %)) and *S. inoxydabilis* strain CBS 425.90 (GenBank GU237693.1; Identities = 321/333 (96.44 %), 2 gaps (0.3 %)). The closest hit using the **tef1α** sequence is *Neodidymella thailandicum* strain MFLUCC 11-0140 (GenBank MG520938.1; Identities = 884/902 (98.0 %), no gaps).

Phylogenetic tree of *Stagonosporopsis* spp. obtained with MrBayes v. 3.2.7 (Ronquist & Huelsenbeck 2003) inferred from the concatenated LSU (1340 bp), ITS (481 bp), *tub2* (363 bp), *rpb2* (596 bp) and *act* (314) sequence alignment. The tree is rooted to *Neoascochyta paspali* CBS 560.81. PP values > 0.50 are shown above or below the branches while thicker branches indicate PP values of 1. Sequences used are those reported in Marin-Felix et al. (2019).

Riccardo Baroncelli, Instituto Hispano-Luso de Investigaciones Agrarias (CIALE), University of Salamanca, Calle del Duero, 12, 37185 Villamayor (Salamanca), Spain; e-mail: riccardobaroncelli@gmail.com

Giovanni Cafà, CABI Europe-UK, Bakeham Lane, Egham, Surrey TW20 9TY, UK; e-mail: g.cafa@cabi.org

Renata Rebellato Linhares de Castro, Thais Bouffleur & Nelson Sidnei Massola Junior, Departamento de Fitopatologia e Nematologia, Escola Superior de Agricultura 'Luiz de Queiroz', Universidade de São Paulo, Caixa Postal 09, CEP 13418-900, Piracicaba-SP, Brazil; e-mail: renata.linhares@usp.br, thaisbouffleur@usp.br & nmassola@usp.br