



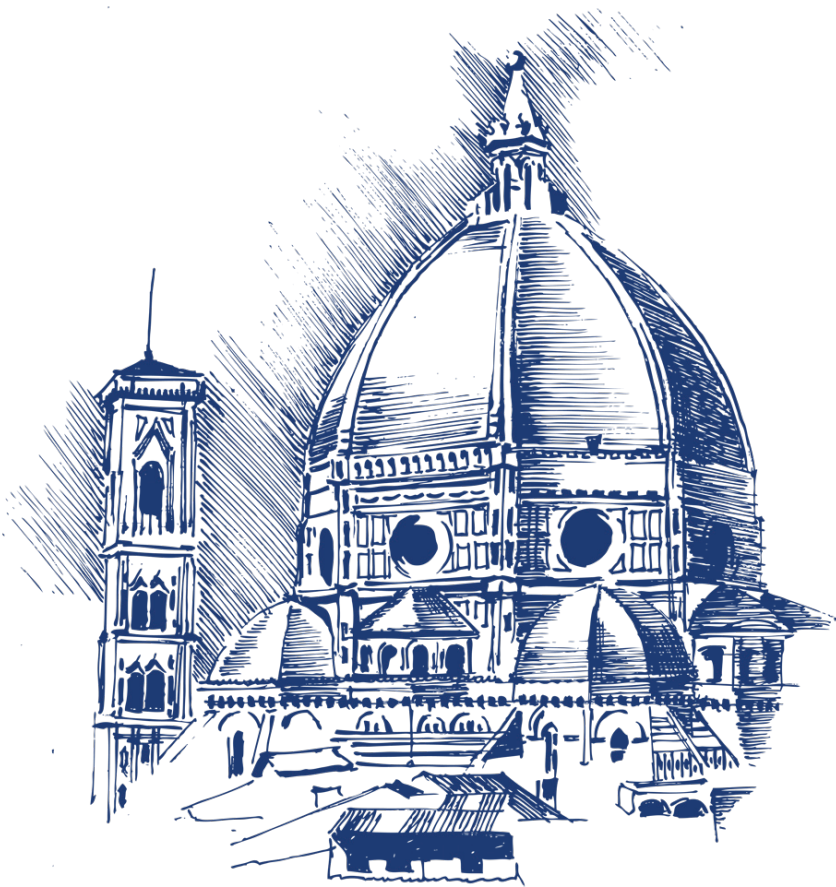
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Programme and Abstracts

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Hyphal morphology, molecular genetics and phylogenetic relationships among commensal and pathogenic vulvovaginal isolates of *Candida albicans*E. Pericolini^{1,2}, A. Sala¹, E. Blasi^{1,2}, A. Tavanti³, C. Rizzato⁴, J. Van Der Schaaf⁵, R.T. Wheeler^{5,6}¹Department of Surgical, Medical, Dental and Morphological Sciences with interest in Transplant, Oncological and Regenerative Medicine, University of Modena and Reggio Emilia, Modena, Italy²Graduate School of Microbiology and Virology, University of Modena and Reggio Emilia, Modena, Italy³Department of Biology, University of Pisa, Italy⁴Dept. of Translational Research and New Technologies in Medicine and Surgery, Univ. of Pisa, Italy⁵Department of Molecular and Biomedical Sciences, University of Maine, Orono, ME, USA⁶Graduate School of Biomedical Sciences and Engineering, University of Maine, Orono, ME, USA

Vaginal candidiasis is a common disorder in women of childbearing age, caused primarily by *Candida albicans*. Since *C. albicans* is a commensal fungus of the vaginal mucosa, a long-standing question is how the fungus switches from being a harmless commensal to a virulent pathogen. Clinical studies and murine vaginitis models suggest that host inflammatory processes drive the onset of symptomatic infection. In previous work with fresh clinical samples, we found that the pro-inflammatory cell wall polysaccharide β -glucan is largely masked from immune recognition during vulvovaginal infection. Enhanced β -glucan availability was only found in hyphae from symptomatic patients with strong neutrophil infiltration. There was high variability in levels of β -glucan exposure and hyphal morphology among colonizing and infection-associated isolates, and we reasoned that this could be explained by fungal-intrinsic factors and/or host-associated traits. We assayed several aspects of *C. albicans* isolated from symptomatic and asymptomatic individuals to determine any associations between fungal-intrinsic traits and virulence: MLST analysis, sequencing of the gene encoding the candidalysin toxin, and propensity to form hyphal cells. Preliminary results suggest that none of these indicators correlates with isolates causing symptomatic infection, indicating that host-intrinsic mechanisms may play the most important role in the occurrence of symptomatic infections.

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Novel probiotics and postbiotics from gut microbiota of Chinese young adultsC. Salvesi^{1,2}, S. Silvi²¹School of Advanced Studies, Università di Camerino, Italia²Scuola di Bioscienze e Medicina Veterinaria, Università di Camerino, Italia

The microbiota of the human body represents a symbiosis of microbial networks spanning multiple organ systems, where the gut microbiota ecosystem is emerging as the preeminent one. The human microbiota has long been known to influence human health and disease, but recently researchers started to appreciate its interaction with the body systems. The bacterial composition is host specific and susceptible to genetic and other factors, such as environment, geographical location, lifestyle, diet and drug consumption. The aim of the present study was to isolate and select from faecal samples of young healthy people from North East of China novel probiotic bacterial strains. Several *Lactobacillus* strains have been characterized for their probiotic properties (gastric acidity and bile salts tolerance, antimicrobial activity), but also non-viable microbial cells, microbial fractions and cell free supernatant have been examined as bioactive compounds, with the purpose to investigate the postbiotic role of these components. Postbiotics contain intermediates and/or final products in metabolism of *Lactobacillus* spp., mainly lactic and acetic acid and antimicrobial peptides known as bacteriocins that may have potential anti-inflammatory and immunomodulatory activities. Till now *in vitro* methods have been used in this study to select the more promising probiotic strains and their postbiotics.