Extended Abstract

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Mycobiome and interkingdom interactions

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Mammalian hosts contain a diverse mycobiome. Colonization sites on the oral and genital mucosa are shared by Candida albicans, Staphylococcus aureus and herpes simplex virus (HSV-1, and HSV-2); however, their interactions are poorly understood. To test whether viral entry into cells results in the differential display of receptors shared between HSV, C. albicans and/or S. aureus, HeLa229 cells were infected with HSV-1 (KOS) gL86 or HSV-2 (KOS) 333gJ- then exposed to S. aureus (ATCC 25923) and/or C. albicans (30 min; 370 C; n=16). Adherence of C. albicans yeast cells and S. aureus to HSV-1 infected HeLa cells varied over time. The level of C. albicans adherence to HSV-1 infected cells was enhanced as compared to controls. Adherence was maximized at 90 min. (191% of control) and 180 min. 146% of control. Interestingly, between 105 and 150 minutes there was inhibition of adherence that ranged from 92% to 97% of control. In contrast, adherence of S. aureus was inhibited. The HSV-mediated inhibition occurred over the initial 120 minutes. Inhibition ranged from a low of 77% of adherence to uninfected homologous controls at 45-60 minutes to restoration of adherence to control levels at 120-165 minutes before decreasing to 92% of control at 180 minutes. Our model suggests that the HSV-1 antagonist interaction with S. aureus as well as its enhancing interaction with C. albicans is a dynamic time-dependent interaction which may correlate with rate of receptor turnover or unmasking as it correlates with the HSV-1 entry process.

Biography:

Balbina J Plotkin has received her PhD from the University of Tennessee. She is a Professor in the Department of Microbiology and Immunology at Midwestern University. Her field of expertise, in which she has published more than 50 papers in peer reviewed journals, is that of identification and characterization of inter-kingdom quorum signaling compounds and their role in biofilm formation and antimicrobial resistance. In addition, she and her colleagues have developed a novel methodology for studying the initial steps in the interactions of microbiome members across the animalis, fungi, and eubacteria kingdoms with herpes simplex virus (HSV-1 and HSV-2)

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