

POSTER PRESENTATION

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Incidence of bla genes among uropathogenic Escherichia coli isolates from HIV and non-HIV patients in South India

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Background

Group 3a/b cephalosporins are currently being used in the treatment of UTI and urosepsis. However, Extended Spectrum Beta-Lactamase (ESBL) mediated resistance has been increasingly reported among uropathogens from HIV patients. We sought to determine the incidence of ESBL genes- bla_{CTX-M} , bla_{TEM} and bla_{SHV} among $E.\ coli$ isolates from HIV (with increased exposure to cephalosporins) and non-HIV antenatal patients.

Methods

PCR detection of bla_{CTX-M} , bla_{TEM} and bla_{SHV} were carried out among ESBL producing urinary $E.\ coli$ isolates from HIV (n=57) and non-HIV antenatal patients (n=22). Fisher's exact test was employed to analyze the statistical significance of the results.

Results

Overall, 31.7%, 59.5% of the *E. coli* isolates carried *bla*_{TEM}, *bla*_{CTX-M} respectively, while none harboured bla_{SHV}. When stratified based on host group, significant difference was observed in the incidence of *bla*_{CTX-M} among the isolates from HIV and non-HIV patients (70.2% vs 31.8% respectively, p = 0.0024; OR 5.042; 95% CI = 1.7441-14.5759). Nonetheless, difference in prevalence of *bla*_{TEM} among the HIV and non-HIV isolates was not statistically significant (29.8% vs 36.4%, p = 0.5979). Co-occurrence of *bla*_{TEM} and *bla*_{CTX-M} was detected among 22.8%, 0% of the *E. coli* isolates from HIV and non-HIV patients respectively (OR 5.1447; 95% CI = 1.3766-19.2273).

Conclusion

Our results augment the fact that frequent exposure to cephalosporins serves as the driving selection force leading to increased incidence of ESBL (bla_{CTX-M}) mediated resistance among the $E.\ coli$ isolates from HIV patients. Hence, the risk associated with antimicrobial exposure needs to be considered in therapeutic decision making.

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