ABSTRACT

The incidence of bacterial infections has been on the increase during past few decades, 25% deaths occur globally due to infectious diseases. *Staphylococcus aureus* is one of the most important pathogens of humans and animals causing wide variety of disease conditions. This organism causes urinary tract infections, wound infection, respiratory tract infection and septicaemia etc and is currently one of the most common causes of hospital acquired infections. The present study aims at determining the prevalence of Methicillin resistant *S. aureus* strains recovered from blood, urine and pus of human patients at Indira Gandhi Medical College and Hospital (IGMC), Shimla, Himachal Pradesh (India). Selective MRSA isolates were characterized based on the PCR amplification of drug resistance gene (mec-A-H, van-A genes) and virulence gene-pvl. Also, the isolates were bacteriophage typed and analysed for plasmid profiling. Clinical isolates of *S. aureus* (n=135) were confirmed as *Staphylococcus aureus* in the Microbiology laboratory at Shoolini University. By MRSA detection kit, 62 (45%) isolates were detected as methicillin resistant. Of these, 44 MRSA isolates were resistant to multiple antibiotics. The amplification of all the genes under study was achieved in the PCR assays in all the isolates examined except a few. On nucleotide sequencing of the amplicons of mec-A-hypervariable region and pvl genes of isolates of different origins, variability was observed. The major substitutions in the predicted amino acids of mec-A-H amplicons were seen at positions 66, 85, 98, 122, 145 and 161 as follows: T66L, Q85K, V98A, N122S, T145K and S161K in these all strains. In case of pvl, the major substitutions in the predicted amino acids were seen at positions: 20, 21, 22, 40, 65, 76, 87 and 98 as follows: N20G(urine-135), E21I(urine-135), L22P(urine-135), H40Q(pus-97), K65R(urine-135), K76E(urine-135), K87R(urine-135) and H98Q(pus-97). Such variations might play role in the pathogenesis of MRSA infections. Out of 40 MRSA isolates examined 36 (90%) isolates harboured a single type of plasmid of ~2 kb. The bacteriophage typing of these isolates revealed mixed phage group (46.87%) and phage group III (37.50%) followed by phage group II (12.5%) and phage group I (3.13%). Phage groups NA and V however, did not lyse any strain. Thus, the characterization of MRSA strains prevalent in this part of the country could be helpful in studying the epidemiology.