Adaptation of *Candida parapsilosis* to hospitalized infant microbiomes

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Abstract

Cases of the fungal disease candidiasis in infants have been increasing over the past two decades, but our understanding of the behavior and evolution of *Candida* spp. outside laboratory models has been lacking. Researchers assembled new *C. albicans* and *C. parapsilosis* genomes using data from premature infant feces, hospital surfaces, clinical samples, and non-hospital environmental samples. Relative to an existing reference genome, the *C. parapsilosis* genomes analyzed had genomic “hotspots” of single nucleotide variants, and the *C. parapsilosis* genomes from premature infants had hotspots that matched hospital and subway surface samples, which may suggest a common ancestor. The researchers also analyzed a microbial gene expression time course in one infant being treated for *Candida* infection. The in situ transcriptomic profiles were highly variable relative to cultured *C. parapsilosis* and genes associated with biofilm formation tended to have lower expression in situ relative to cultured samples of the same strain. Although the gene expression data presented here is only from one infant, these results underscore the importance of in situ research, and the genomic results outline potential evolutionary processes and hospital strain persistence.