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ARTICLE

Species distribution and susceptibility profile to fluconazole, voriconazole and MXP-4509 of 551 clinical yeast isolates from a Romanian multi-centre study

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Abstract This is the first multi-centre study regarding yeast infections in Romania. The aim was to determine the aetiological spectrum and susceptibility pattern to fluconazole, voriconazole and the novel compound MXP-4509. The 551 isolates were identified using routine laboratory methods, matrix-assisted laser desorption ionisation time-of-flight mass spectrometry (MALDI-TOF MS) and DNA sequence analysis. Susceptibility testing was performed using the European Committee for Antimicrobial Susceptibility Testing (EUCAS T) method and breakpoints. The yeasts originated from superficial infections (SUP, 51.5 %), bloodstream infections (BSI, 31.6 %) and deep-seated infections (DEEP, 16.9 %), from patients of all ages. Nine genera and 30 species were identified. The 20 *Candida* species accounted for 94.6 % of all isolates. *C. albicans* was the overall leading pathogen (50.5 %). *Lodderomyces elongisporus* is reported for the first time as a fungaemia cause in Europe. *C. glabrata* and *Saccharomyces cerevisiae*, as well as the non-*Candida* spp. and non-*albicans Candida* spp. groups, showed decreased fluconazole susceptibility (<75 %). The overall fluconazole resistance was 10.2 %. *C. krusei* accounted for 27 of the 56 fluconazole-resistant isolates. The overall voriconazole resistance was 2.5 % and was due mainly to *C. glabrata* and *C. tropicalis* isolates. Fluconazole resistance rates for the three categories of infection were similar to the overall value; voriconazole resistance rates differed: 4 % for BSI, 3.2 %

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