Bacterial Species and Antimicrobial Resistance Patterns in Infected Wounds Kelsey Resler, AGNP, CWCN

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Introduction

Infection is one of the leading causes of delayed healing in chronic wounds. If left undiagnosed, wounds can remain stagnant for weeks, months, and even years. The goal of this retrospective study was to identify both the most prevalent high growth bacteria responsible for chronic wound infections as well as the antimicrobial resistance genes most commonly found within these bacteria. By identifying these, practitioners can implement targeted treatment plans to improve patient outcomes.

Methods

In this retroactive study, PCR wound cultures were collected from chronic wounds from October 2023 to November 2024 from a suburban-based outpatient wound clinic. PCR (Polymerase Chain Reaction) is a lab test that identifies specific DNA to detect bacteria, fungus, and resistance genes in a wound culture swab sample. Samples were obtained utilizing a "Z" pattern across the entire surface of the wound for ~ 15 seconds after sharp debridement and thorough cleansing of the wound bed with a pH balanced wound cleanser. Out of all samples collected, 74 grew high loads of bacteria which were the only samples used in this study.

Results

After isolating the high growth cultures, 16 species were identified and analyzed for their susceptibility patterns to antimicrobials. The 5 most prevalent bacteria were a mixture of gram positive and gram negative bacteria with Staphylococcus aureus being the most prevalent bacteria. Of the samples, 42% had high growth of Staphylococcus aureus, 18% had high growth of Pseudomonas aeruginosa, 18% had high growth of Enterococcus faecalis, 14% had high growth of Escherichia coli, and 10% had high growth of Enterobacter cloacae.

Out of these 5 most prevalent bacteria, every single one had 3 significant gene resistances to Tetracycline, Methicillin, and Macrolide-Lincosamide-Streptogram B; 80% carried Tetracycline resistance genes, 68% carried Methicillin resistance genes, and 66% carried Macrolide-Lincosamide-Streptogram B resistance genes. Tetracyclines most commonly include Doxycycline. Methicillins most commonly include <u>Penicillins</u>, <u>Cephalosporins</u> (Cephalexin) and Carbapenems (Ertapenem & Meropenem). Macrolide-Lincosamine-Streptogram B most commonly include Clindamycin, Erythromycin, Azithromycin, and Clarithromycin.

Overall, this data represents many commonly prescribed antibiotics are inappropriate due to the bacteria in these chronic infections being resistant to them.



/ancomvcin 🔳 3% Quinolone 5% 7% 68% 84% Reterences Leaper D, Assadian O, Edmiston CE. Approach to chronic wound infections. Br J Dermatol. 2015 Aug;173(2):351-8. doi: 10.1111/bjd.13677. Epub 2015 Mar 15. PMID: 25772951. Maheswary, T.; Nurul, A.A.; Fauzi, M.B. The Insights of Microbes' Roles in Wound Healing: A Comprehensive Review. Pharmaceutics 2021, 13, 981. https://doi.org/10.3390/ pharmaceutics13070981

Tetracycline

Carbapenems B- lactamase

Extended Spectrum Macrolide-Lincosamide Streptogram B



Conclusions

Many commonly prescribed antibiotics are not effective at treating the bacteria found in infected, chronic wounds. By isolating not only the most common bacteria that are causing infections in chronic wounds, but also their most common antibiotic resistance genes, providers can better understand how to guide their treatment for these antibiotic-resistant infections. This will produce better outcomes for the patient including infection resolution, wound healing, and overall improved physical and mental health as well as decreased healthcare costs, hospital admissions, and follow-up care.

MOST COMMON RESISTANT GENES

% of 74 Total Cultures with Resistance Genes