

Impact of Respiratory *Staphylococcus aureus* Abundance on Risk for Ventilator-Associated Pneumonia During Long-Term Care

James J. Harrigan, MD, PharmD¹; Hatem Abdallah¹; Erik L. Clarke, PhD²; Ebbing Lautenbach, MD, MPH, MS^{1,2}; Emily Reese, MS²;
Magda Wernovsky¹; Pam Tolomeo²; Zygmunt Morawski⁴; Jerry Jacob, MD, MS^{1,4}; Michael A. Grippi, MD^{3,4}; Brendan J. Kelly, MD, MS^{1,2}

¹Division of Infectious Diseases; ²Department of Biostatistics, Epidemiology, and Informatics; ³Division of Pulmonary and Critical Care, University of Pennsylvania; ⁴Good Shepherd Penn Partners, Philadelphia, PA

Objectives

- We sought to evaluate the impact of respiratory *Staphylococcus aureus* colonization and bacterial community dominance, both diagnosed and undiagnosed, on subsequent *S. aureus* VAP and VAE during long-term acute care.

Introduction

- Clinically-diagnosed ventilator associated pneumonia (VAP) is common in the long-term acute care hospital (LTACH) setting.^{1,2}
- VAP may contribute to adverse ventilator-associated events (VAE).³
- S. aureus* is a common causative organism of VAP.^{4,5}
- Healthcare exposure results in significant microbiome disruption, particularly in the setting of critical illness, and may contribute to risk for healthcare-associated infections (HAIs) including VAP.⁶ Bacterial community dominance has been shown to be a useful index of microbiome disruption, which is associated with risk for VAP.⁵

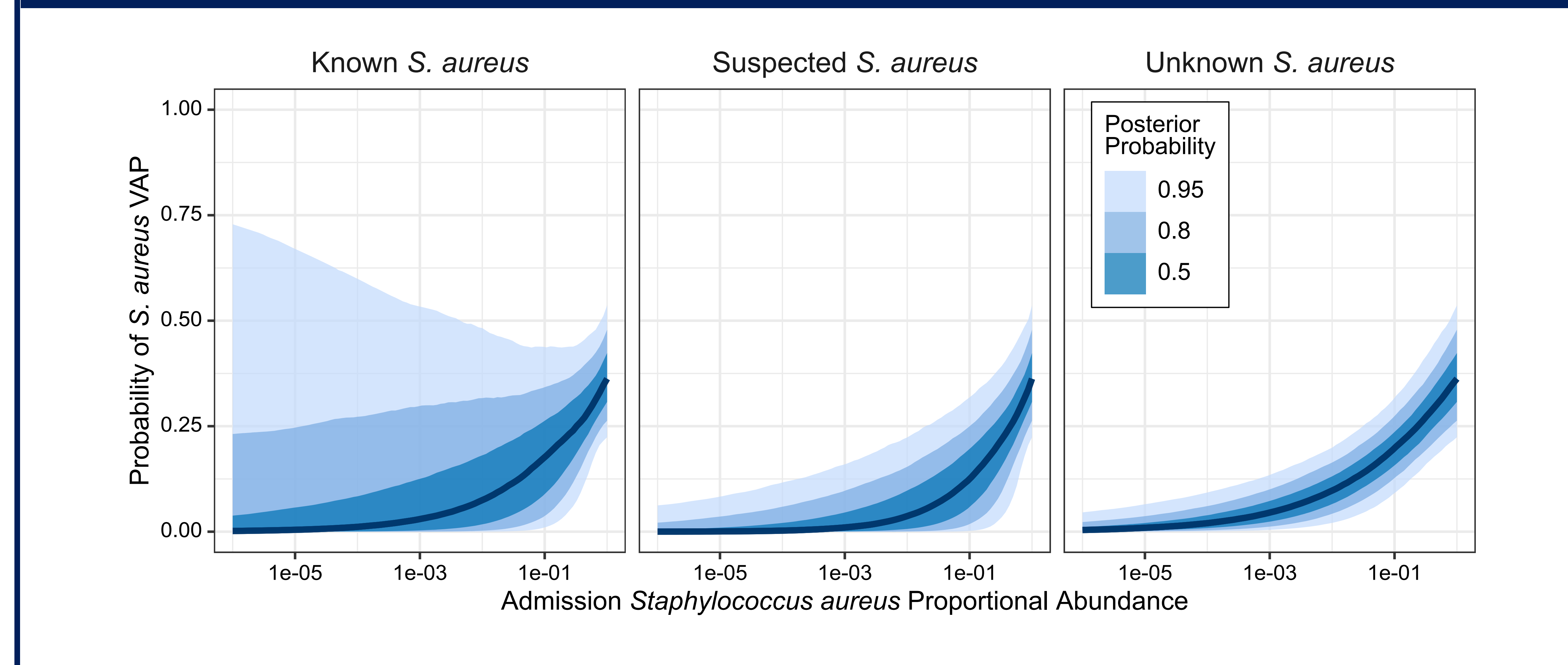
Study Population

- We enrolled 83 subjects on LTACH admission for ventilator weaning: 8 were diagnosed with *S. aureus* pneumonia during the 14 days prior to admission ("Known *S. aureus*"), 17 received anti-*S. aureus* antibiotics within 48 hours of admission ("Suspected *S. aureus*"), and 58 had neither ("Unknown *S. aureus*").

Methods

- We performed longitudinal sampling of endotracheal aspirates, followed by 16S rRNA gene sequencing (Illumina HiSeq).
- Bacterial community profiling was performed to detect error-corrected amplicon sequence variants (ASVs) using QIIME2, and bacterial community diversity was determined from ASV count data.
- 16S rRNA gene quantitative PCR (qPCR) was performed to determine total bacterial abundance.
- Clinically-suspected VAP were defined as a positive endotracheal aspirate culture accompanied by a new or revised antibiotic prescription.
- VAE were defined according to National Healthcare Safety Network (NHSN) surveillance criteria.
- Statistical analysis was performed with R and Stan; mixed effects (slope and intercept) models were fit to relate the admission *S. aureus* abundance to subsequent, clinically-diagnosed *S. aureus* VAP and VAE.

Results: *Staphylococcus aureus* Impact on VAP



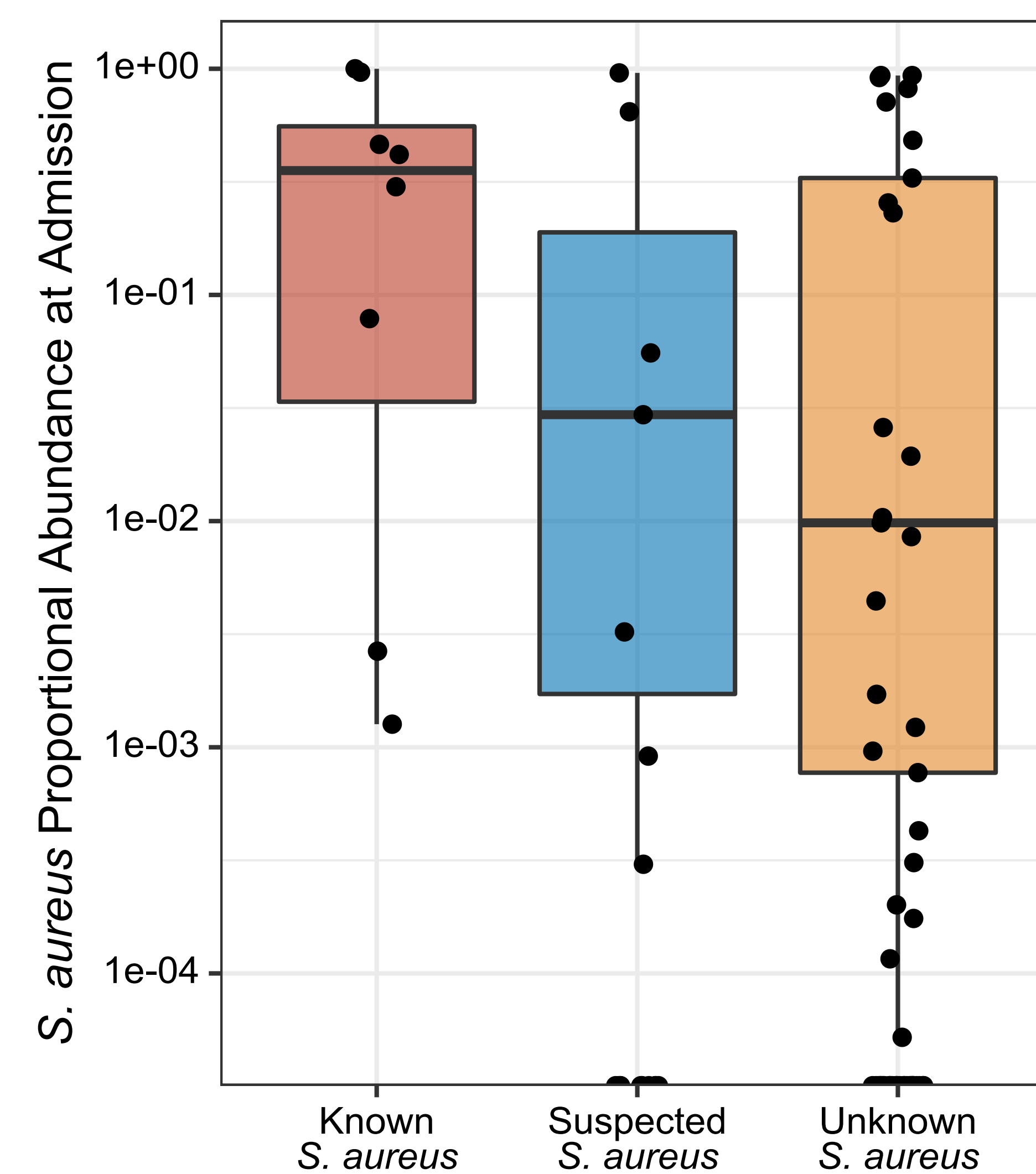
Conclusions

- We identified a high prevalence of unrecognized respiratory *S. aureus* colonization among patients admitted to LTACH for weaning from mechanical ventilation.
- The admission *S. aureus* proportional abundance was associated with increased risk of incident *S. aureus* VAP among these subjects.
- Of note, the association between admission *S. aureus* proportional abundance and risk for incident *S. aureus* VAP was strongest among subjects without recognized *S. aureus* colonization.
- An association between *S. aureus* proportional abundance and VAE was also observed among subjects without recognized *S. aureus* colonization.

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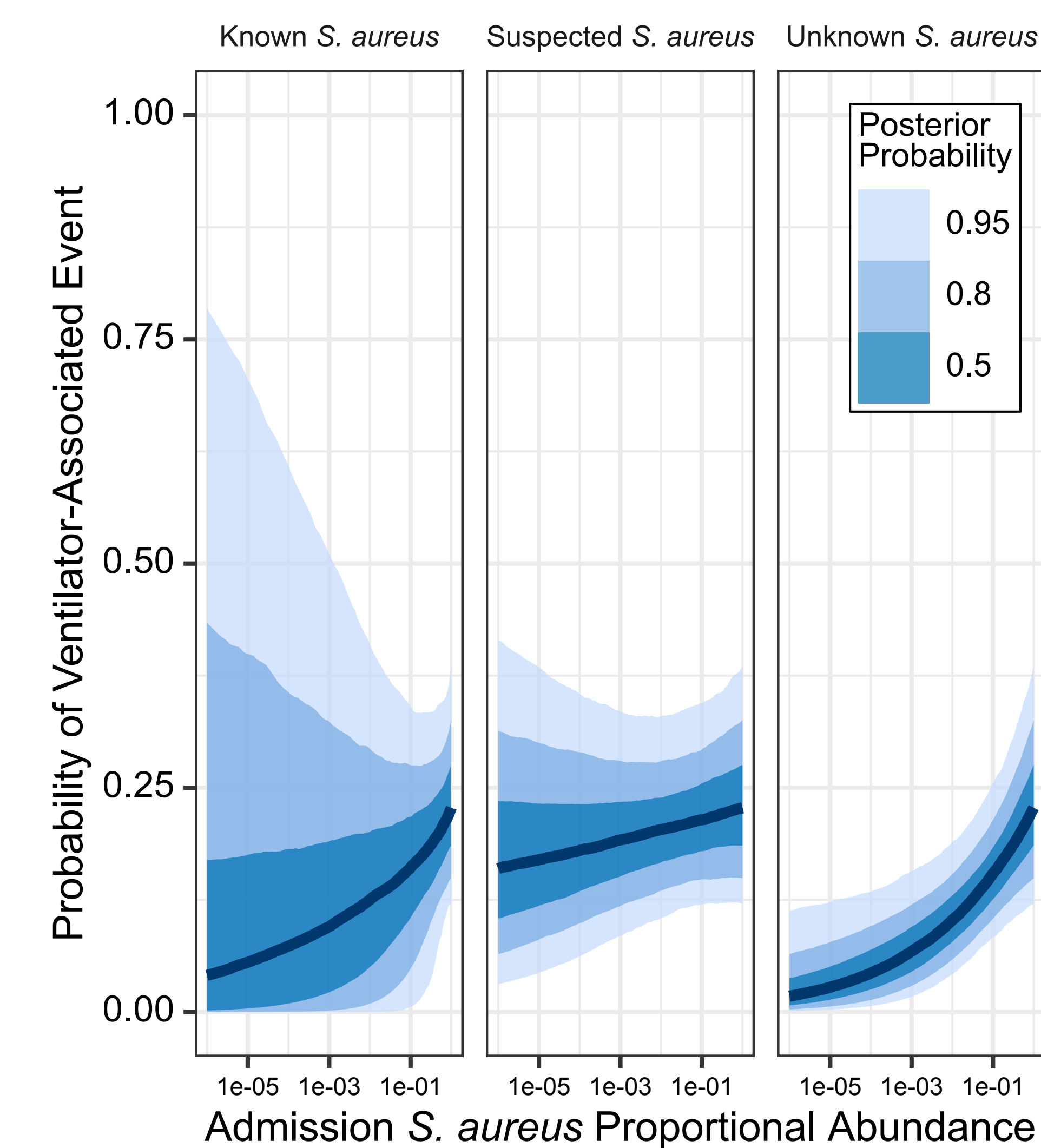
Results: *S. aureus* Colonization Prevalence



- All of the Known *S. aureus* group 8 had *S. aureus* detectable by 16S sequencing, with elevated admission *S. aureus* proportional abundance (median 0.36; range 0.0013 - 1). In the Suspected *S. aureus* group, only 7 had *S. aureus* detectable by 16S sequencing, with a wide range of proportional abundance (median 0; range 0 - 0.96). 25 of 58 subjects in the Unknown *S. aureus* group also had detectable respiratory *S. aureus*, with a wide range (median 0; range 0 - 0.93).

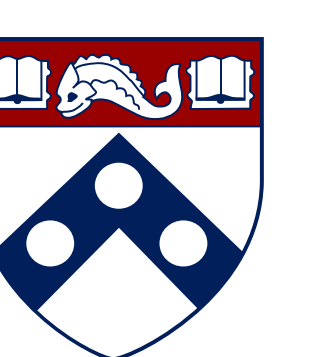
Results: *S. aureus* Impact on VAP & VAE

- Incident *S. aureus* VAP was observed within 30 days among 2 (25%) of Known *S. aureus* subjects, 0 (0%) of Suspected *S. aureus* subjects, and 3 (5.17%) of Unknown *S. aureus* subjects. VAE was observed within 30 days among 0 (0%) of Known *S. aureus* subjects, 3 (18%) of Suspected *S. aureus* subjects, and 1 (1.7%) of Unknown *S. aureus* subjects. Admission *S. aureus* abundance was positively associated with 30-day VAP risk in the Suspected (type S error < 0.001) and Unknown (type S error < 0.001) groups, and 30-day VAE risk in the Unknown group (type S error < 0.007).



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Contact Information

- Email: brendank@penmedicine.upenn.edu
- Code: github.com/bjklab
- Phone: 215.662.6932