

**ABSTRACT**

*Acinetobacter* species were isolated from human and animal clinical samples and were studied at molecular level. 100 samples were collected. Samples were identified by using preliminary biochemical tests and an identification kit (Remel RapidID ONE system). Moreover isolates were diagnosed at molecular level by 16S rRNA gene sequencing. Polymerase chain reaction was performed for 16S ribosomal RNA gene amplification and was sequenced. Antibiotic resistance profile was also determined which showed that the percentage resistance of isolates toward Lincomycin, Ciproflocacin, Kanamycin, Ofloxacin, Tetracyclin, Imipenem, Cefixime, Ampicillin, Chloremphinicol, Amoxicillin was 90, 70, 90, 90, 60, 70, 60, 60, 50 and 80 percent respectively. Polymerase chain reaction and sequencing were also done for the amplification of specific antibiotic resistant gene that was *gyrA*. Comparative analysis was done using NCBI-BLAST and CLUSTAL W. On the basis of *gyrA* gene, phylogenetic tree of *Acinetobacter* was also created by the method known as neighbor-joining method using MEGA 5 software.