Conclusions

1. Out of 300 patients with ExPEC infection 10% died, 18% relapsed and 72% recovered without sequelae.
2. Mortality was higher in patients with sepsis (25%).
3. Female sex was a risk factor for UTI while carcinoma, advanced age and diabetes mellitus were the common risk factor for ExPEC infection,
4. While diabetes was associated with recurrences, carcinoma was associated with mortality.
5. 24% ExPEC isolates were found to be β- haemolytic, 10% had atypical characters and around 40% were biofilm producers.
6. Phenotypically 70% E.coli isolates were ESBL producers, 32% were AmpC producers and 10% carbapenemase producers of which 7% were MBL producers.
7. Our isolates showed high degree of resistance to commonly used antibiotic such as ampicillin (87%), Piperacillin (75%), ciprofloxacin (35%), Norfloxacin (40%) respectively.
8. Our isolates were sensitive to cefoperazone/sulbactam (65%), piperacillin/tazobactam (75%), Amikacin (84%), nitrofurantoin (89%) and carbapenem group of drugs (approx 95%) respectively.
9. We recommended that BL+BI combination should be used for infection such as UTI or wound infection and for more serious infection such as sepsis, meningitis, pneumonia carbapenem is the drug of choice. Nitrofurantoin and Amikacin cannot be used for inpatients but can be used for outpatient setup.
10. Sixty one isolates were found to belong to phylogroup A and 27 strains to group B1, both phylogroups which are known to be commensal groups. Among the virulent groups (phylogroups B2 & D), 104 were from group B2 and 108 were from group D.
11. On analysis of virulence genes among the isolates, we found maximum number were carrying fimH (90%) gene followed by iutA (68%), papC (45%), hlyA (23%), cnf1 (23%) and neuC (5%) respectively.
12. Of the 300 isolates, 70% isolates were found to be positive for ESBL genes. A total of 62% strains were positive for bla\_CTX-M gene, 14% isolates were found to be positive for bla\_TEM and only 4% isolates were found to be positive for bla\_SHV. Approximately 92% bla\_CTX-15 producers were found to be positive for bla\_CTXM-15.
13. CIT type of plasmid mediated AmpC were seen only in 12% of isolates.
14. Very few isolates were carrying bla\_NDM1 gene (6%).
Conclusions

15. There was significant correlation between α-haemolysin (phenotypic) expression and the possession of the virulence genes \( \text{papC, cnf1 and iutA} \) indicating that the haemolytic strains carry maximum number of virulence genes.

16. Among the atypical \( \text{E.coli, iutA, hlyA and neuC} \) genes were significantly higher indicating that atypical \( \text{E.coli} \) are more virulent.

17. There was no significant difference in distribution of virulence genes among the biofilm producing isolates and non producing isolates.

18. In ESBL phenotypic testing we found around 2% isolates showed false negative results in comparison to molecular detection.

19. There is a significant discrepancy in-between phenotypic detection of AmpC producing isolates and genotypically positive isolates which was due to the fact that we did not do chromosomal AmpC detection.

20. It was observed that 16 out of 17 NDM1 positive isolates were phenotypically carbapenemase positive, as well as MBL producers and only one isolate was not detected by the phenotypic methods.

21. There was a significant association between the \( \text{iutA} \) gene and invasive isolates.

22. It was found that \( \text{iutA} \) also plays a significant role in clinical severity as indicated by higher APACHE II score.

23. In correlation between outcome of infection with possession of virulence and drug resistance genes we found that \( \text{papC, cnf1, neuC and hlyA} \) play an important role in recurrent infections. There was no correlation between clinical recovery or mortality with the possession of virulence and drug resistance genes indicating that host factors, early use of appropriate antibiotics may influence outcome.

24. Among the tested VFs we found a statistically significant higher prevalence of \( \text{papC, cnf1, hlyA and iutA} \) genes among the virulent (B2 &D) strains.

25. Possession of antimicrobial resistance genes such as ESBLs, pAmpC and NDM-1 indicated that beta lactamase producing isolates occurred with greater frequency in group A and B1 isolates when compared with B2 and D.

26. In correlation with phenotypically susceptible and resistance isolates with virulence genes we found that \( \text{hlyA, iutA, cnf1} \) genes were significantly less in fluoroquinolone-resistant isolates when compared to fluoroquinolone-susceptible isolates.

27. There was a significant negative association between \( \text{hlyA} \) and \( \text{cnf1} \) genes with ESBL negative isolates. In case of \( \text{pAmpC} \) and \( \text{NDM-1} \) producing isolates we also
observed a negative correlation where we found that pAmpC and NDM1 positive isolates were carrying less virulence genes when compared to negative isolates.

Hence we conclude that there is inverse relationship between resistance and virulence with reference to extraintestinal *E.coli* infections.

**Limitation of our study:**

1. Clinical outcome can be influenced by host factors, time of presentation and antibiotic choice in addition to the phenotypical and genotypical characters of the infecting *E.coli* strains.
2. Recommendation of antibiotics based on our study is reliable for ESBL producers. For ampC and carbapenemase producers we have not included cefepime and polymyxins in our culture studies and our recommendation is only theoretical.
3. The presence of only plasmid mediated AmpC β-lactamase genes was targeted and other possible mechanisms of cefoxitin resistance like chromosomal hyper-producers or porin loss mutants were not detected.