Abstract

**Background:** Characterization of phenotypic/genotypic properties of pathogenic *E. coli* causing extraintestinal infections (ExPEC) and to correlate findings with clinical outcome of patients.

**Methods:** The descriptive study was conducted on 300 in-patients with ExPEC infection. Production of haemolysin, biofilm & β-lactamase enzymes were detected by phenotypic methods. Phylogenetic analysis (*chuA, yjaA and TSPE4.C2*), virulence (*fimH, hlyA, papC, cnfl, iutA, neuC*) and drug resistance (*ESBL: TEM, SHV, CTXM, CTXM-15*; plasmid mediated ampC: *MOX, CIT, DHA, ACC, EBC & FOX*; MBL: *NDM-1*) genes were determined by multiplex PCR. Patient’s follow up were done for up to 1 year. Clinical data from the patient’s were collected in a structured proforma.

**Results:** Of 300 patients with ExPEC infection, 10% expired, 18% had relapses and 72% recovered. Phenotypic methods detected 24% isolates as β-haemolytic, 40% expressed biofilm, 70% were ESBL producers (32% AmpC +, 7.5% carbapenemase + & 5% MBL +). Phylogenetic analysis revealed 61 isolates belonged to phylogroup A, B1 (27), B2 (104) and D (108). Among virulence genes, percentage strains carrying *fimH* was 90%, followed by *iutA* (68%), *papC* (45%), *hlyA* (23%), *cnf* (23%) and *neuC* (5%) respectively. Among drug resistance genes, 70% possessed ESBL genes, 12% *CIT*-AmpC & 5% carried bla<sub>NDM1</sub>.

**Conclusion:** Results indicate there is an inverse relationship between resistance and virulence with reference to ExPEC causing extraintestinal infections. Virulence of infecting strain, as well as patient related factors are equally responsible for development and outcome of infections.