

Abstract

Background: ESBL producers are an important cause of drug resistant infection world-wide. No studies have been done to assess the genotype of this emerging threat in Sri Lanka.

Methods : The study was conducted in 2004 on sequentially collected clinical samples presumptively identified as *Escherichia coli* & *Klebsiella spp* by colony appearance & gram stain during a three month period. The samples were screened using the NCCLS screening criteria for ESBL . Confirmatory tests for ESBL using the Oxoid combination disk method was done on the screening positive isolates .The combination disks used were Ceftazidime/Clavulanic acid & Cefotaxim/Clavulanic acid . The positive isolates were confirmed as being *Escherichia coli* & *Klebsiella spp* by biochemical tests . 50 ESBL positive isolates thus obtained were tested by PCR for blaSHV & blaTEM genes by the following primers

blaSHV – Forward GGT TAT GCG TTA TAT TCG CC

Reverse TTA GCG TTG CCA GTG CTC

blaTEM – Forward ATG AGT ATT CAA CAT TTC CG

Reverse CTG ACA GTT ACC AAT GCT TA

Results : The gene for TEM , blaTEM was found in 19 out of 50 isolates tested (38%) . The gene for SHV , blaSHV was found in 16 out of 50 isolates (32%). Both blaSHV & blaTEM was found in 7 isolates (14%) Either of the genes could not be demonstrated in 22 isolates (44%). 17 isolates were *Klebsiella spp* (34%) out of which 10 had blaSHV (59%) 6 had blaTEM (35%) 5 had both (29%) 6 had neither (35%) . 33 isolates were *Escherichia coli* of which 10 had blaTEM (30%) 4 had blaSHV (12%) 1 had both (3%) 20 had neither (60%)

Conclusion : More research has to be done in this area as little is known on the distribution , prevalence phenotypic and genotypic characteristics of ESBL in this country