The Ethanol Induced Bacteriostatic Response of *Staphylococcus aureus*

Short title: The ethanol bacteriostatic response

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Methods and Results: The ethanol MICs and MBCs of 106 MRSA strains were determined. Two unrelated MRSA that expressed unique ethanol susceptibility levels were then scrutinized by: microarray profiling following 15 min 10 % (v/v) ethanol challenge, qRT-PCR array validation and analysis of the EIBR transcriptional alterations by the *S. aureus* microarray metadatabase (SAMMD) analysis. Ethanol MICs of MRSA ranged between 6 % and 11 %, and MBCs ranged between 9 % and > 15 %. SAMMD revealed that 600 altered genes were common to both of the EIBRs investigated and some of the highest EIBR up-regulated genes were heat shock genes (*groES-groEL*, *hrcA-grpE-dnaK*, *ctsR-mscAB-clpC*, *clpC*, and *clpB*). SAMMD analysis also revealed that the EIBR overlapped greatest with the stringent response and led to the altered expression of a large number of translational and transcriptional genes. Consistent with this finding, a putative gene encoding a GTP pyrophosphokinase (*ywaC*) was highly up-regulated following ethanol exposure and amino acid addition led to increased ethanol MICs. Conclusions: We propose that the down-regulation of numerous transcription and translation genes during the EIBR allows energy to be channeled into the protection and restructuring of essential proteins and structures altered by ethanol exposure.

Significance and impact of study: This study analyzes the EIBR of a pathogen targeted by ethanol-based hand disinfection programs and adds to what is known about the bacteriostatic effects of ethanol.