

fact that echinocandins are able to penetrate bone tissue¹⁰, combined with their good safety profile, makes this group of antifungals an attractive option for the treatment of *Candida* MOE extending to the skull base.

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***Mycoplasma genitalium*: Using a commercial molecular technique that facilitates rapid detection of mutations associated with resistance to macrolides[☆]**



***Mycoplasma genitalium*: utilización de una técnica molecular comercial que facilita el análisis rápido de mutaciones asociadas con resistencia a macrólidos**

The bacterium *Mycoplasma genitalium* (MG) is a species recently described as a cause of sexually transmitted infections, with particular importance due to its resistance to some antibiotics.¹ The accepted empirical treatment in episodes of non-gonococcal urethritis is doxycycline (IUSTI and ECDC guidelines) and azithromycin (CDC guidelines). The indicated dosage of azithromycin is 500 mg/first day and 250 mg/four further days. The reports in the literature of variable and increasing rates of MG macrolide resistance make it necessary to analyse its susceptibility to these antibiotics. The IUSTI European guidelines recommend the use of molecular tests for the detection of MG and associated resistance, as they provide a clinical advantage and propose the most appropriate treatment. As little is known in Spain about the susceptibility of MG to macrolides,^{2,3} we decided to carry out a study of the mutations associated with macrolide resistance on strains isolated at our hospital.

We studied 20 clinical samples frozen at 80 °C from 17 patients, corresponding to 17 episodes of infection. In these samples, MG had been previously detected by commercial PCR (BD Max

Mycoplasma/Ureaplasma®, Madrid, Spain). There were 15 samples from 12 males (eight urethral exudate, four rectal exudate, two balanopreputial exudate and one semen sample) and five samples from five females (four endocervical exudate and one vaginal exudate). These patients were studied in the Urology, Gynaecology, Infectious Diseases and Accident and Emergency Department of Hospital Virgen de las Nieves in Granada, from April 2017 to September 2018. The mean age of the patients was 26.2 years (18–36 years). All samples were analysed simultaneously using the ResistancePlus® MG kit (Speedx), a multiplex qPCR which, in a single well, detects MG and five mutations in 23S rRNA associated with azithromycin resistance (A2058G, A2059G, A2058T, A2058C and A2059C).

Of the 20 samples studied, three were negative for the detection of MG. In the identification by BD MAX, these samples had shown some amplification cycle (Ct) values greater than 30. Of the 17 positive samples, corresponding to 15 infection episodes, mutations were found in six samples corresponding to four episodes (26.7%). These six samples belonged to four patients (three males and one female). After reviewing their medical records as far as it was documented, it seemed that given the absence of any subsequent specific treatment, the positive result for MG had not been assessed by the treating physician.

This study needs to be extended with more positive MG samples to assess the level of resistance in the different study populations. The ResistancePlus® MG test was simple to perform and adapted to the routine practice of our laboratory. The PlexPCR® technique failed to detect MG in three samples. However, considering its relatively high Ct values, we assume a low positivity which, added to the freeze/thaw process, may explain the negative result. The results of the test used are in accordance with the latest recommendations for the management of patients infected with MG with the aim of

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optimising antibiotic therapy and potentially reducing the transmission of azithromycin resistance. In conclusion, it is important to recommend the early analysis of macrolide susceptibility in MG, in this case facilitated by the use of a commercial technique.

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First case of non-invasive fungal rhinosinusitis by *Aspergillus melleus*[☆]



Primer caso de rinosinusitis fúngica no invasiva por

Non-invasive fungal rhinosinusitis is a clinical condition with a variable inflammatory response which usually affects immunocompetent patients. This condition typically involves the occupation of multiple sinuses by mucoid material containing fungal hyphae. The main aetiological agents are dematiaceous fungi and *Aspergillus* spp., particularly *A. flavus*.¹

We describe the case of a 46-year-old immunocompetent woman whose only relevant medical history was endoscopic sinus surgery two and a half years previously for central facial pain, in which mucoid material occupying the left sphenoid sinus was aspirated. Some 22 months after the procedure, the patient reported persistence of the pain, in addition to hyposmia and difficulty breathing through her nose. A CT scan showed complete expansive occupation of the left sphenoid sinus with posterior wall bone erosion and complete occupation of the maxillary sinus, ethmoid cells and frontal sinus on the left side, with underlying polyp. Six months later the patient had repeat endoscopic nasal-sinus surgery, with removal of purulent material from the left maxillary, sphenoid and ethmoid sinuses, which was sent to pathology and microbiology for testing.

Pathology reported mucoid material rich in eosinophils and the presence of septate hyphae.

Microbiology received three samples of pus drained from the left maxillary, sphenoid and ethmoid sinuses, which were seeded in Sabouraud-chloramphenicol agar (bioMerièux) culture media and incubated at 37 °C and 30 °C. After 72 h of incubation, several 4-cm colonies with a yellowish centre and white periphery had grown in the three cultures incubated at 30 °C (Fig. 1A). Microscopic examination revealed radiate, biserial conical heads (Fig. 1B).

Initially, the identification was carried out using MALDI-TOF mass spectrometry (Bruker Daltonics), obtaining a score of 1.8

for *Aspergillus ochraceus*. To confirm this result, the β -tubulin gene was amplified with conventional PCR, which can discriminate between species of *Aspergillus*,^{2,3} and with its subsequent sequencing *Aspergillus melleus* was definitively identified with 100 % similarity to the sequence deposited in GeneBank® (FJ491523.1).

The patient was discharged home after surgery. She was prescribed antibiotic treatment (amoxicillin-clavulanic acid 875 mg/125 mg every 8 h for 7 days) and nasal lavage with normal saline followed by inhalations of mometasone furoate in each nostril. Four months later, she had made a good recovery.

Aspergillus melleus belongs to the subgenus *Circumdati*, section *Circumdati* and the group *Aspergillus ochraceus*.^{2,4} It is a fungus of ubiquitous distribution, found in soil, plantations or food,⁵ and has the ability to produce proteolytic enzymes⁶ and insecticidal compounds.⁷ Like other species in the group, it can also produce ochratoxin, although in small quantities.⁴ To our knowledge, *A. melleus* has only been described as a human pathogen in certain cases of onychomycosis,^{8,9} so the case we describe would be the first case of fungal rhinosinusitis due to *A. melleus* and the first infection other than an onychomycosis caused by this microorganism.

In terms of therapeutic management, the fact that it was a non-invasive condition in an immunocompetent patient meant that the use of systemic antifungals was not necessary¹⁰; the main treatment being the drainage of the mucous material occupying the sinus cavities. Despite this being an immunocompetent patient with no risk factors for an *Aspergillus* spp. infection, the anatomical alteration of her nasal sinuses in conjunction with the previous surgery may have played a significant role in the infection and proliferation of the fungus.

By way of conclusion, we would like to emphasise on the one hand the importance of nucleic acid amplification techniques to precisely identify the species of the *Aspergillus* genus, and on the other, to raise the possibility that *A. melleus* cases are underdiagnosed. This is primarily due to their low severity, which means that very often only empirical treatment is considered necessary and microbiological diagnosis is not requested. Another reason is the difficulty in establishing a definitive diagnosis with techniques other than nucleic acid amplification, such as microscopy or MALDI-TOF, which are much more widely available in microbiology laboratories.

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