S2:1
DIFFERENCES IN MORTALITY BETWEEN PATIENTS INFECTED WITH DIFFERENT CANDIDA ALBICANS GENOTYPES
J. Schmidl, S. Bretagne2, N. Zhang1, M. Bendall1, M. Desnos-Ollivier2, F. Dromer2, 2, the YEASTS group; 1Institute of Molecular Biosciences, Palmerston North, NEW ZEALAND, 2Institut Pasteur, Paris, FRANCE

The yeast Candida albicans is a major opportunistic pathogen of humans, capable of causing life-threatening systemic disease. Strains of C. albicans general-purpose genotype (GPG) are more frequent than other genotypes in humans as agents of various forms of candidiasis and as commensals. Circumstantial evidence suggests that they could also be more virulent. To test this hypothesis, we used a PCR assay to distinguish GPG strains from other strains in 90 patients with candidemia and investigated, using logistic regression, if isolation of GPG strains from the bloodstream was associated with higher mortality. GPG strains increased the odds of death 3.77-fold in non-surgery patients after removing the effect of age in a logistic regression model. Age increased the odds of death and the probability of isolation of non-GPG strains from the bloodstream. For every 10 years of age, the odds of having a non-GPG strain isolated from the bloodstream increased 1.36-fold. Our data indicate that GPG strains may be more virulent and more frequent as pathogens in younger patients.

S2:2
MOLECULAR PHYLOGENETIC ANALYSIS OF CANDIDA ALBICANS ISOLATES FROM HUMANS AND NON-MIGRATORY WILDLIFE IN CENTRAL ILLINOIS
L. Wrobel1, J. K. Whittington1, C. Pujol1, S. Oh1, M. O. Ruiz1, M. A. Pfalter2, D. J. Diekema1, D. R. Soil1, L. L. Hoyer1, 1University of Illinois, Urbana, IL, 2University of Iowa, Iowa City, IA

Candida albicans strains can be subdivided into discrete genetic clades. While strains from different clades can be found side-by-side in the same locale, their distribution varies between geographical areas (Soll and Pujol, 2003; EMIS Immunol Med Mycol 39:1-7; Odds et al., 2007 Eukaryot Cell 6:1041-1052). This finding is unanticipated considering the high frequency of human travel that should homogenize the worldwide distribution of C. albicans clades. These observations suggest a local reservoir of C. albicans strains that maintain the association between certain clades and a specific geographic area. This work tested whether local non-migratory wildlife species serve as a reservoir for human C. albicans isolates. Oral and anal/occaal swabs were collected from non-migratory wildlife species immediately upon their admission to the University of Illinois Wildlife Medical Clinic. Twenty-one C. albicans isolates were obtained from a variety of avian, mammalian and reptilian species. A geographically matched set of 45 C. albicans oral isolates was collected from normally healthy human volunteers who attended the annual College of Veterinary Medicine Open House. Multilocus sequence typing (MLST) (Bougnoux et al., 2003; J Clin Microbiol 41:5265-5266) revealed that the clade distribution of the human isolates is similar to that described for North American isolates from a larger strain collection (Odds et al., 2007). The wildlife isolates had a significantly different clade distribution, particularly diploid sequence type (DST) 69, were the most common. The wildlife isolates had a significantly different clade distribution resulting mainly from a deficit of clade 1 isolates and enrichment for clade 8 strains. DST90 was particularly common among clade 8 wildlife strains, but was not found among the human isolates. Although we observed differences in clade distribution for human and wildlife isolates, in several instances, strains collected from wildlife and human sources shared the same DST. Nevertheless, none of these cases suggested that there was contact, and hence recent transmission, between the animal and human subject. In most instances, isolates with the same DST could be discriminated from each other by mating type, ABC type and/or by typing based on ALS gene tandem repeat domain lengths. Antifungal susceptibility testing of the strain collection showed similar caspofungin and fluconazole MICs for human and wildlife isolates. A significantly lower amphotericin B MIC was observed for wildlife isolates (P = 0.004), although the difference was approximately one dilution. These studies suggest that although highly similar strains can colonize humans and wildlife, wildlife does not appear globally to serve as a reservoir for C. albicans in a specific geographic locale. Ongoing analysis of C. albicans isolates from domestic animals will indicate whether their clade distribution is more similar to human or wildlife isolates.

S2:3
A STUDY OF ORAL CANDIDIASIS IN A PORTUGUESE DENTAL CLINIC DURING A ONE YEAR PERIOD
M. I. Martins1, M. Henrique1, A. P. Ribeiro1, R. Fernandes1, V. Goncalves1, A. Seabra1, J. Azered1, R. Oliveira1, 1University of Minho, Braga, PORTUGAL, 2Clinica Dentária dos Congregados, Lda, Braga, PORTUGAL

Candida species are frequently found in the oral cavity. This has been attributed to the ability of yeasts to adhere to oral surfaces and to host factors that favour Candida colonization and subsequent infection. Indeed, asymptomatic carriage may compel individuals to a higher risk of complications through yeast infections if they become immunosuppressed. Therefore, Candida species identification could be used in general dental practice for treatment control, risk evaluation and even for patient motivation in the prevention of disease. To the authors’ knowledge, evaluation of oral candidiasis prevalence and etiologic evaluation is not yet available in Portugal. Thus, the main aim of this study was to determine the incidence rate of oral Candida species among patients of a Portuguese dental clinic in Braga. A total of 111 patients were analysed. Samples were collected and directly cultured in CHROMagar - Candida. Isolated yeasts were identified by polymerase chain reaction (PCR). Specifically, genomic DNAs were extracted using the commercially available QI Aamp® DNA mini kit. Species identification of the isolates was performed by PCR using primers for Candida DNA topoisomerase II genes [1]. The frequency of candidiasis, defined by the recovery of at least one Candida species in culture, was found to be 58.6% (65 out of 111). Candida albicans was the most frequent species found (81.8%). Among Non-C. albicans Candida (NCAC) species recovered, Candida glabrata and Candida parapsilosis accounted for 5.2%, each, Candida tropicalis, 2.6% and Candida guilliermondii, 1.3%. Three CHROMagar - Candida isolates (3.9%) were not identified. Polymicrobial cultures with two different Candida species occurred in eight patients (12.3%). The most common combination of Candida species was C. albicans and C. glabrata (50.0%). C. albicans with C. tropicalis occurred in 25.0% of the cases, while C. albicans with C. parapsilosis and C. guilliermondii with C. parapsilosis were both found in 12.5% of the situations. The results showed that the main etiological agent of oral candidiasis is C. albicans. However, there is an important participation of NCAC species. Notably, besides C. parapsilosis, all the other NCAC species were exclusively recovered from polymicrobial cultures. This study suggests that the incidence rate of oral candidiasis in the Portuguese population is similar to the observed in other countries.