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Case Report

Schizophyllum commune – A rare isolate from fungal sinusitis

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ABSTRACT

Schizophyllum commune is a basidiomycete that has been occasionally reported to cause sinusitis, allergic bronchopulmonary mycosis, and co-infection with allergic bronchopulmonary aspergillosis. Even though it is an environmental fungus, cases have been reported with vascular and tissue invasion and even presented as brain abscess in immunocompromised individuals. As there are reports of *S.commune* as an emerging fungal pathogen causing rhinosinusitis, laboratories should not ignore this as an environmental contaminant. Microbiologists must consider this as a possible pathogen and should report with clinical correlation. We present a case report of *S.commune* fungal sinus infection, as it is a rare occurrence and since we have noticed it for the first time in our hospital.

1. Introduction

Chronic rhino sinusitis is a common disorder that affects all parts of the world. The various factors that play a causal role in chronic rhino sinusitis are microorganisms, allergic and non-allergic immune-mediated inflammation.[1] In previous days, most cases of rhino sinusitis were diagnosed clinically and attributed to allergic causes. With recent advances in endoscopy techniques, accurate sampling, and microbiological culture systems, a greater number of cases are attributed to bacterial and fungal etiologies. Among the fungal pathogens, Aspergillus and Mucor are the major causes of fungal sinusitis. Occasionally, there may be fungi like *Schizophyllum commune* (*S. commune*), which is a common basidiomycete fungus that is rarely involved in human disease can cause fungal sinusitis.

S.commune is a basidiomycete found in trees, dry logs, and dead wood.[2] It is a very rare pathogen in humans and has been occasionally reported to cause sinusitis, allergic bronchopulmonary mycosis, and co-infection with allergic bronchopulmonary aspergillosis.[1,3] Infective propagules in the fungus spread through aerosols and can cause infections in both immunocompetent and immunocompromised individuals.[3,4] As it is an environmental contaminant, the growth can be ignored easily. In few studies, DNA sequencing has been done and the clinical correlation of *S.commune* infection in sinus samples has been reported as the causative agent, it is necessary to carry out repeated culture or sequencing to confirm the isolate. We present this case report of a *S.commune* fungal sinus infection, as it is a rare occurrence and since we have noticed it for the first time in our hospital.

2. Case History

A 76-year-old female came with complaints of watery nasal discharge, sneezing, and nasal block on the left side of the nasal cavity to our tertiary care hospital located in South India. She was a known case of diabetes and hypertension on medications. There was no history of

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previous surgery, facial trauma, and distant travel. On examination, the left nasal cavity showed allergic mucins, edematous middle turbinate, and nasal mucosa. The right side of the nasal cavity, ear, and throat were normal. Her hematological parameters were within normal limits. Her tests for HIV were negative. The chest X-ray finding was unremarkable. Her total WBC count was 12,000/cumm, with differential counts showing eosinophils at around 4%. CT paranasal sinuses showed a left sinonasal polyp with possible inspissated secretions in the left maxillary sinus and an "s"-shaped deviated nasal septum. A presumed diagnosis of left maxillary fungal sinusitis was made, and functional endoscopic sinus surgery (FESS) was planned. Sub mucous resection was done, gross septal deflection to the left was corrected, and left uncinectomy, MMA, and anterior ethmoidectomy were done. During the procedure, fungal debris was seen and cleared, which was sent for fungal culture.

Specimens sent to microbiology were subjected to KOH immediately. Direct microscopy of a KOH preparation of the surgical specimen showed the presence of hyaline septate hyphae, which was communicated by the laboratory to the surgeon (Figure 1). The patient was scheduled to be reviewed after 15 days, and on follow-up, she was relieved of her symptoms. Fungal cultures at 25°C and 37°C on Sabouraud's dextrose agar containing gentamicin grew white to pale buff, densely woolly fungi on the third day of incubation. Initially, the revere was white, and then it turned pale brown as the colony aged. It produced a strong, disagreeable odour. Identification of the S.communae species mainly based on macroscopic features is challenging as it does not produce spores and grows like a wooly white coloured colonies which is not so distinguishing from other fungus.[4] Examination of colonies using Lacto phenol Cotton Blue Mount showed hyphae of various widths and hyaline septate hyphae, often with clamp connections or lateral pegs (Figure 2). Even after the isolate was held for several months and subcultured on potato dextrose agar media, it has failed to sporulate under any conditions. Banana peel culture was not tried. Aerobic and anaerobic bacteria cultures showed no growth.

The culture was sent for genomic sequencing. Isolation of DNA was performed by the Chromous kit (Chromous Pvt. Ltd., Bangalore), and PCR products were subjected to sequence analysis. After sequencing, the nucleotide sequences were compared with ITS sequence data strains available at the public databases Genbank (http://www.ncbi.nem.nih.gov) by using the BLASTN sequence match was done. The sequences were aligned using the CLUSTAL W programme, and phylogenetic and molecular evolutionary analyses were performed using MEGA6. The phylogenetic reformation was performed using the neighbour joining (NJ) algorithm, with bootstrap values calculated from 1000 replicate runs using the software routines included in the MEGA software. The isolate was confirmed to be *Schizophyllum commune*, with the GenBank accession number referred to as follows: SUB4088751 Seq1 MH392740.

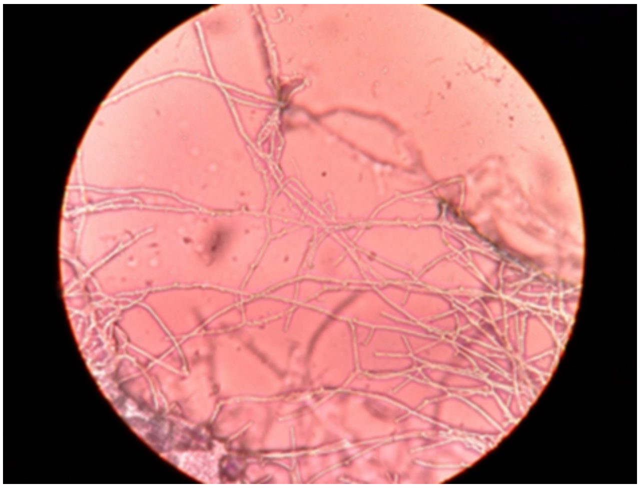

Fig. 1: KOH mount of the sample showing hyaline septate hyphae

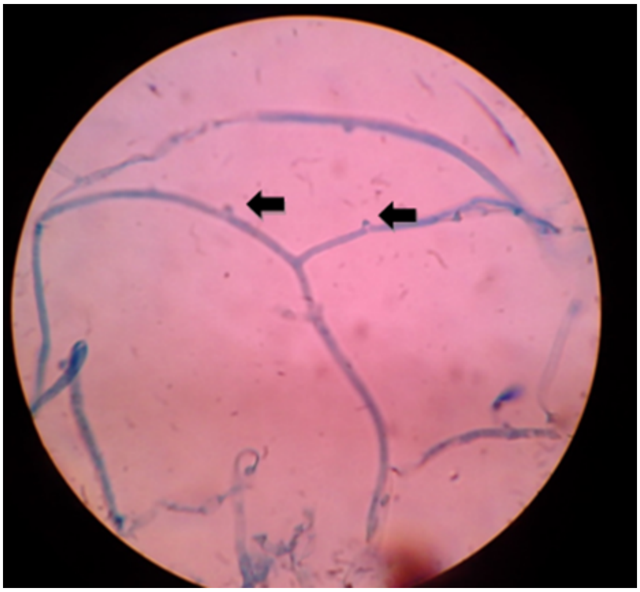

Fig. 2: Lacto phenol Cotton Blue mount showing hyphae of various widths, hyaline septate hyphae with clamp connections and lateral pegs

3. Discussion

Even though *S.commune* is widely seen in the environment, its occurrence in humans as a pathogen is rare.[5] *S. commune* has presented as a cause of non-invasive form of fungal sinusitis in this patient with no bony destruction and intact intersinus septa in ethmoid labyrinths as evidenced in the imaging of paranasal sinuses. Cases have reported that it can present with vascular and tissue invasion, as brain abscess and with pneumonia or as allergic bronchopulmonary mycosis in immunocompromised individuals.[6–8] Till date there is no single factor associated with *S. commune* infection, but it is mostly associated with young, male patients who are agricultural workers. In our patient, we noticed that it had occurred in an elderly female patient from an urban background.

As there are reports of *S.commune* which is an emerging fungal pathogen causing rhinosinusitis, microbiology laboratories should not ignore this as an environmental contaminant. Microbiologists should include this as a possible pathogen and should report with clinical correlation. Though the macroscopic culture looks familiar with the common fungal pathogens, there are characteristic findings of clamp connections and hyphal tubercles that needs to be cautiously looked and can confirm with gene sequencing based on the availability of resources. Colonies of white, non-sporulating mould that grows on routine SDA media should be carefully identified as a possible isolate of *S. commune* before being discarded as a sterile contaminant. In recent times, accurate identification and confirmation of pathogenicity is achieved by molecular methods using nucleotide sequencing of the internal transcribed spacer (ITS) or by 18S rRNA gene.[9] Literature has shown that metagenomic next generation sequencing is also now used for the identification of rare pathogens like *S.commune*.[10]

As of now, there is no targeted therapy for *S. commune* infections, and the utility of azoles for the same is uncertain. The role of surgery and antifungal therapy in cases of a fungal ball caused by *S. commune* remains unclear due to the rarity of reports presented clearly so far. The data on antifungal susceptibility testing methods and cut off values for breakpoints are not available for *S.commune* specifically.[11] In a study, it was found that there were five tested clinical isolates of *S.commune* that were found to be susceptible to itraconazole, voriconazole and amphotericin B.[12] Based on the previous case study of *S. commune* causing ulceration of the hard and soft palate, Amphotericin B is the therapy that looks promising.[5] The duration and dosing of therapy remain uncertain. The therapy relies mainly on appropriate surgical drainage or debridement in combination with antifungal therapy.[5] In this patient, treatment was done by thorough drainage of the paranasal sinuses for maxillary fungal sinusitis. Antifungal therapy was not started as the patient was clinically improving after thorough drainage of sinuses and it was a non-invasive presentation. There was no recurrence documented with a follow up of 2 years. Overall, the prognosis of *S.commune* infections were mild, self limiting to some cases requiring anti fungal therapy. So far, only one case of fatal empyema thoracis has been reported due to delay in diagnosis and co-existing diseases.[13]

4. Conclusion

S.commune, a rare fungal infection in humans can cause fungal sinusitis. Based on this case report, we suggest the microbiologists to clinically correlate and consider the possibility of this environmental isolate which could be an etiological agent for sinus infections. Appropriate debridement or drainage helps in managing with antifungal therapy warranted mostly in invasive cases.

5. Conflict of Interest

None.

6. Source of Funding

None.

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