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ePoster Viewing
Antibacterial activity and drug interactions - miscellaneous organisms and agents

VIRULENCE PROFILES, ANTIMICROBIAL RESISTANCE AND GENETIC DIVERSITY OF ESCHERICHIA COLI STRAINS OF UROSEPSIS AND SOFT TISSUE INFECTIONS FROM INDIA AND SEPTICAEMIA ISOLATES FROM GERMANY

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Background

Urinary tract infection (UTI) is the most common extraintestinal infection caused by *Escherichia coli* (*E. coli*). In addition, *E. coli* can cause several invasive extra urinary infections such as septicaemia, soft tissue infections, meningitis and pneumonia. Several studies on different extraintestinal infections regarded *E. coli* to be syndrome specific by giving it different designations such as: Uropathogenic *E. coli* (UPEC), neonatal meningitis *E. coli* (NMEC), septicaemia associated *E. coli* (SEPEC) and Avian pathogenic *E. coli* (APEC). However, there are reports that suggest these different pathotypes can cause cross infections at multiple anatomical sites.

Objective

It appeared pertinent to ask whether there are similarities in properties such as phylogenetic background, virulence profile, drug resistance mechanisms and genotypes between *E. coli* of different pathotypes and geographic origins, so as to identify which of these factors is contributing to the generic and/or specific pathogenicity of *E. coli* implicated in uroseptic infections.

Bacterial samples

We present here an analysis of 58 *E. coli* from cases of Urosepsis and 21 *E. coli* associated with soft tissue infections from two hospitals in India (jan2009- dec2012), along with 44 genomic DNA samples (2009) of septicaemia *E. coli* from Germany. All Indian isolates have been characterized by several phenotypic and genotypic methods. German *E. coli* isolates were only characterized genotypically.

Results

Phylogenetic grouping placed majority of Urosepsis and German septicaemia isolates in groups B2 and D, whereas the soft tissue infection associated *E. coli* were mainly affiliated to phylogroup A. Antimicrobial susceptibility towards six different non β-lactam antibiotics revealed higher resistance rates in Urosepsis as compared to soft tissue infections with 67 % of multidrug resistance (MDR), 82% Extended spectrum β-lactamase producers (ESBL) and 43% MDR, 76% ESBL in Urosepsis and soft tissue infection associated *E. coli* respectively. Majority of the Indian *E. coli* isolates produced alpha haemolysis irrespective of pathotypes. Genotyping of antimicrobial resistance demonstrated no unique resistance gene profiles between *E. coli* associated with Urosepsis and soft tissue infections from India and German septicaemia isolates. Among the twelve ExPEC virulence genes sought, the different pathotypes did not differ significantly for the presence of virulence genes except for *cvaC*, *traT*, *sfaD/E* and *usp* in german isolates with *SfaD/E*, *usp* and *cvaC* being totally absent in *E. coli* from soft tissue infections. Fingerprinting by ERIC PCR revealed genetic diversity among the three pathotypes by demonstrating a more or less disease and geographic specific clustering.

Conclusion

The most important finding of our study is that, although the *E. coli* belonging to different pathotypes and geographic origin are genetically diverse, there is considerable overlap in *E. coli* obtained from different disease specifications and geographic origin with respect to their affiliation to phylogroups, virulence profiles and drug resistance features.