

**Table 1**

The *E. coli* isolates from different sources and distribution of major virulence genes with regard to subtilase possession

No. of Isolates	Virulence genes				No. of isolates (No. of <i>subAB</i> +)			
	<i>stx1</i>	<i>stx2</i>	<i>eae</i>	<i>ehly</i>	Sheep (n=15)	Goats (n=25)	Cattle (n=50)	Other species (n=11)
6	+					5 (3)	1	
7		+					7	
1	+	+					1	
23	+	+		+	3 (3)	9 (9)	8	3 <sup>b</sup> (3)
17		+		+		1	15 (12)	1 <sup>c</sup> (1)
26	+			+	11 (11)	11 (11)	1	3 <sup>d</sup> (3)
13	+		+	+			13	
6		+	+	+			2	4 <sup>e</sup>
1	+	+	+	+			1	
1	+		+				1	
28		+ <sup>a</sup>	+					
Total Positive (%)					14 (93.3)	24 (92.0)	12 (24.0)	7 (63.6)

<sup>a</sup> *stx2f*<sup>+</sup>

<sup>b</sup> Persian follow deer (n=2), Caspian pony (n=1)

<sup>c</sup> Persian follow deer

<sup>d</sup> Diarrheic children

<sup>e</sup> *Macaca mulatta*

**Table 2**

Distribution of Subtilase variants, Shiga toxin gene(s), O-serogroups and phylogenetic groups among *E. coli* isolates from various sources

Genetic traits	Hosts (no. of subAB+ isolates)				Total (57)
	Sheep (14)	Goat (24)	Cattle (12)	Others <sup>a</sup> (7)	
Subtilase profiles <sup>b</sup>					
<i>subAB1</i>			12		12
<i>subAB2-1</i>		1		1 <sup>D</sup> , 1 <sup>P</sup>	3
<i>subAB2-2</i>	1				1
<i>subAB2-1/2-2</i>	13	23		3 <sup>H</sup> , 2 <sup>D</sup>	41
Shiga toxin profiles					
<i>stx1</i>	11	14		3 <sup>H</sup>	28
<i>stx1/stx2</i>	3	9		2 <sup>D</sup> , 1 <sup>P</sup>	15
<i>stx2</i>		1	12	1 <sup>D</sup>	14
Sero-group					
O5	7				7
O113		2	10	2 <sup>D</sup> , 1 <sup>H</sup>	15
O128		2			2
Unknown	7	20	2	3 <sup>H</sup> , 1 <sup>D</sup>	33
Phylo- group					
A		1	1	2 <sup>D</sup> , 1 <sup>P</sup>	5
B1	14	23	10	3 <sup>H</sup> , 1 <sup>D</sup>	51
E			1		1

<sup>a</sup>Other sources are indicated as superscripts, H (Humans), D (Deer), P (Pony)

<sup>b</sup>Subtilase AB2-3 was negative in all isolates

**Table 3**

Virulence gene combinations, subtilase variants, serogroups and phylo-groups of Shiga toxin-producing *E. coli* strains isolated from different reservoirs

Virulence gene profile											Sero-group	<i>subAB</i>			Source	Phylo-group	Total
<i>stx1</i>	<i>stx2</i>	<i>ehly</i>	<i>tia</i>	<i>saa</i>	<i>espP</i>	<i>epeA</i>	<i>terD</i>	<i>astA</i>	<i>Lpf<sub>O113</sub></i>	<i>iha</i>		<i>1</i>	<i>2-1</i>	<i>2-2</i>			
+									+	+	O128	+	+		goat	B1	2 <sup>b</sup>
+		+							+	+	ND <sup>a</sup>	+	+		sheep	B1	2
+		+							+	+	O5	+	+		sheep	B1	2
+		+	+						+	+	O5	+	+		sheep	B1	2
+		+	+						+	+	ND	+	+		sheep	B1	4
+		+	+						+	+	ND	+	+		goat	B1	6
+		+	+						+		ND	+	+		goat	B1	5
+		+	+						+		O5	+	+		sheep	B1	1
+		+	+	+					+	+	ND	+	+		human	B1	3
+			+						+	+	ND	+			goat	B1	1
+	+	+							+	+	O5	+	+		sheep	B1	2
+	+	+									ND		+		sheep	B1	1
+	+	+	+						+		ND	+	+		goat	B1	1
+	+	+	+						+	+	ND	+	+		goat	B1	7
+	+	+	+					+			O113	+	+		goat	A	1
+	+	+	+	+			+	+	+	+	O113	+	+		deer	A	1
+	+	+	+	+			+	+	+	+	O113	+			deer	A	1
+	+	+	+	+			+	+	+	+	O113	+			pony	A	1
	+	+	+						+	+	ND	+	+		deer	B1	1
	+	+						+			O113	+	+		goat	B1	1
	+	+		+	+				+		ND	+			cattle	A	1
	+	+		+	+					+	ND	+			cattle	E	1
	+	+		+	+	+			+	+	O113	+			cattle	B1	10

<sup>a</sup> Not-Defined

<sup>b</sup> One strain yielded an specific amplicon for *cdt* gene