

ABSTRACT

Objectives : This study aim to classified the phylogenetic *Extended-spectrum β -lactamase-producing Escherichia coli* in intestinal flora of neonates into groups A, B1, B2, D and tracing the presence of transmission between hospes because of double impact occurred by *Escherichia coli* from phylogenetic group of B2 and D which are generally dominant in *E. coli* infections.

Methods : Triplex classified the phylogenetic *E. coli* ESBL into groups komensal (A, B1) and pathogen (B2, D). Tracing transmission of *E. coli* ESBL using RAPD-PCR method with two random primers to observe the RAPD-type.

Results : The phylogenetic distribution from 34 samples were correlated with the age of early neonates (ages 0-7 days) and postneonatus (age > 28 days-1 year) showed insignificant results ($p = 0,388$). Total groups A (11,8%), B1 (5,9%), B2 (32,4%) and D (38,2%) were found and the rest were not identified. The dominance of pathogenic groups B2 and D as much as 70,6%. From 34 samples was found 31 types of RAPD. Similar types were found in RT VI with 2 isolates and RT VII with 3 isolates, all of isolates are phylogenetic group D.

Conclusions : Statistical analysis between two age groups of neonatus had no relation on the types of filogenetik groups. Indication of strain transmission from host to other host is rarely occurs in naonatus patients who have interaction at the health service center.

Keywords : *Escherichia coli*, ESBL, neonates, phylogenetic, phylogrup, pathogen, transmission