
MOLECULAR IDENTIFICATION OF RHIZOMUCOR PUSILLUS AS A CAUSE OF SINUS-ORBITAL ZYGOMYCOSIS IN A PATIENT WITH ACUTE MYELOGENOUS LEUKEMIA

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Introduction. *Rhizomucor pusillus* is recognized as an uncommon cause of human disease. Accurate identification of this pathogen through the development of zygospores requires time-consuming culture methods not readily available to most clinical diagnostic laboratories. We describe a case of sinus-orbital zygomycosis caused by *R. pusillus* using a PCR-based method to identify the pathogen from culture. **Case Report.** A 62-year old male rancher from the Midwest with acute myelogenous leukemia received standard induction and consolidation chemotherapy followed by a low-intensity related allogeneic peripheral stem cell transplant. He received fluconazole prophylaxis. At day 8-post transplant (PT), the patient complained of nasal congestion with peri-orbital edema noted on day 13-PT, at which time the neutropenia resolved. A CT scan showed pan-sinusitis, leading to surgical debridement of the sinus with culture of the tissue which was negative for viral, bacterial and fungal pathogens. Amphotericin B (AMB) lipid complex (5 mg/kg/day) was begun for presumed fungal sinusitis, in addition to ongoing antibacterials. At day 16-PT, the patient developed pain, proptosis, and blurred vision in the right eye. Extensive sinus debridement and a right orbitotomy were performed. An exam of tissue showed fibrovascular changes with acute inflammation and necrosis containing non-septate hyphae. A presumed *Rhizopus* species was identified from culture after 4 days of growth. Increased dosing of AMB lipid complex to 7.5 mg/kg/day, AMB nasal irrigation, and GM-CSF were initiated. Additional orbital and sinus debridement were performed on day 24-PT with no evidence of fungus. The patient was discharged at day 33-PT in stable condition. Shortly after discharge, the patient developed mental status changes with a progressive respiratory deterioration, ultimately leading to death on day 55-PT. No postmortem exam was performed. **Molecular testing.** DNA was extracted from the culture and evaluated by PCR using consensus fungal primers to amplify a 607 bp product which included the complete internal transcribed spacer 1 and 2 regions and the 5.8S rDNA gene of the fungal genome. The amplicon was sequenced and evaluated by comparison sequence analysis using the BLAST search engine available within the GenBank database (NCBI, Washington, DC). The sequence showed >99% homology when aligned to a *Rhizomucor pusillus* sequence within the database. The isolate was subsequently submitted to a reference laboratory where morphological and mating studies confirmed the identity as *R. pusillus*. **Conclusion.** This report highlights the value of molecular testing for the accurate identification of fungal species and expands the conditions of infections caused by *R. pusillus* in immunocompromised patients.