Abstract:
The blood microbiome in CLABSI neonates clustered separately from the uninfected blood samples in beta diversity plots. We found that the microbiome signature in catheter biofilm and blood of neonates with CLABSI is different than the microbiomes of non-CLABSI neonates” Pammi et al (2020).

Neonates are at high risk for central line associated bloodstream infections (CLABSI). Biofilm formation is universal on indwelling catheters but why some biofilms seed the bloodstream to cause CLABSI is not clearly understood. With the objective to test the hypothesis that catheter biofilm microbiome in neonates with CLABSI differs than those without infection, we prospectively enrolled neonates (n = 30) with infected and uninfected indwelling central catheters. Catheters were collected at the time of removal, along with blood samples and skin swabs at the catheter insertion sites. Microbiomes of catheter biofilms, skin swabs and blood were evaluated by profiling the V4 region of the bacterial 16S rRNA gene using Illumina MiSeq sequencing platform. The microbial DNA load was higher from catheter biofilms of CLABSI patients without differences in alpha diversity when compared to that of the non-CLABSI neonates. Proteus and unclassified Staphylococcaceae were more abundant in infected catheter biofilms while Bradyrhizobium, Cloacibacterium, and Sphingomonas were more abundant in the uninfected catheters. A blood microbiome was detected in uninfected samples. The blood microbiome in CLABSI neonates clustered separately from the uninfected blood samples in beta diversity plots. We found that the microbiome signature in catheter biofilm and blood of neonates with CLABSI is different than the microbiomes of non-CLABSI
neonates.

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