Antibiotic Susceptibility Testing, Molecular Profiling, and 16S rRNA-Based Identification of *Pseudomonas aeruginosa* Isolates from Musculoskeletal Infections

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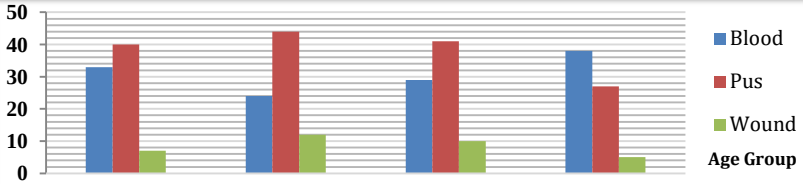
Background

Gram-negative opportunistic pathogen *Pseudomonas aeruginosa* causes musculoskeletal infections in immunocompromised individuals. The primary goal of this research was to describe antibiotic resistance and identification of virulence genes in *Pseudomonas aeruginosa.*

Materials & Methodology

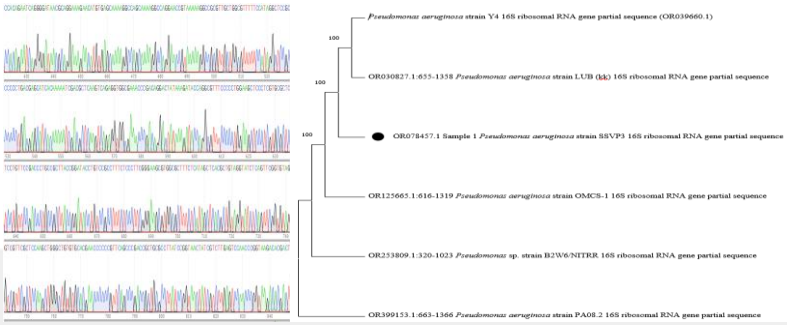
The study was cross-sectional, featuring a randomized selection of samples. Conducted from January to December 2023, the study encompassed a sample size of 320 including blood, pus, and wound swabs [Mele:169(52.8%), Female 151(47.1%)]. Age-based categories were ascertained, G1:13-20 years, G2:21-40 years, G3:41-60 years, G4:61-80 years. Identification tests for *Pseudomonas aeruginosa* included API20NE (bioMérieux®, France). Antimicrobial susceptibility testing was following the CLSI,2020 for the Disc Diffusion Test.DNA extraction and purification were carried out through a Genome Jet DNA Purification kit and 16S rRNA primers for the identification of resistance genes exoA and oprL. Phylogenetic and taxonomic identification was conducted via ribosomal RNA sequencing of PCR-amplified products(BIO-RAD T100TM Thermocycler) and sequencing with an automated sequencer (Illumina MiniSeqTM). Phylogenetic tree was constructed by MEGA11.p-value<0.05 was statistically significant.



Graphical distribution of sample distribution according to age groups

Samples	Quantity	Percentage
Tissue swab	53	19%
Wound swab	35	13.05%
Pus swab	110	41.02%
Blood	70	26.11%

The positive isolates were collected from different specimens.



Molecular characterization of *Pseudomonas aeruginosa*

Results

Prevalence of *Pseudomonas aeruginosa* was 22%. Positivity was recorded from pus (152/320:47.5%),blood(124/320-38.75%) and wound swabs(44/320-1 3.75%).G4 showed maximum positive isolates(91.25%).Maximum resistance was exhibited against Meropenem(76%) and Imipenem(70%).PCR identified the presence of resistance genes,exoA gene(125 bp), and oprL(105 bp). The phylogenetic tree was constructed through ribosomal RNA.The gene bank accession number for 16S rRNA gene *of P. aeruginosa* is PQ269824.

Conclusion

Antimicrobial susceptibility testing helps improve the treatment alternatives for stubborn strains . The presence of resistance genes highlights how research at the molecular level enhances treatment approaches for managing multi-drug resistant pathogens.