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P1485 Genotyping of extended-spectrum beta-lactamase producing Escherichia coli isolates from gut among patients with hemoblastoses

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Background: The aim of this study was to evaluate the molecular relatedness of extended-spectrum beta-lactamase (ESBL) producing *Escherichia coli* isolated at admission and during hospitalization.

Materials/methods: Prospective study was performed from April 2013 to October 2014. ESBL colonization of gut was evaluated in patients with newly diagnoses acute myeloid leukaemia (AML) and lymphoma at admission and during 96 days of hospital stay. Rectal swabs were obtained at admission and every week up to 96 days. ESBL-production was confirmed by phenotypic tests (EUCAST, 2013). ESBL producing *E.coli* isolates were examined by enterobacterial repetitive intergenic consensus method (ERIC-PCR). Analysis of genomic fingerprinting were performed using GelJ v.1.3 software by unweighted pair group method using arithmetic averages (UPGMA). Strains were considered genetically related if the similarity index was ≥ 80%.

Results: Study included 73 patients (median age 46 years; 43 female and 30 male) with AML (n=25) and lymphoma (n=48). A total 66 ESBL producing Enterobacteriaceae (ESBL-E) isolates were identified: 22 – at admission of those 54.5% were *E. coli* (n=12), 44 – during hospital stay of those were 61.4% *E. coli* (n=27). ERIC-PCR was performed for all 39 *E. coli* producing ESBL. Genetically related *E. coli* strains were not detected among isolates at admission. Genotyping of 27 *E. coli* isolates obtained during hospital stay revealed a genetic identity in 16 (59%) isolates with similarity index 83-100%. From two patients hospitalized in different departments two closely related (similarity index 100%) isolates were obtained with interval 40 days.

Conclusions: DNA fingerprinting by ERIC-PCR revealed diversity of ESBL-E isolates obtained at admission and 59% of isolates were probably transmitted from patient to patient during hospital stay. Molecular analyses showed both multiclonal and monoclonal paths of ESBL-E dissemination. This diversity could be due to the dissemination of particular plasmids between isolates and spread of epidemiological strains. The surveillance of ESBL-E colonization can provide guidelines to prevention of colonization and infection with the same bacteria.