years, our contamination rates were well below the CLSI recommendation; however, a significant reduction in blood culture contamination was observed after the use of a Red Top discard tube (0.8% vs. 1.9%) (Figures 1–3).

Fig. 1

	2017 (ChloraPrep + Red Top discard			2016 (ChloraPrep)		
	Volume	Contaminated	% Contaminated	Volume	Contaminated	% Contaminated
June	1356	10	0.74	1059	25	2.36
July	1404	9	0.64	1227	24	1.96
August	1228	10	0.81	1240	17	1.37
September	1304	12	0.92	1643	34	2.07
October	1291	13	1.01	1433	31	2.16
November	1192	9	0.76	1424	25	1.76
December	1358	10	0.74	1232	22	1.79
Total	9233	73	0.8	9258	178	1.9

Fig. 2

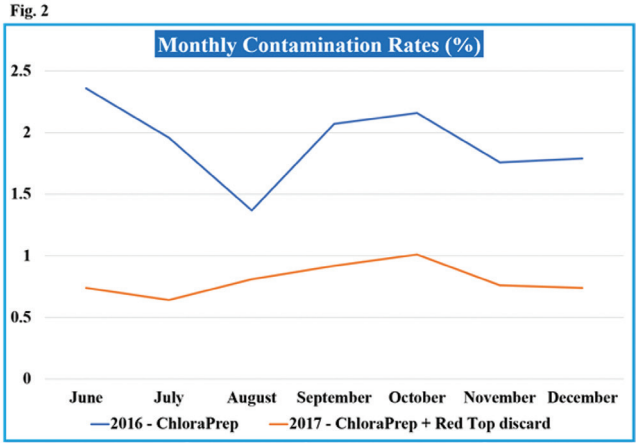
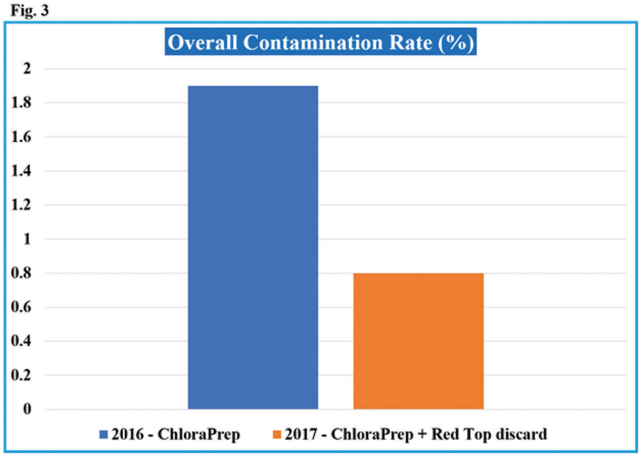


Fig. 3



Conclusion. The cost of a standard blood draw with Red Top tubes is minimal (few cents) while a single collection using an initial specimen diversion device (ISDD) can range from $15 to $18. During the course of this study, the use of a standard Red Top discard cost approximately $456 (2017); if an ISDD was used instead, this would have generated $136,995 in healthcare cost. At our institution, we were able to keep our contamination rates below 1% after the implementation of a standard Red Top discard tube. This suggests that the use of a Red Top discard prior to blood culture collection is an effective means for reducing and maintaining a low blood contamination rate.

Disclosures. **All authors:** No reported disclosures.

158. The Effect of Insurance Coverage on Appropriate Selection of Hospital Discharge Antibiotics for *Staphylococcus aureus* Bacteremia

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Session: 45. Cool Findings in Bacteremia and Endocarditis
Thursday, October 4, 2018: 10:30 AM

Background. Inappropriate or inadequate antimicrobial therapy of *Staphylococcus aureus* bacteremia (SAB) is associated with worsened outcomes. The impact of insurance coverage on appropriate selection of antibiotics is poorly understood. In patients diagnosed with SAB, we assessed the impact of insurance coverage on appropriate selection and duration of antibiotics at discharge.

Methods. We analyzed 273 patients who were diagnosed with SAB during their hospitalization at Nebraska Medicine and were discharged on antibiotics in 2015 and 2016. Antimicrobial therapy was deemed inappropriate if (i) total treatment duration was less than 14 days, (ii) oral delivery route was used, (iii) vancomycin was used to treat methicillin sensitive *S. aureus* in non-β-lactam allergic patients, or (iv) any penicillin or cephalosporin was used to treat methicillin-resistant *S. aureus*. Insurance was categorized broadly into (i) no insurance, (ii) Medicaid, (iii) Medicare, and (iv) Commercial. We collected data on a suite of additional variables that included: type of infectious disease (ID) inpatient consult and location of discharge. Logistic regression was used to determine the odds of being prescribed inappropriate therapy in univariate and multivariate analyses and likelihood ratio tests (LRT) were used to evaluate the strength of evidence.

Results. In unadjusted models, not having insurance was associated with inappropriate antimicrobial therapy (Reference Group: Any insurance; OR No insurance 4.71; LRT $P = 0.027$). Two additional risk factors for inappropriate therapy were identified in unadjusted models: discharge location (Refrence Group: Nursing assistance; OR Home without assistance 3.37; 95% CI 1.34–8.46; LRT $P = 0.008$) and lack of an ID consult (Reference Group: Academic team; OR Not consulted 26.8, 95% CI 7.66–93.8; LRT $P < 0.001$).

Conclusion. We found strong evidence that not having insurance, being discharged to home without assistance, and not having an inpatient ID consult are risk factors for being prescribed inappropriate antimicrobial therapy for SAB upon hospital discharge; however, the sparsity of outcomes prevents us from drawing causal inferences. This study adds to the extensive body of evidence that has shown that uninsured patients tend to have suboptimal therapeutic choices.

Disclosures. **All authors:** No reported disclosures.

159. Genomic Epidemiology of MRSA at Intake to a Large Inner-City Jail: Evidence for Community Transmission Networks?

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Session: 46. Healthcare Epidemiology: Special Populations
Thursday, October 4, 2018: 10:30 AM

Background. USA300 is endemic in the community, with congregate settings potentially facilitating spread. The impact of community MRSA transmission networks on importation of MRSA into urban jails is unknown. We examined MRSA colonization isolates entering the jail and determined whether there are community transmission networks for MRSA that precede incarceration.

Methods. HIV-infected and HIV-negative males incarcerated at the Cook County Jail were enrolled within 72 hours of intake. Surveillance cultures (nares, throat, and groin) were collected to determine prevalence of MRSA colonization. A survey was administered to identify predictors of colonization. Whole-genome sequencing (WGS) and phylogenetic analysis were integrated with epidemiologic data to identify community transmission networks.

Results. A total of 800 males were enrolled (83% AA and 9% Hispanic); 58% were HIV-infected. The prevalence of MRSA colonization at intake was 19%. In multivariate analysis, methamphetamine use (METH), unstable housing, and prior jail incarceration were significant predictors of MRSA. Among HIV patients, injection drug use and HIV care at outpatient Clinic A that emphasize comprehensive care to the LGBTQ community were significant predictors of MRSA. Of the 31 (45%) patients with care at Clinic A, 14 had MRSA colonization. We sequenced 145 isolates from unique individuals, with 102 and 13 closely related to USA300 and USA500 reference genomes, respectively. USA300 strains from intake were diverse (median pairwise SNV distance = 109), with several small clusters noted. WGS revealed the high prevalence of MRSA in Clinic A was not due to clonal spread but rather an intermingling of distinct community transmission networks (strains were highly diverse; median pairwise SNV distance = 410). We did identify a 13-member community transmission network underlying spread of USA500 (figure). Members of this network were more likely to be HIV-infected ($P < 0.004$), MSM ($P < 0.001$), and METH ($P < 0.001$).

Conclusion. A high proportion of individuals enter jail already colonized with MRSA and colonization risk factors provide clues to community reservoirs for MRSA. WGS extended epidemiologic analysis and revealed community transmission networks that could be a potential focus for an intervention.