



ABSTRACT

Staphylococci are one of the leading causes of urinary tract infections (UTIs) in humans. The emergence of multiple drug resistance (MDR) among *Staphylococci* poses a serious challenge in antimicrobial therapy for UTIs. The current study was conducted to establish a baseline profile of drug resistance in *Staphylococci* isolates from urinary tract infections. A total of 20 isolates from urinary tract infections were screened and 13 were found to have *Staphylococci* which were identified biochemically and confirmed by molecular methods. Using disc diffusion method, drug resistance was observed against erythromycin (100%), gentamycin, azithromycin and tetracycline (92.3%), ampicillin and oxytetracyclin (84.6%), amikacin and srteptomycin (76.9%), methicillin (69.2%), vancomycin (53.8%) and cephradine, cefaclor and cefazolin (53.8%). In an effort to find relevant drug resistance genes, twenty different genes were targeted by PCR: among these *tetM* gene was found to be most prevalent (46.1%) followed by *tetK* (30.7%), *aac(6')/aph(2'')* (30.7%), *aacA-aphD* (23%), *ermA* (23%), *blaZ* (23%), *mecA* (23%) *bla_{TEM-1}* (23%), *Mecca* (23%), *mecA* (15.3%) and *pta* (7.6%) genes. The targeted genes for vancomycin resistance were *vanR*, *vanS*, *vanH*, *vanA*, *vanX*, *vanY*, and *vanZ* but none of these isolates was positive for any of these genes. The salient finding was that all *Staphylococci* isolates were multiple drugs resistant as they showed resistance against at least three structurally different antimicrobial agents. It is concluded that in addition to the mostly used antimicrobial agent vancomycin, the cephalosporins including cephradine, cefaclor and cefazolin are also the drugs of choice against UTIs caused by *Staphylococci*.