BACKGROUND:

*Staphylococcus aureus* is a major cause of community- and hospital-acquired infections worldwide. *S. aureus* has a remarkable ability to adapt to a biofilm mode of growth in response to the host environment, and this is crucial for its leading role in device-related infections. The staphylococcal transcriptome was studied in vivo and the joint fluid metabolome in a prosthetic joint infection using deep RNA sequencing and nuclear magnetic resonance spectroscopy, respectively. We compared our findings with the genome, transcriptome and metabolome of the *S. aureus* joint fluid isolate grown in vitro and in a guinea pig infection model.

RESULT:

From the transcriptome analysis we found increased expression of siderophore synthesis genes and multiple known virulence genes in vivo. The regulatory pattern of catabolic pathway genes indicated that the bacterial infection in vivo was sustained on amino acids, glycans and nucleosides. Upregulation of fermentation genes and the presence of ethanol in joint fluid indicated severe oxygen limitation in vivo. The gene expression profiles showed adaptation to the hypoxic and acidic environment during infection development in the guinea pig infection model.

CONCLUSION:

Understanding the function and pathogenesis of bacteria in vivo, both in mono- and multiple species biofilms is an important next step for optimized diagnosis and treatment.