

# The role of phylogenetic groups of *Escherichia coli* in childhood recurrent urinary tract infections

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## Introduction

Urinary tract infection (UTI) is one of the leading infection sites in children. The most common bacterial species causing UTI is *Escherichia coli*. The *E. coli* strains have been assigned to four main groups – A, B1, B2 and D. Strains from phylogenetic group B2 and D are generally more virulent, but also less resistant and contain resistance-encoding integrons to a lesser extent than strains from groups A and B1. The latter phylogenetic groups are considered to be commensal with low virulence, but have a higher resistance rate accompanied by the occurrence of integrons. Recently, contradicting data about the higher resistance of uropathogenic *E. coli* strains belonging to phylogenetic group B2 have been published.

Information about the clonality of recurrent UTI isolates is important in understanding the essence of the infection. The persistence of the primary infecting strain or re-infection with a new strain may challenge different treatment strategies. At the same time, the role of phylogenetic groups in clonal and non-clonal recurrences of chronic childhood UTI is not elucidated yet.

## Objectives

We aimed to compare the role of phylogenetic groups of *E. coli*, antibacterial susceptibility and containment of class 1 integrons in relation to first infectious attack and subsequent recurrences of urinary tract infection caused by relapsing or re-infecting strains.

## Methods

Altogether 89 urinary *E. coli* isolates from 41 children (35 girls and 6 boys) were included. Index isolates (n=41) from a first acute pyelonephritis and isolates from recurrent UTI episodes (n=48) were studied. Phylogenetic groups and occurrence of class I integrons were detected by PCR. E-tests were used for antimicrobial susceptibility testing. PFGE was applied to compare the consecutive 74 isolates of 26 patients with recurrences.

Table. Phylogenetic characterization and antibacterial resistance of isolated *Escherichia coli* strains (n=89); SXT- trimethoprim-sulfamethoxazole

<i>E. coli</i> phylogenetic group	No of strains				
	Total No of strains	First attack of APN	Recurrent episodes	Betalactam resistant	SXT resistance
A	16	4	12	6	7
B1	4	1	3	1	0
<b>B2</b>	<b>51</b>	<b>25</b>	<b>26</b>	<b>20</b>	<b>13</b>
D	18	11	7	10	5
Total	89	41	48	37	25

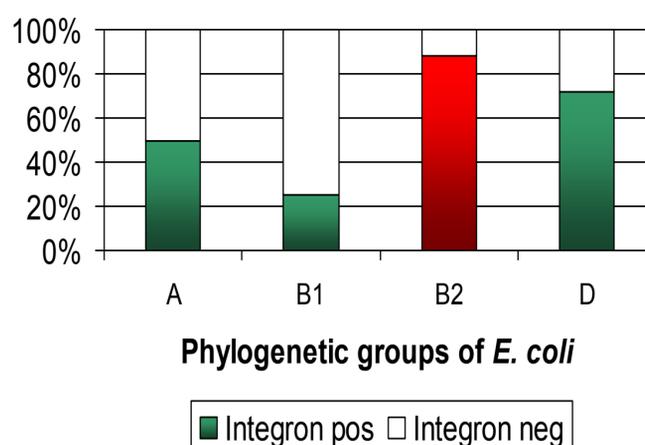


Figure. Class I integron containment of different phylogenetic groups of *Escherichia coli* isolates (n=89) in childhood urinary tract infection.

## Results

More than half (51/89; 57%) of isolates belonged to the phylogenetic group B2 (Table). Group A (16/89; 18%) and D (18/89; 20%) were found with similar frequency, and B1 was the least common (4/89; 4%). Group B2 was also the most frequent as an index episode (25/41; 61%). Antibiotic resistance was detected to trimethoprim-sulfamethoxazole (28%), ampicillin (44%), cefuroxime (27%), cefotaxime (3%) and gentamicin (2%). There was no association between antibiotic susceptibility and phylogenetic groups.

PFGE revealed the unique clonal strains in 20/26 (77%) of patients, presenting as relapses. When comparing clonal relapses caused by the same strain as the initial infectious episode, the phylogenetic group B2 (13/16, 81%) was shown to be prevalent when compared to groups A (0/16), B1 (1/16, 6%) and D (2/16, 13%). Clonal strains compared to individual ones had lower sensitivity to cefotaxime (MIC median 0.079 vs. 0.032, respectively; p=0.004) and gentamicin (MIC median 0.75 vs. 0.5, respectively; p=0.011). Strains of phylogenetic group B2 consisted more often integrons than group A (45/51 vs. 8/16, respectively; p=0.003) (Figure). Intl pos compared to neg strains had higher MIC values to cefuroxime (MIC median 4.0 vs. 2.0, respectively; p=0.001), cefotaxime (MIC median 0.079 vs. 0.032, respectively; p=0.014), gentamicin (MIC median 0.75 vs. 0.44, respectively; p=0.003).

## Conclusions

Group B2 was the most common cause of the first episode of pyelonephritis as well as the persistence of the same strain in children and also contained most frequently class I integrons. Though the integron positive strains of *E. coli* express higher MIC values, the phylogenetic group diversity is not associated with antibiotic susceptibility or