ΔCulture-Independent Pilot Study of Microbiota Colonizing Open Fractures and Association with Severity, Mechanism, Location, and Complication From Presentation to Early Outpatient Follow-up

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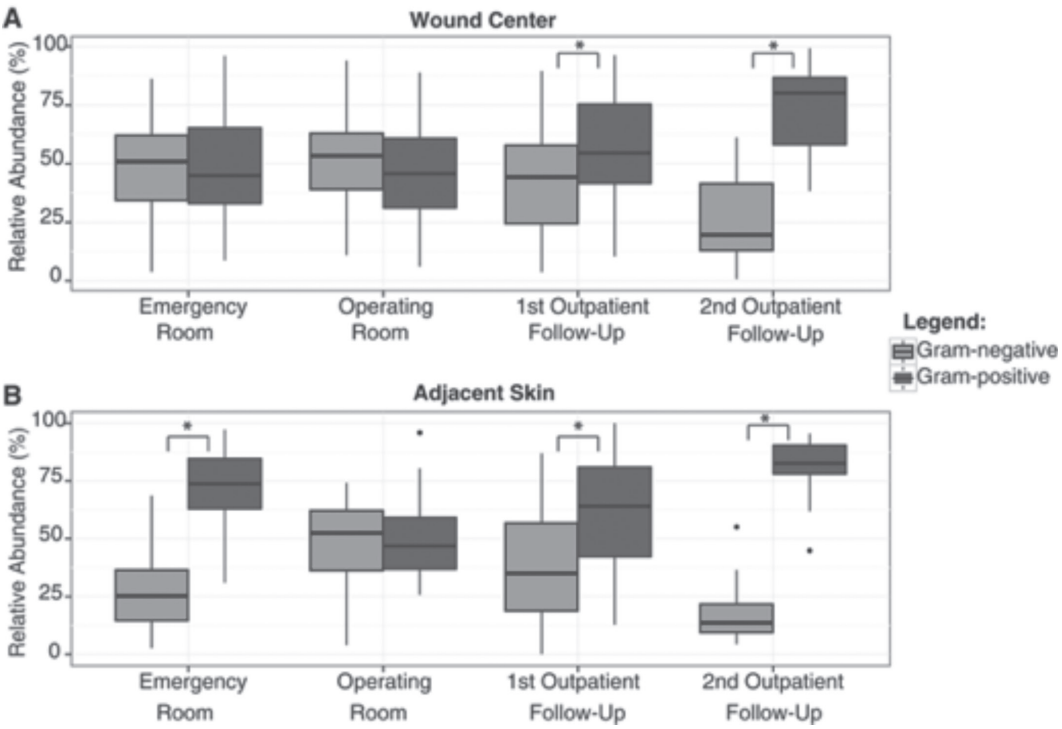
Purpose: Precise identification of bacteria associated with post-injury infection, comorbidities, and outcomes could have a tremendous impact in the management and treatment of open fractures.

Methods: We characterized microbiota colonizing open fractures using culture-independent, high-throughput DNA sequencing of bacterial 16S ribosomal RNA genes, and analyzed those communities with respect to injury mechanism, severity, anatomical site, and infectious complications.



Gram-positive and gram-negative bacteria in the open fracture wound and on the adjacent skin. Open fracture wound relative abundance is shown in (A) and adjacent skin relative abundance is shown in (B). The upper and lower box hinges correspond to the first and third quartiles. Lines within the box depict median, and the whiskers extend to the highest and lowest values within 1.5 times the IQR (interquartile range). Outliers of the IQR are depicted with black dots above or below the whiskers. *$p < 0.05$ (Wilcoxon rank-sum test).

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Results: 30 subjects presenting to our Level I trauma center for acute care of open fractures were enrolled in a prospective cohort study. Microbiota was collected from wound center and adjacent skin upon presentation to the emergency department, intraoperatively, and at two outpatient follow-up visits at approximately 25 and 50 days following initial presentation. Bacterial community composition and diversity colonizing open fracture wounds became increasingly similar to adjacent skin microbiota with healing. Mechanism of injury, severity, complication, and location were all associated with various aspects of microbiota diversity and composition.

Conclusion: The study demonstrates the diversity and dynamism of the open fracture microbiota, and their relationship to clinical variables. Validation of these preliminary findings in larger cohorts may lead to the identification of microbiome-based biomarkers of complication risk and/or to aid in management and treatment of open fractures.

See pages 99 - 147 for financial disclosure information.