Diabetes Metab Syndr. 2018 May;12(3):417-421.

Molecular and culture based assessment of bacterial pathogens in subjects with diabetic foot ulcer.

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Expeditious and precise discerning of bacterial pathogens is a fundamental grail, of clinical diagnostic microbiology. Genotypic detection is a budding substitute to recognize phenotypic culture based processes in bacterial identification. We report a comparative evaluation of biochemical and genomic-based assays for exploring the commonest bacterial flora of infected diabetic foot ulcers along with clinical variables of subjects enrolled. The pathogens selected (i) Staphylococcus aureus ii) Pseudomonas aeruginosa, iii) Escherichia coli and iv) Klebsiella pneumonia, stood for the most frequent isolates of diabetic footinfection in previous studies from Northern India. Identification of these pathogens were done by conventional assays and polymerase chain reaction. Of 50 specimens obtained from infected DFUs, 74% of cases were affirmative by bacteriological assays and 90% showed positivity via polymerase chain reaction (PCR). Among processed samples 44 isolates were detectable through phenotypic analysis and 65 bacteria by species-specific PCR. Thirteen samples and 21 isolates could not be scrutinized by phenotypic identification systems. The most prevalent pathogens identifiable were Klebsiella pneumonia, followed by Staphylococcus aureus, Pseudomonas aeruginosa, and Escherichia coli. We have shown that PCR-based diagnostic methods improved the identification compared to conventional methods and highlight the incorporation of PCR due to shorten turnaround time translating into improved clinical outcomes.