

Purpureocillium*, a new genus for the medically important *Paecilomyces lilacinus

Jennifer Luangsa-ard¹, Jos Houbraken², Tineke van Doorn², Seung-Beom Hong³, Andrew M. Borman⁴, Nigel L. Hywel-Jones⁵ & Robert A. Samson²

¹Phylogenetics Laboratory, National Center for Genetic Engineering and Biotechnology, NSTDA Science Park, Pathum Thani, Thailand; ²Department of Applied and Industrial Mycology, CBS-KNAW Fungal Biodiversity Centre, Utrecht, The Netherlands; ³Korean Agricultural Culture Collection, NIAB, Suwon, Korea; ⁴HPA UK Mycology Reference Laboratory, HPA Southwest, Bristol, UK; and ⁵Mycology Laboratory, BIOTEC, NSTDA Science Park, Pathum Thani, Thailand

Correspondence: Robert A. Samson, Department of Applied and Industrial Mycology, CBS-KNAW Fungal Biodiversity Centre, Utrecht 3584 CT, The Netherlands. Tel.: +31 30 212 2600; fax: +31 30 251 2097; e-mail: r.samson@cbs.knaw.nl

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Abstract

Paecilomyces lilacinus was described more than a century ago and is a commonly occurring fungus in soil. However, in the last decade this fungus has been increasingly found as the causal agent of infections in man and other vertebrates. Most cases of disease are described from patients with compromised immune systems or intraocular lens implants. In this study, we compared clinical isolates with strains isolated from soil, insects and nematodes using 18S rRNA gene, internal transcribed spacer (ITS) and partial translation elongation factor 1- α (TEF) sequences. Our data show that *P. lilacinus* is not related to *Paecilomyces*, represented by the well-known thermophilic and often pathogenic *Paecilomyces variotii*. The new genus name *Purpureocillium* is proposed for *P. lilacinus* and the new combination *Purpureocillium lilacinum* is made here. Furthermore, the examined *Purpureocillium lilacinum* isolated grouped in two clades based on ITS and partial TEF sequences. The ITS and TEF sequences of the *Purpureocillium lilacinum* isolates used for biocontrol of nematode pests are identical to those causing infections in (immunocompromised) humans. The use of high concentrations of *Purpureocillium lilacinum* spores for biocontrol poses a health risk in immunocompromised humans and more research is needed to determine the pathogenicity factors of *Purpureocillium lilacinum*.

Introduction

Paecilomyces lilacinus is a ubiquitous, saprobic filamentous fungus commonly isolated from soil, decaying vegetation, insects, nematodes and laboratory air (as contaminant), and is a cause of infection in man and other vertebrates. This species can colonize materials such as catheters and plastic implants and can contaminate antiseptic creams and lotions, causing infections in immunocompetent and immunocompromised patients (Castro *et al.*, 1990; Orth *et al.*, 1996; Itin *et al.*, 1998). The prevalence of *P. lilacinus* in patients has increased recently (Carey *et al.*, 2003; Rosmaninho *et al.*, 2010). A review of 119 infections caused by *P. lilacinus* after 1964 showed that the most frequent manifestation is keratitis, but other sites of the body were also affected (Pastor & Guarro, 2006). Keratitis caused by *P.*

lilacinus typically occurs by external invasion. Common predisposing factors are chronic keratopathy, environmental trauma, implant surgery following lens and/or cornea replacements and extended use of contact lenses (Domniz *et al.*, 2001; Yuan *et al.*, 2009). *Paecilomyces lilacinus* infections are reported in patients taking immunosuppressant drugs for transplant surgery for liver, kidneys, bone marrow and heart (e.g. Castro *et al.*, 1990; Orth *et al.*, 1996; Lott *et al.*, 2007; Schooneveld *et al.*, 2007). Although commonly reported as a component of the soil mycobiota, the source of *P. lilacinus* infections in humans has rarely been traced. Exceptions are a catheter-related *P. lilacinus* fungemia in an immunocompromised child (Tan *et al.*, 1992), a sodium bicarbonate solution used as a neutralizing agent for a sodium hydroxide sterilizer for artificial lenses (Pettit *et al.*, 1980) and a skin lotion used by patients in a

haematology–oncology and bone marrow transplant wards (Orth *et al.*, 1996; Itin *et al.*, 1998).

The first aim of the current study was to clarify the phylogenetic position of *P. lilacinus* and to find out whether purple-spored species with morphologies similar to *P. lilacinus* form a monophyletic assemblage within the *Hypocreales*. The second aim was to determine whether there are clades within *P. lilacinus*, which only comprise vertebrate or invertebrate pathogens. Towards this aim, translation elongation factor 1- α (TEF) gene and internal transcribed spacer (ITS) sequences from strains obtained from clinical specimens were compared with those from isolates of soil, insects and indoor environments or used as biocontrol agents.

Materials and methods

Strains

Strains isolated from various clinical specimens and hospital environments are emphasized in our selection of *P. lilacinus* isolates. These strains are supplemented with isolates from various other substrates (soil, indoor environment, insects and nematodes), and originate from various collections worldwide. An overview of isolates and sources is shown in Supporting information, Table S1.

Morphological examination

A selection of isolates (Table S1) were grown for 7–14 days on malt extract agar (MEA) and were incubated in darkness at 25, 30 and 37 °C. Furthermore, three-point inoculations were made on MEA and incubated for 7 days at 25 °C in darkness (medium compositions in Samson *et al.*, 2010). After incubation, colony diameters were measured and cultures were investigated with a light microscope.

Sequencing and phylogeny

Isolates were grown on MEA for 5–10 days, incubated at 25 °C. Total DNA was extracted using the Ultraclean™ Microbial DNA isolation Kit (MBio, Solana Beach, CA) according to the manufacturer's instructions. DNA sequences of the 18S rRNA gene were obtained from the GenBank database, and amplification of the ITS regions and a part of the TEF gene was performed as described by Houbbraken *et al.* (2011) and Dodd *et al.* (2002), respectively. The ITS and TEF dataset was combined and maximum likelihood analysis was performed using RAXML version 7.2.8. Each dataset was treated as a separate partition. Two *Cryptococcus neoformans* sequences (GenBank nos AJ560317 and AJ560313) were used to root the 18S rRNA gene phylograms. The phylogram based on combined TEF and ITS sequences were rooted with *Paecilomyces marquandii* DTO 145E5.

Nucleotide sequence accession numbers

The sequences used for building the 18S rRNA gene phylogram were downloaded from the NCBI GenBank database. Newly generated sequences are deposited in GenBank under accession numbers HQ842812–HQ842841.

Results

Generic delimitation

The phylogenetic analysis of the 18S rRNA gene region confirms the data of Luangsa-ard *et al.* (2004), showing the polyphyletic nature of *Paecilomyces*. Figure 1 shows that the type species of *Paecilomyces*, *Paecilomyces variotii*, is located in the family of the *Trichocomaceae* (*Eurotiales*) near *Aspergillus*, *Penicillium* and related species, forming a sister clade with the *Onygenales*. On the other hand, *P. lilacinus* belongs to the *Ophiocordycipitaceae*, a family recently introduced by Sung *et al.* (2007). The purple-spored species *P. marquandii* is phenotypically similar to *P. lilacinus*, but failed to group with *P. lilacinus* in the phylogenetic analysis using 18S rRNA gene sequences, and this species grouped with green-spored species within the family of *Clavicipitaceae*. Detailed phylogenetic analysis showed that the purple-colored species *Paecilomyces nostocoides*, *P. lilacinus*, *Isaria takamizusanensis* and *Nomuraea atypicola* are closely related (Sung *et al.*, 2007; this study) and the former three species have identical partial 18S sequence. None of these species are types of a genus, which warrants the introduction of the new genus *Purpureocillium* for these species. Phenotypically, *Paecilomyces sensu stricto* (*s. str.*) (*P. variotii*) can be differentiated from *Purpureocillium* by its rapid growth on agar media. Species belonging to *Paecilomyces s. str.* have a higher optimum and maximum growth temperature (30–45 °C) compared with *Purpureocillium* (25–33 °C). Furthermore, the conidial color of *Paecilomyces s. str.* is olive-brown and chlamydo-spores are frequently formed, while the conidia of *Purpureocillium* are lilac and chlamydo-spores absent.

Variability within *P. lilacinus*

Figure 2 shows the results of the maximum likelihood analysis of the combined ITS and TEF sequences and three clades are present in this phylogram. The *P. lilacinus* isolates split up in two clades. The type culture of *P. lilacinus* CBS 284.36^T is present in one clade, together with the type strain of *P. nostocoides* and all the examined strains originating from clinical specimens and hospital environments. Furthermore, the majority of *P. lilacinus* strains from soil, indoor environment, insect larvae, nematodes and decaying vegetation are located in this clade. Minor differences among the ITS and TEF sequences are present within the *P. lilacinus* clade; however, in various cases, strains originating from insects, nematodes, (indoor) environment and clinical

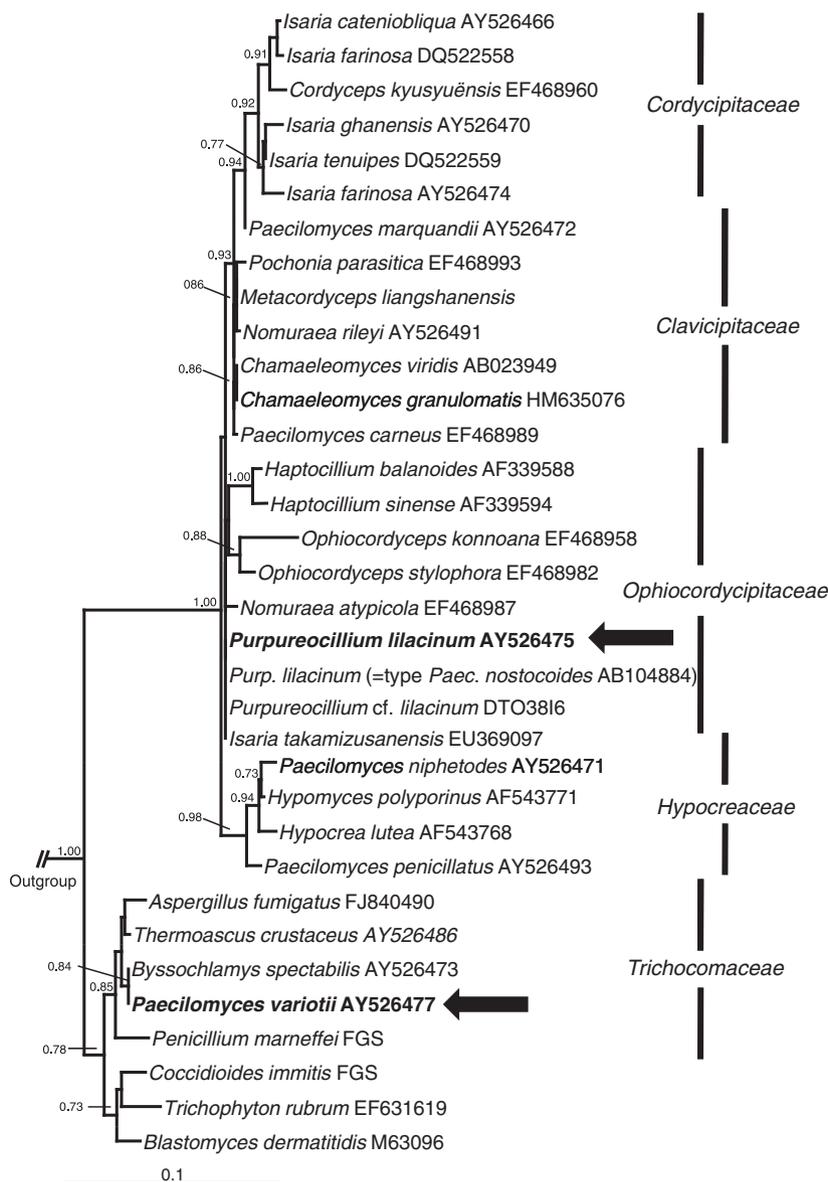


Fig. 1. Phylogram based on partial 18S rRNA gene sequences showing that *Purpureocillium lilacinum* belongs Ophiocordycipitaceae and *Paecilomyces variotii* to the Trichocomaceae.

specimens share the same ITS and TEF sequence. No clinical *P. lilacinus* isolates were present in the other smaller clade. The *P. lilacinus* isolates from this group are saprobes and seem to have a worldwide distribution (India, Ghana, Israel, Australia). This clade represents a new species and will be described in future (unpublished data). Also *I. takamizusanensis* and *P. nostocoides* grouped well with *P. lilacinus*. The former species is associated with insects, and the latter with corn cyst nematodes. Both species share the ability to form purple-colored conidia. Our results show that *P. nostocoides* is phylogenetically closely related to *P. lilacinus*. Comparison of an ITS sequence originating from the ex-type culture of *P. nostocoides* and deposited in GenBank (AB104884) shows that this sequence is similar to those generated in this study

on *P. lilacinus*. The main difference is the presence of a 29-nucleotide gap in the ITS1 region of *P. nostocoides* (GenBank AB104884). The ITS regions of the ex-type culture of *P. nostocoides* (DTO 149E4) were reanalyzed in this study, and in contrast to the sequence deposited on GenBank, these data could not confirm the presence of this 29-nucleotide gap in the ITS1 region. The absence of this gap and the high similarity of the partial TEF sequence of this strain to other *P. lilacinus* indicates that *P. nostocoides* is conspecific with *P. lilacinus*. Furthermore, *N. atypicola* is phylogenetically related to *P. lilacinus* (Sung *et al.*, 2007) and possesses lavender-colored conidia similar to those of *P. lilacinus* (Hywel-Jones & Sivichai, 1995). The taxonomy of the genus *Purpureocillium*, including the phylogenetic relationship

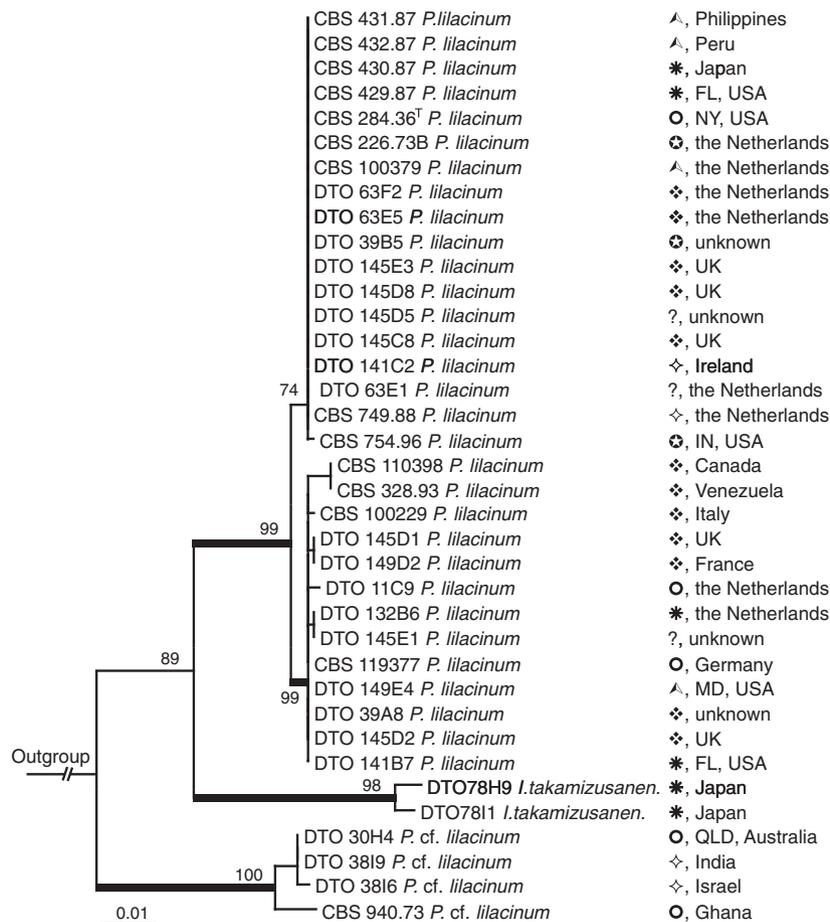


Fig. 2. Phylogram based on the ITS regions (including 5.8S rRNA gene) and partial TEF sequences showing the diversity among *Purpureocillium lilacinum* isolates and the relationship with other closely related species. Animal: ✧, human; ▲, nematode; ✱, entomogenous; ⊕, other; ○ (indoor) environment/soil; ✧, miscellaneous; ?, undetermined.

between *I. takamizusanensis*, *N. atypicola*, *P. nostocoides* and *P. lilacinus*, will be treated elsewhere.

Taxonomy

Purpureocillium Luangsa-ard, Hywel-Jones, Houbraken & Samson gen. nov. Mycobank MB 519529

= *Paecilium* Luangsa-ard, Hywel-Jones & Samson nomen provisorium – Compendium of soil fungi, 2nd edn, p. 322, 2007.

Type: *Penicillium lilacinum* Thom.

Latin diagnosis: Conidiophora ex hyphis submersis oriunda, seu mononematosa, phialibus vix in collulum extensi, seu laxis synnematis connexa, rigida, verticillata; phialidibus collulo distincte angustato praeditis. Conidia in catenis siccis divergentibus adhaerentia, cylindrica (recta vel modice curvata) vel ellipsoidea vel fusiformia, rugulosa, hyalina, aggregata purpurea.

Etymology: The generic name refers to the purple colored conidia produced by its type species, *Purpureocillium lilacinum*.

Colonies on MEA moderately to fast growing consisting of either a basal or compact crustose felt of numerous

conidiophores with a floccose overgrowth of aerial mycelium. Colonies at first white, becoming pink and lilac with the onset of sporulation. Reverse usually in shades of purple or yellow. Conidiophores arising from submerged hyphae, mononematous, stiff, verticillate; phialides ovate to cylindrical with distinct neck or erect and densely grouped, forming verticils of branches and cylindrical phialides without or with very short necks. Conidia in dry divergent chains, straight to slightly curved or ellipsoidal to fusiform, slightly roughened, purple in mass.

Purpureocillium lilacinum (Thom) Luangsa-ard, Houbraken, Hywel-Jones & Samson, **comb. nov.** Mycobank MB 519530

Basionym: *Penicillium lilacinum* Thom – *Bull Bur Anim Ind US Dep Agric*, **118**: 73 (1910).

= *Paecilomyces lilacinus* (Thom) Samson – *Stud Mycol* **6**: 58 (1974).

= *Paecilomyces nostocoides* Dunn – *Mycologia* **75**: 179 (1983).

Colonies on MEA (Oxoid) fast growing, attaining a diameter of 25–35 mm after 7 days at 25 °C; no or restricted growth at 37 °C, 0–10 (–20) mm. Colonies consisting of a



Fig. 3. *Purpureocillium lilacinus*: (a–c) 14-day-old culture on MEA. (a) DTO 63E5, typical sporulating colonies; (b) DTO 63E1, typical sporulating colonies; (c) floccose colonies, DTO 141C2, (d, e) well-defined conidiophores; (f) typical fusiform conidia; (g, h) *Acremonium*-like conidiophores; DTO 141C2; (i) cylindrical conidia formed near the agar; DTO 141C2. Scale bar = 10 µm.

basal felt with or without floccose aerial overgrowth (Fig. 3a and b), some isolates strongly floccose (Fig. 3c), white at first, becoming vinaceous; reverse mostly in shades of purple or sometimes uncolored. Conidiophores arising from submerged hyphae 4–6 µm in length, occasionally forming loose synnemata up to 2 mm high; stalks with roughened

thick walls 3–4 µm wide consisting of verticillate branches with whorls of two to four phialides. Phialides 6–9 × 2.5–3 µm, having a swollen basal portion tapering into a short distinct neck about 1 µm wide. Conidia in divergent chains, ellipsoidal to fusiform, smooth-walled to slightly roughened, hyaline, purple *en masse*, 2–3 × 2–4 µm.

Conidial structures formed near the agar atypical: phialides solitary or in verticils, 2–4, variable in length (Fig. 3g and h); shaped like typical *Purpureocillium lilacinum* phialides, or very long (up to 30 µm) and *Acremonium*-like. Cylindrical, occasionally slightly curved conidia formed in ‘slimy heads’ on these *Acremonium*-like structures, conidia on these structures variable in size, measuring 2.0–14 × 1.5–2.5 µm (Fig. 3i). This conidiogenesis was also observed by Okada *et al.* (1995) for *P. nostocoides* (= *Purpureocillium lilacinum*). Chlamydospores absent.

Discussion

Identification of *Paecilomyces* spp.

Species previously assigned to *Paecilomyces* causing human mycoses include *Paecilomyces farinosus*, *Paecilomyces javanicus*, *P. lilacinus*, *P. marquandii*, *Paecilomyces taitungiacus* (= anamorph of *Thermoascus taitungiacus*), *P. variotii* and *Paecilomyces viridis*. Of these, *P. variotii* is retained in the genus *Paecilomyces* (as it is the type), *P. javanicus* and *P. farinosus* have been returned to the genus *Isaria* in the *Hypocreales* (Luangsa-ard *et al.*, 2004), *P. viridis* has been transferred to *Chamaeleomyces* (Sigler *et al.*, 2010) and *P. lilacinus* is accommodated here in the genus *Purpureocillium*. *P. marquandii* is currently maintained in *Paecilomyces*; however, this species is unrelated to *P. variotii* and should to be transferred to a new genus. *Paranomuraea* was suggested for *P. marquandii* and *Paecilomyces carneus* (Domsch *et al.*, 2007), but this genus has yet not been published validly. Samson (1974) considered *P. lilacinus* and *P. marquandii* to be very close to each other, based on overall morphology and spore color. *Paecilomyces marquandii* differs from *Purpureocillium lilacinum* by its hyaline conidiophores and the typical yellow reverse. Although both species have a similar morphology, phylogenies show them to be separated in two families of the *Hypocreales* (Sung *et al.*, 2007). Some clinical isolates have been identified as *P. marquandii* (Castro *et al.*, 1990; Naldi *et al.*, 2000). These isolates need to be re-examined using sequence-based methods to determine whether *P. marquandii* genuinely has the potential for human pathogenicity or whether this is merely a misidentification of *Purpureocillium lilacinum*. Correct identification is crucial because *Purpureocillium lilacinum* is significantly more resistant to amphotericin B than *P. marquandii* (Aguilar *et al.*, 1998).

Purpureocillium lilacinum in clinical settings

Our results and those of other studies show that *Purpureocillium lilacinum* is a commonly occurring saprobic species and this species is isolated from soil, decaying vegetation, insect and insect larvae, nematodes, humans, animals and (indoor) air (Samson, 1974; Castro *et al.*, 1990;

Itin *et al.*, 1998). This species can contaminate antiseptic creams and (skin) lotions, sodium bicarbonate solutions used as a neutralizing agent for a sodium hydroxide sterilizer for artificial lenses, and colonize materials such as catheters and plastic implants (Pettit *et al.*, 1980; Orth *et al.*, 1996; Itin *et al.*, 1998). A 3-year surveillance study showed that *Purpureocillium lilacinum* was frequently found in water distribution system of a bone marrow transplantation unit. *Purpureocillium lilacinum* positive sites included water from water tanks and showers, sinks, showers (including drains), toilets and air. This species can thrive on wet and moist surfaces of water distribution systems and form a biofilm, together with other species such as *Aspergillus*, *Fusarium* and *Acremonium* (Anaissie *et al.*, 2003). Although biofilm formation by filamentous fungi has been poorly studied, it is postulated that adhesion, colonization and matrix formation are key criteria in the biofilm formation process (Martinez & Fries, 2010). The capacity of *Purpureocillium lilacinum* to adhere to the waxy host cuticle of nematodes and its ability to colonize surfaces under harsh conditions with low nutrient concentrations (fungal biofilters, plastics) and low oxygen levels (Mountfort & Rhodes, 1991; Viguera *et al.*, 2008) suggested that this species is able to form a biofilm. Concordant with our results, Okada *et al.* (1995) showed that *Purpureocillium lilacinum* is a dimorphic species and is able to form an *Acremonium*-state in and/or on agar media. This *Acremonium*-state phenotypically resembles *Fusarium solani*, a fungal pathogen causing severe corneal disease and the causal agent of an outbreak of lens-associated keratitis. Remarkably, the most frequent manifestation of *Purpureocillium lilacinum* is also keratitis (Pastor & Guarro, 2006), suggesting that both species might have similar properties besides their phenotypic similarity. In this respect, it needs to be noted that Imamura *et al.* (2008) showed that *F. solani* has the ability to form biofilms on lenses; however, this appears to be strain rather than species dependent.

Antifungals and *Purpureocillium lilacinum*

Paecilomyces can cause hyalohyphomycosis, and two species, *Purpureocillium lilacinum* (= *P. lilacinus*) and *P. variotii*, are the most frequently encountered (Walsh *et al.*, 2004; Houbraken *et al.*, 2010). The phylogenies described here and elsewhere explain why some treatments will work for one species and fail for the others. Major differences in antifungal susceptibility profiles were found between *P. variotii* and *Purpureocillium lilacinum* *in vitro*. Amphotericin B showed good activity against *P. variotii* and related species *in vitro*, as was the case for flucytosine (Aguilar *et al.*, 1998; Castelli *et al.*, 2008; Houbraken *et al.*, 2010). However, these antifungals are not active against *Purpureocillium lilacinum*, and treatments of infections may therefore be complicated.

Also itraconazole has limited efficacy against *Purpureocillium lilacinum* *in vitro*. Voriconazole, terbinafine, ravuconazole and posaconazole were active against *Purpureocillium lilacinum*, with posaconazole being the drug with the best *in vitro* activity (e.g. Martin *et al.*, 2002; Pastor & Guarro, 2006; Sponzel *et al.*, 2006; Houbraken *et al.*, 2010). Posaconazole may be the only appropriate alternative agent, although the lack of an intravenous formulation and limited penetration into the cerebrospinal fluid might limit its use (Rodríguez *et al.*, 2009; Houbraken *et al.*, 2010). On the other hand, Ortoneda *et al.* (2004) showed that a combination of terbinafine combined with ravuconazole and voriconazole gave the best results *in vitro*.

The *in vitro* susceptibility of *Purpureocillium lilacinum* for itraconazole seems to be strain dependent and both susceptible and resistant strains are reported (Pastor & Guarro, 2006; Castelli *et al.*, 2008; Houbraken *et al.*, 2010). Kitami *et al.* (2005) and Zendri *et al.* (2006) found that orally administered itraconazole successfully treated cutaneous infections. Recently, a large body of literature has accumulated on the successful treatment of keratitis and other *Purpureocillium lilacinum* infections with voriconazole alone or in combination with terbinafine (Martin *et al.*, 2002; Chang *et al.*, 2008; Yuan *et al.*, 2009). The efficacy of voriconazole was also successfully demonstrated in a murine model, when compared with amphotericin B (Rodríguez *et al.*, 2010).

Purpureocillium lilacinum in biocontrol and other benefits

There is a significant body of literature that has demonstrated the negative impact of *Purpureocillium lilacinum* to mankind in the form of medically important infections. However, there is also a wealth of literature reporting the use of *Purpureocillium lilacinum* for the control of nematode pests (e.g. Brand *et al.*, 2003; Kalele *et al.*, 2007). It is therefore possible that isolates of *Purpureocillium lilacinum* used as biological control agents of nematodes could form opportunistic mycoses in humans as well as other vertebrates. Literature suggests that *Purpureocillium lilacinum* is most often a problem in immunocompromised patients with very few instances of it occurring in apparently immunocompetent subjects. Our ITS and TEF data suggest that it is not possible to separate harmful from beneficial isolates of *Purpureocillium lilacinum*. Other genotyping techniques such as multilocus sequence typing, microsatellite analysis or amplified fragment length polymorphism have a higher resolution and might show a genetic structure within *Purpureocillium lilacinum*. Furthermore, these typing techniques might enable tracking of the biocontrol *Purpureocillium lilacinum* strain(s) released into the environment.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Table S1. *Purpureocillium lilacinum* isolates examined in this study.

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