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Itinerary

Session 276 - Sunday Late-Breaker Poster Presentations

LB-082 / LB-082 - Metagenomic Evaluation of Sink Trap Biofilms as a Nosocomial Reservoir for Carbapenemase Producing Gammaproteobacteria

June 19, 2016, 12:30 - 2:30 PM

Authors

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Disclosures

P. Subramanian,
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N. A. Hasan,
CosmosID, Inc. Role(s): Self, D. Employee.
C. Grim, None..
A. Mathers, None.
R. Colwell,
CosmosID, Inc. Role(s): Self, A. Board Member.
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Abstract

Background: Carbapenemase producing bacteria are an increasing threat to hospitalized patients and a full understanding of nosocomial transmission has yet to be realized. The biofilm in sink traps has long been recognized as a biologically active community but little is known about how to evaluate the presence of highly resistant organisms or the risk they could pose to patients. We adapted a novel genomic approach to evaluate a sink trap as a hospital reservoir for carbapenemase organisms. **Method:** 15 *Klebsiella pneumoniae* carbapenemase (bla_{KPC}) *Aeromonas* sp. and Enterobacteriaceae clinical isolates collected between 2/2012-5/2013 paired with 9 sink trap biofilm samples from the same hospital (3/2014) underwent whole genome shotgun sequencing using an Illumina MiSeq and metagenomic analysis using CosmosID's MetaGenID software. To determine if patient isolates were present in the biofilm, their genomes were added to the MetaGenID bacterial database. The biofilm metagenomes were examined using this supplemented database. Both biofilm samples and patient isolates were also profiled using the MetaGenID antimicrobial resistance and virulence gene database. Genes with partial match to a biofilm sample at >50% coverage and > 80% isolate coverage were aligned, using BLAST, to a characterized bla_{KPC} plasmid. **Result:** 7 patient isolates were identified as present in the sink biofilms indicating that the sink trap biofilm can act as a sustained reservoir over time. Of 303 antibiotic resistance and virulence associated genes found in the biofilm samples and patient isolates, the majority (n=190) were plasmid associated. The remaining genes not on the plasmid, with the exception of a single virulence factor, were found only in the biofilms. All genes present and common to multiple biofilm samples and patient isolates (including those isolates not identified in the biofilms) were plasmid associated. **Conclusion:** We have applied a novel approach to understand a nosocomial reservoir of drug resistance which can sustain plasmid based genes of resistance shared between environmental and patient isolates. Based on these results, we conclude that biofilms can create a niche for sustaining clinically relevant multidrug resistance organisms (MDROs) in a hospital.