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

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Diabetic foot ulcerations (DFUs), a dreadful micro-vascular complication is responsible for substantial increase in morbidity and mortality. DFU is a complicated amalgam of, neuropathy, peripheral arterial diseases, foot deformities and infection. Spanning the spectrum from superficial cellulitis, microbial flora leads to chronic ostemyelitis and gangrenous extremity requiring surgical interventions and lower limb amputations. Though expeditious and precise discerning of bacterial pathogens is a fundamental grail, of clinical diagnostic microbiology but when conventional methodologies are implemented in identifying bacteria, interpretation of test results requires substantial slanted judgment. Therefore, genotypic detection is budding as substitute to known phenotypic culture based processes. Typically, genotypic identification of bacteria involves the use of conserved sequences within phylogenetically informative genetic targets. Also time required in conventional diagnosis delays the selection of antibiotic regime making and adversely affects the outcome. Therefore, we report a comparative evaluation of biochemical and genomic based assays for exploring the common bacterial flora in infected DFU patients along with clinical variables of subjects enrolled. The pathogens selected (i) Kleibseilla pneumonia, ii) Pseudomonas aeruginosa, iii) Escherichia coli and iv) Staphylococcus aureus , stood for the most frequent isolates of diabetic foot infection (DFIs) in previous studies from Northern India. Of 50 specimens obtained from infected DFUs, 74% of cases were affirmative by bacteriological assays and 95% showed positivity via PCR methodologies. Among processed samples 44 isolates were detectable through phenotypic analysis and 73 bacteria by species specific PCR. 13 samples and 19 isolates could not be scrutinized by phenotypic identification systems. The most prevalent pathogens identifiable by both assays were *Klebseilla pneumonia*, followed by *Staphylococcus aureus, Pseudomonas aeruoginosa* and *Escherichia coli*. We have shown that PCR based diagnostic methods improved the identification of common aerobic pathogens compared to conventional phenotypic methods. The outcome of this study expresses that polymerase chain reaction provides rapid, unambiguous identification of clinical bacterial isolates. The results highlight the incorporation of PCR technique in bacterial identification due to shorten turnaround time and may translate into improve clinical outcomes by early use of appropriate antibiotic along with other principles followed in diabetic foot management.

Biography

Saba Noor is a PhD scholar, working under the supervision of Professor Jamal Ahmad at Rajiv Gandhi Centre for Diabetes and Endocrinology, Faculty of Medicine, J N Medical College. She has completed her Master's and Graduation in Biochemistry from Department of Biochemistry, Faculty of Life Sciences from the same university. She has published one original article and one review in peer-reviewed reputed international journals and presently working to improvise the diagnostic tools implemented in exploring microbial spectrum and immunological studies among diabetic foot patients.

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