colonization, it is challenging to quantify the relative importance of different transmission mechanisms and assess control efficacy. By identifying clusters of transmission, whole-genome sequencing (WGS) provides an opportunity to overcome these challenges.

Methods. We sought to apply cluster analysis techniques to WGS data for MRSA, in order to assess MRSA prevalence, transmissibility, the degree of transmission heterogeneity and the potential effectiveness of control. Our model builds upon previous work that showed a direct relationship between the size distribution of infection clusters, the effective reproduction number (R) and the dispersion parameter (k). To demonstrate its functionality, our model was applied to existing WGS data for MRSA isolates collected during a 12 month period in the East of England (DOI: 10.1126/scitranslmed.aak9745)

Results. The effective reproduction number for the East of England data is 0.29 (95% CI: 0.24–0.36). The dispersion parameter is 0.09 (0.03–0.33) reflecting a high degree of transmission heterogeneity. This implies all transmission is caused by just 12% of the cases. Targeted control of these cases could have decreased overall burden of MRSA colonization by 29% during the time period of the study.

Conclusion. The high degree of transmission heterogeneity seen in MRSA transmission suggests that the risk for infection is variable.This observation motivates the need for more detailed mechanistic modeling of hospital-based MRSA transmission that integrates patients-specific factors, movement data and genome sequencing. Such models could be used to forecast which patients are at greatest risk for either acquiring or transmitting MRSA, thereby improving targeted control.

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561. Genomic Epidemiology of Methicillin-Resistant *Staphylococcus aureus* in Two Cohorts of High-Risk Military Trainees

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Background. Methicillin-resistant Staphylococcus aureus (MRSA) skin and soft-tissue infections (SSTIs) are common among military recruits. Identifying which strains are responsible for SSTI and understanding the underlying transmission dynamics is critical to developing appropriate interventions for this high-risk population.

Methods. A cohort study of US Army Infantry trainees at Fort Benning, GA (June and September 2015). Participants from two training Companies were screened for colonization on multiple anatomic sites throughout the 14-week cycle as well as the time of clinical infection. MRSA+ samples were sequenced with Illumina HiSeq. Multi-locus sequence type (MLST) and virulence genes were identified in silico. Single nucleotide polymorphism (SNP) distances between soldiers' bacteria were compared with assessing for potential transmission.

Results. Of 383 soldiers enrolled, 84 (22%) were colonized with MRSA during the study. Forty-two of 84 had a single positive colonization sample, of which 76% were from anatomical sites other than the nares (36% oropharyngeal, 26% perianal, 14% inguinal). Twelve trainees had MRSA SSTI during training (50% had colonization detected prior to or at infection). All were PFGE-type US300 (ST8) and were lukS/lukF-positive. SNP-based phylogenetic analyses and epidemiologic data indicate that most MRSA positives at baseline were due to unique importations from various community origins, suggesting that the ongoing MRSA epidemic is not due to a single endemic strain circulating on base. Following importation, extensive transmission then occurred, with multiple STs implicated. Transmission appeared restricted to within Companies, and predominantly within platoons.

Conclusion. Frequent colonization at baseline suggests a need for extensive MRSA screening and decolonization upon arrival to base, followed by ongoing infection control measures throughout training to prevent recolonization/infection. As multiple anatomical sites appear to play a role in transmission of MRSA, this may have important implications for screening protocols and control both in community and hospital-based settings.

Table 1 Risk factors for bloodstream infection within the first year in kidney transplant recipients by Cox Proportional Hazard Models

Risk factors	Univariate analysis		Multivariate analysis	
	HR (95% CI)	P value	HR (95% CI)	P value
Recipient age (per 10-year)	1.16 (0.85-1.60)	0.36		
Recipient female sex	1.71(0.79-3.70)	0.17		
Donor age (per 10-year)	1.20 (0.90-1.60)	0.21		
Donor infection	0.36 (0.02-1.72)	0.24		
Underlying diabetes mellitus	1.55 (0.58-4.10)	0.38		
Underlying hypertension	0.40(0.18-0.93)	0.03	0.52 (0.21-1.29)	0.16
HLA mismatch ≧ 3	1.15 (0.53-2.58)	0.72		
Positive panel-reactive antibody	2.31 (0.84-5.43)	0.10		
Deceased donor kidney transplantation	1.64(0.71-3.76)	0.25		
The second kidney transplantation	6.97(2.09-23.28)	0.002	4.55 (1.24-16.79)	0.02
Carbapenem for peri-operative prophylaxis	0.77 (0.18-3.25)	0.72		
Re-operation	3.50(0.47-25.90)	0.20		
Receiving induction therapy	3.11(1.18-8.27)	0.02	3.05 (1.15-8.10)	0.03
Double filtration plasmapheresis	2.41 (0.13-11.37)	0.45		
Tacrolimus vs. cyclosporine maintenance therapy	1.51 (0.62-4.52)	0.39		
Duration of urinary catheter (per 1-day)	0.98 (0.82-1.02)	0.58		
Duration of drainage (per 1-day)	0.99 (0.90-1.04)	0.73		
Duration of double J stent (per 1-day)	0.97 (0.84-1.02)	0.39		

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

562. Reducing MRSA Bacteremia in Adult Patients through MRSA Decolonization Bundle

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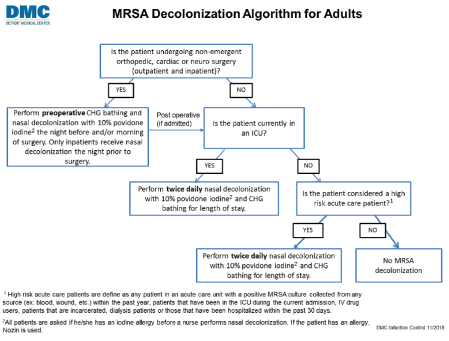
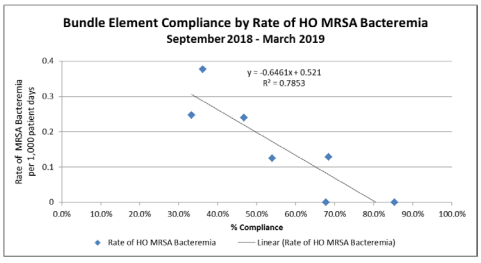
Background. Patients colonized with methicillin-resistant Staphylococcus aureus (MRSA) are at an increased risk of developing a subsequent MRSA infection. Moreover, these individuals may serve as an endogenous reservoir to spread the bacteria to other patients. In an attempt to reduce MRSA bacteremia rates, a decolonization protocol was developed and implemented at a tertiary teaching hospital in Detroit, Michigan. In this study, we evaluate the intervention's impact on community-onset (CO) and hospital onset (HO) MRSA bacteremia rates.

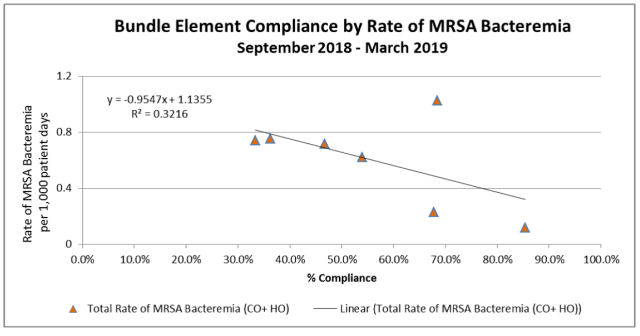
Methods. Infection Control developed an MRSA decolonization bundle for adults that consisted of daily Chlorhexidine gluconate (CHG) bathing and twice-daily nasal swabs with 10% Povidone–iodine (PI) or Nozin for individuals with iodine allergies. Patients with known risk factors for developing an MRSA infection, such as patients residing in an intensive care unit and/or undergoing specified procedure, were prescribed the bundle for their length of stay (Figure 1). Countraindications for nasal decolonization included inhalation injuries, CSF leaks, ENT surgeries, and transphenoidal surgeries. A retrospective chart review of high-risk patients was conducted to determine compliance with the elements of the MRSA decolonization bundle. Rates of CO and HO MRSA bacteremia per 1,000 patient-days were graphed against compliance with bundle elements (2 nasal swabs and 1 CHG bath per day). To quantify the correlation, a linear regression model and the Pearson coefficient was used.

Results. Approximately 2,000 and 1,000 opportunities for nasal decolonization and CHG bathing, respectively, were identified between September 2018 and March 2019. The data suggest a strong correlation between compliance with MRSA decolonization elements and rate of HO MRSA bacteremia ($R^2 = 0.785$) and a moderate association between nasal decolonization and rate of CO bacteremia ($R^2 = 0.322$) (Figures 2 and 3).

Conclusion. The MRSA decolonization bundle of CHG bathing and nasal swabs appears to be an effective strategy to decrease HO MRSA bacteremia rates with higher bundle compliance being associated with lower rates of infection.







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