Case Report

Cutaneous hyalohyphomycosis due to Petriella setifera following traumatic inoculation in an immunocompetent host

Carlie Cerne a,*, Seyedmojtaba Seyedmousavi b, John E. Bennett c

a Infectious Diseases, Walter Reed National Military Medical Center, Bethesda, MD, 20889, USA
b Microbiology Service, Department of Laboratory Medicine, Clinical Center, National Institutes of Health, Bethesda, MD, 20892, USA
c Laboratory of Clinical Immunology and Microbiology, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD, 20892, USA

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ABSTRACT

A common cause of subcutaneous mycoses in immunocompetent patients is traumatic inoculation. This is the first reported case of cutaneous infection with Petriella setifera in a human host. A 49-year-old immunocompetent man sustained a splinter from his wooden deck, which resulted in a chronic cutaneous lesion. Originally identified as Scedosporium species on microscopic examination, genome sequencing of the internal transcribed spaces (ITS) region of ribosomal DNA (rDNA) identified the mold as Petriella setifera, a common environmental fungus responsible for wood rot. The patient underwent excision and antifungal therapy with cure.

1. Introduction

In the immunocompetent host, localized cutaneous mold infections can occur following traumatic environmental inoculation. It is important to be able to identify the species as accurately as possible since many molds have vastly different antifungal susceptibility profiles. Current identification techniques such as DNA sequence-based and MALDI-TOF MS used in clinical microbiology laboratories make accurate diagnosis more obtainable [1].

Petriella setifera is an environmental mold classically associated with wood rot that has yet to be reported in human infection. It is a close phylogenetic relative of the genera Scedosporium and Lomentospora and belongs to the family Microascaceae [2].

Here, we report a case of localized cutaneous Petriella setifera infection in an immunocompetent male following inoculation from a wooden deck splinter that was successfully treated with excision and antifungal therapy, which to the authors’ knowledge is the first reported human infection of this species.

2. Case

A 49-year-old man was seen in the Dermatology clinic for a nodular skin lesion on his right forearm that he noticed after sustaining a splinter from his wooden deck on day 0 in April 2019 [Fig. 1]. He initially sought care at his primary care clinic when 7 days after manually removing the splinter, he developed a 1 cm erythematous nodule at the site of injury. He was diagnosed with localized cellulitis and prescribed cephalaxin. An incision and drainage were attempted with no purulent fluid able to be expressed. His skin findings did not improve with antibiotic treatment. Over the following months he described occasional clear drainage from the nodule without any visible granules. The nodule was not painful and did not change in size. He has Fitzpatrick type II skin and had a history of basal cell carcinoma of the forehead and superficial melanoma of the cheek, both treated with Mohs micrographic surgery. He had no drug allergies and took no medications. He denied any recent insect or animal bites.

The patient underwent an excisional biopsy of the skin lesion on day 314. He was diagnosed with a ruptured epidermal inclusion cyst based on the appearance during the procedure.

Tissue samples were submitted to both Microbiology and Pathology departments at Walter Reed National Military Medical Center, Bethesda MD. The histopathological exam showed neutrophilic infiltration, but no fungal elements or grains were seen on gomori methenamine silver stain (Figure not shown). A pure heavy growth of a greyish-white mold grew within 5 days on Sabouraud’s Dextrose Agar (SDA). The patient expressed. His skin findings did not improve with antibiotic treatment.

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recurred [Fig. 2].

The Mycology laboratory technician reported the mold as *Scedosporium* although its morphological features were slightly different than classic *Scedosporium* and *Lomentospora* species. The sample was referred to the Mycology Section of Department of Laboratory Medicine, National Institute of Health Clinical Center, Bethesda, MD for species level identification. Specific identification was attempted by colony morphology, microscopic characteristics, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI Biotyper® Bruker Daltonics Inc. Billerica, MA - USA) and PCR-sequencing of the internal transcribed spaces (ITS) region of ribosomal DNA (rDNA).

Colonies grew rapidly on SDA (Fig. 3 Top image), were dirty white with dark grey spots and became fungiculose (aggregated into rope-like strands) (Fig. 3. A) and granular (Fig. 3. B) in texture (due to perithecial production) after approximately 5 days incubation at 30 °C. No melanin pigmentation was observed. Colonies on Brain Heart Infusion agar grew faster and sporulated more densely than on SDA. Microscopic examination of the culture revealed long delicate conidiophores bearing small ovoid (Fig. 4. A.) to cylindrical (Fig. 4. B.) smooth-walled conidia (7–14 × 3–4 μm) with protruding basal scar sitting directly on supporting structure, without stalk or denticle. Hyphal bundles of immature synnemata with liberating conidia were observed, indicating the mold was in a graphium stage of reproduction. The conidiogenous cells raised from undifferentiated hyphae morphologically matched a member of genera *Scedosporium* and *Lomentospora*. Using MALDI Biotyper, the NIH Bruker Daltonics database was also able to identify protein spectra of the isolate as *Petriella setifera* and *Scedosporium apiospermum* with the spectral scores of 1.87 and 1.80, respectively. The resulting DNA sequences were aligned to both the NCBI Genbank (http://www.ncbi.nlm.nih.gov/ genbank) and the International Mycological Association-Westerdijk Fungal Biodiversity Institute (http://www.mycobank.org) databases. Comparison of concatenated ITS sequence (~500 nucleotides) to both databases yielded sequence identity of >99.6% to *P. setifera* type strains, which were considered sufficient data to conclude that the isolate is *P. setifera*. The corresponding sequences were submitted to Genbank (accession number: MW405800). A phylogenetic tree including related taxa of clinical relevance in the *Scedosporium* and *Lomentospora* genera is shown in Fig. 5.

Antifungal susceptibility testing was conducted in accordance with the Clinical and Laboratory Standards Institute CLSI M38-A3 guidelines. Minimum inhibitory concentrations (μg/ml) were as follows in increasing order: Voriconazole 1 μg/ml, Amphotericin B 2 μg/ml, Posaconazole 2 μg/ml, Terbinafine >2 μg/ml, Micafungin >8 μg/ml. No clinical breakpoints are currently available for *Petriella* spp.

3. Discussion

The species of *Petriella setifera* (Alf. Schmidt) Curzi belongs to the family Microascaceae of the division Ascomycota, Kingdom Fungi, and is primarily found in enriched soil by, e.g. dung, manure, composts or decayed wood [3,4]. It is known to secrete the chemical cellulase, which is responsible for the breakdown of wood [5]. It undergoes a reproductive graphium stage which is characterized by the presence of synnemata which bear compacted conidiophores that are fused together. A mixed subcutaneous infection in a captive dolphin was reported by Poelma et al. in 1974 and is the only other reported clinical infection with *Petriella setifera* [6]. There is no known treatment for *Petriella setifera* and our treatment decisions were based on antifungal susceptibility data and extrapolated from literature on scedosporiosis [7,8]. Complete excision is likely the key to successful treatment.

This case highlights the utility of molecular identification of molds and illustrates the concept that we probably underestimate the clinical
relevance of environmental fungi. As sequencing techniques continue to
develop and become more available, we will likely see more diverse
pathogens emerge.

Declaration of competing interest

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Fig. 3. Colony morphology on Sabouraud’s dextrose agar (A.1. and B.1.) and Brain Heart Infusion media (A.2. and B.2.). The images represent fungal growth
following direct inoculation of skin lesion onto agar plate (top image), and consecutive subculture of two colony types growing on initial culture with slightly
different appearances after approximately 5 days incubation at 30 °C.

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**Fig. 4.** Lactophenol cotton blue wet preparation showing long delicate conidiophores with ovoid (A) to cylindrical (B.) smooth-walled conidia. Scale bar = 10 μm. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

**Fig. 5.** Phylogenetic relations between members of clinical relevance in *Scedosporium* and *Lomentospora* genera, based on sequences from the internal transcribed spaces (ITS) region of ribosomal DNA (rDNA).
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