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20-5960 Whole genome analysis and phylogenetic characteristics of *Escherichia coli* isolated from urine and stones in calcium oxalate stone patients

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Results

Table 1. Distribution of antimicrobial resistance in *E. coli* strains isolated from urine (EUC) and stones (ESC).

Antimicrobial	ESC(n=50)		EUC(n=33)		p
	R/No	%	R/No	%	
Amikacin	2/50	4.0	2/33	6.1	1.0
Amoxicillin/Clavulanate	5/50	10.0	4/33	12.1	1.0
Ampicillin	29/37	78.4	10/12	83.3	1.0
Aztreonam	13/36	36.1	5/12	41.7	0.743
Cefazolin	21/49	42.9	20/31	64.5	0.059
Cefepime	14/49	28.6	9/32	28.1	0.965
Cefoperazone/Subactam	4/47	8.5	1/32	3.1	0.621
Cefotaxime	24/50	48.0	18/33	54.6	0.559
Cefoxitin	6/48	12.5	6/33	18.2	0.479
Ceftazidime	13/47	27.7	11/33	33.3	0.586
Ceftriaxone	24/49	49.0	18/33	54.6	0.621
Cefturoxime	23/46	50.0	14/33	42.4	0.506
Ciprofloxacin	15/37	40.5	5/12	41.7	0.945
Ertapenem	2/50	4.0	0/33	0	0.515
Gentamicin	15/37	40.5	9/12	75.0	0.081
Imipenem	2/50	4.0	0/33	0	0.515
Levofloxacin	20/48	41.7	13/33	39.4	0.838
Meropenem	2/47	4.3	0/33	0	0.509
Nitrofurantoin	4/45	8.9	0/24	0	0.289
Piperacillin/Tazobactam	3/49	6.1	2/32	6.3	0.981
Sulfamethoxazole	28/50	56.0	17/33	51.5	0.688
Tobramycin	4/35	11.4	5/12	41.7	0.061

R: resistance; No: number.

Table 2. Distribution on phylogenetic groups and sequence types (ST) in 83 *E. coli* isolates. Number (%).

	Total (n=83)	ESC (n=50)	EUC (n=33)	p
Phylogenetic group				
B2	50(60.2)	27(54.0)	23(69.7)	0.153
D	25(30.1)	16(32.0)	9(27.3)	0.646
A	6(7.2)	5(10.0)	1(3.0)	0.443
B1	2(2.4)	2(4.0)	0	0.666
Sequence type (ST)				
ST1193	15(18.1)	6(12.0)	9(27.3)	0.077
ST131	11(13.3)	6(12.0)	5(15.2)	0.933
ST73	6(7.2)	3(6.0)	3(9.1)	0.921
ST69	5(6.0)	4(8.0)	1(3.0)	0.646
ST12	4(4.8)	3(6.0)	1(3.0)	0.925
ST224	4(4.8)	4(8.0)	0	0.254
ST648	4(4.8)	3(6.0)	1(3.0)	0.925
ST62	3(3.6)	1(2.0)	2(6.1)	0.712
ST156	3(3.6)	2(4.0)	1(3.0)	1.0
ST162	3(3.6)	2(4.0)	1(3.0)	1.0
ST6756	2(2.4)	2(4.0)	0	0.151
ST405	2(2.4)	1(2.0)	1(3.0)	1.0
ST550	2(2.4)	1(2.0)	1(3.0)	1.0
ST3177	2(2.4)	1(2.0)	1(3.0)	1.0
ST4381	2(2.4)	1(2.0)	1(3.0)	1.0
ST6807	2(2.4)	1(2.0)	1(3.0)	1.0
other	13(15.7)	9(18.0)	4(12.1)	0.68

EUC: *E. coli* isolated from urine.

ESC: *E. coli* isolated from stones

Table 3. General characteristics of 16 whole genome sequenced isolates of *E. coli* from urine (EUC) and stones (ESC) in 8 patients.

Patient No.	Isolate	Source	ST	Raw Data (Mb)	Genome Size (Mb)	%GC content	No. of contigs (>500 bp)	N50 Length(bp)	Total Length(bp)	GenBank accession no
1	ESC1	stone	1193	848	5.68	50.60	41	237,323	4,934,974	SAMN09829079
	EUC1	urine	1193	861	5.62	50.45	59	233,866	5,032,283	SAMN09829087
2	ESC2	stone	1193	921	5.87	50.60	64	222,076	5,090,175	SAMN09829080
	EUC2	urine	1193	861	5.55	50.59	69	222,466	5,105,378	SAMN09829088
3	ESC3	stone	1193	859	5.61	50.59	66	207,532	5,106,238	SAMN09829081
	EUC3	urine	1193	841	5.51	50.54	70	210,541	5,189,592	SAMN09829089
4	ESC4	stone	1193	862	5.35	50.63	52	222,472	4,988,410	SAMN09829082
	EUC4	urine	1193	862	5.39	50.61	67	222,076	5,060,440	SAMN09829090
5	ESC5	stone	1193	855	5.84	50.43	62	201,068	5,054,441	SAMN09829083
	EUC5	urine	1193	859	6.13	50.58	70	216,510	5,095,647	SAMN09829091
6	ESC6	stone	131	845	5.3	50.77	64	353,825	5,120,644	SAMN09829084
	EUC6	urine	131	860	5.35	50.76	59	353,825	5,110,513	SAMN09829092
7	ESC7	stone	131	859	5.0	50.73	66	238,968	4,945,649	SAMN09829085
	EUC7	urine	131	847	5.04	50.74	69	238,458	4,951,026	SAMN09829093
8	ESC8	stone	131	865	5.89	50.68	82	248,754	5,305,291	SAMN09829086
	EUC8	urine	131	844	5.8	50.69	87	239,941	5,323,603	SAMN09829094



In summary

- The phylogenetic groups B2 and D, the genotypes ST1193 and ST131 were most common E.coli strain isolated from urine and stone in CaOx stone patients.
- Consistent antimicrobial susceptibility profiles.
- Consistent genotypes, as well as virulence and resistance genes.