

Table S1: Antimicrobial susceptibility (S) and resistance (R) against *E. coli* strains of Humans, Animals and Environmental origins.

Drugs	Breakpoints		Samples isolated					
	(mm)		Humans		Animals		Environmental	
	S	R	(n=20)	(n=20)	(n=20)	(n=20)	(n=20)	(n=20)
			R	S	R	S	R	S
CIP	≤ 21	≥ 26	n=17	n=03	n=09	n=11	n=08	n=12
			85%	15%	45%	55%	40%	60%
LEV	≤ 16	≥ 21	n=17	n=03	n=07	n=13	n=09	n=11
			85%	15%	35%	65%	45%	55%
CTX	≤ 22	≥ 26	n=18	n=02	n=15	n=05	n=13	n=07
			90%	10%	75%	25%	65%	35%
CAZ	≤ 17	≥ 21	n=20	n=00	n=18	n=02	n=17	n=03
			100%	00%	90%	10%	85%	15%
CN	≤ 12	≥ 15	n=16	n=04	n=17	n=03	n=15	n=05
			80%	20%	85%	15%	75%	25%
AK	≤ 14	≥ 17	n=03	n=17	n=09	n=11	n=07	n=13
			15%	85%	45%	55%	35%	65%
TGC	≤ 15	≥ 18	n=09	n=11	n=14	n=06	n=08	n=12
			45%	55%	70%	30%	40%	60%
TE	≤ 11	≥ 15	n=14	n=06	n=05	n=15	n=08	n=12
			70%	30%	25%	75%	40%	60%
IMP	≤ 19	≥ 23	n=05	n=15	n=02	n=18	n=02	n=18
			25%	75%	10%	90%	10%	90%
MEM	≤ 19	≥ 23	n=05	n=15	n=02	n=18	n=02	n=18
			25%	75%	10%	90%	10%	90%
AMP	≤ 13	≥ 17	n=20	n=00	n=18	n=02	n=17	n=03

			100%	00%	90%	10%	85%	15%
SXT	≤ 10	≥ 16	n=18	n=02	n=01	n=19	n=05	n=15
			90%	10%	05%	95%	25%	75%
AZT	≤12	>12	n=4	n=16	n=3	n=17	n=5	n=15
			20%	80%	15%	85%	25%	75%
AZM	≤ 4	≥ 16	n=1	n=19	n=3	n=17	n=2	n=18
			5%	95%	15%	85%	10%	90%

CIP=ciprofloxacin, LEV=levofloxacin, CTX=cefotaxime, CAZ=ceftazidime, CN=gentamicin,
AK=amikacin, TGC=tigecycline, TE=tetracycline, IMP=imipenem, MEM=meropenem, AM=ampicillin,
SXT=trimethoprim-sulfamethoxazole, AZT=aztreonam, AZM= Azithromycin

Table S2: Biofilm and non-biofilm producer strains of human, animal and environmental origin.

Biofilm production	<i>E. coli</i> strains			
	Human	Animal	Environment	Total
	(n=20)	(n=20)	(n=20)	(n=20)
Strong positive	05	04	04	13 (21.6%)
Moderate positive	07	06	05	18 (30.0%)
Weak positive	03	06	08	17 (28.3%)
Non biofilm producers	05	04	03	12 (20.0%)

Table S3: ERIC-PCR based fingerprints of genetic profiles.

Band Size (bp)	Genomic Profiles																	
	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	P14	P15	P16	P17	P18
6000												+						
4500				+														
4000													+					
3800			+															
3500														+				
2900	+									+		+	+		+			
2400							+											
1700			+								+	+			+			
1600	+	+		+					+	+			+			+		
1500					+													
1400							+	+	+	+	+	+	+					
1300					+													
1200				+		+	+		+									
1100	+	+	+	+	+		+	+		+	+		+	+	+	+	+	+

850	+	+				+		+			+	+			+
750			+	+		+	+	+		+	+	+	+	+	+
650								+							
400			+	+		+	+	+							+
350								+							
250				+		+									

Table S4: Geographical locations of sampling sites

Sources	No. of Isolates (n=60)	Geographical Distribution of Sampling Sites
Wastewater	13	Kala Shah Kaku
		Sundar industrial estate,
		Kasur,
		College Road,
		Valencia town,
Soil	07	Thokar Niaz Baig
		Ada plot
		Bedian Road,
		Manga mandi,
		Raiwind,
Cattle faeces	09	Ravi interchange
		Kasur
		Animal samples were collected from 5 different farms, Johar town block F,
		Edwn lane villas 2,
		Khna nau kahna,
Rectal swab	06	Valencia town and
		Sarwar
		Uol Teaching hospital, Lahore
		Sharif city complex, Lahore
		Jinnah hospital, Lahore
Milk	05	Rehman Medical complex, Peshawer
		Nishter hospital, Multan
		District Head Quarter Hospital, Rawalpindi
Urine	06	
Pus	05	
Sputum	05	
Blood culture	02	
Tissue culture	02	

Table S5: Primer sets used in the study

Primers	Primer Type	Primer sequences (5'→3')	Annealing Temperature (°C)	Product Size (bp)
<i>uidA</i>	Forward	TGGTAATTACCGACGAAAACGGC	57	162
	Reverse	ACGCGTGGTTACAGTCTTGCG		
<i>hlyA</i>	Forward	GCATCATCAAGCGTACGTTCC	60	534
	Reverse	AATGAGCCAAGCTGGTTAAGCT		
<i>Stx1</i>	Forward	ACACTGGATGATCTCAGTGG	58	614
	Reverse	CTGAATCCCCCTCCATTATG		
<i>Stx2</i>	Forward	CCATGACAACGGACAGCAGTT	56	779
	Reverse	CCTGTCAACTGAGCAGCACTTTG		
<i>eaeA</i>	Forward	GACCCGGCACAAGCATAAGC	58	384
	Reverse	CCACCTGCAGCAACAAGAGG		

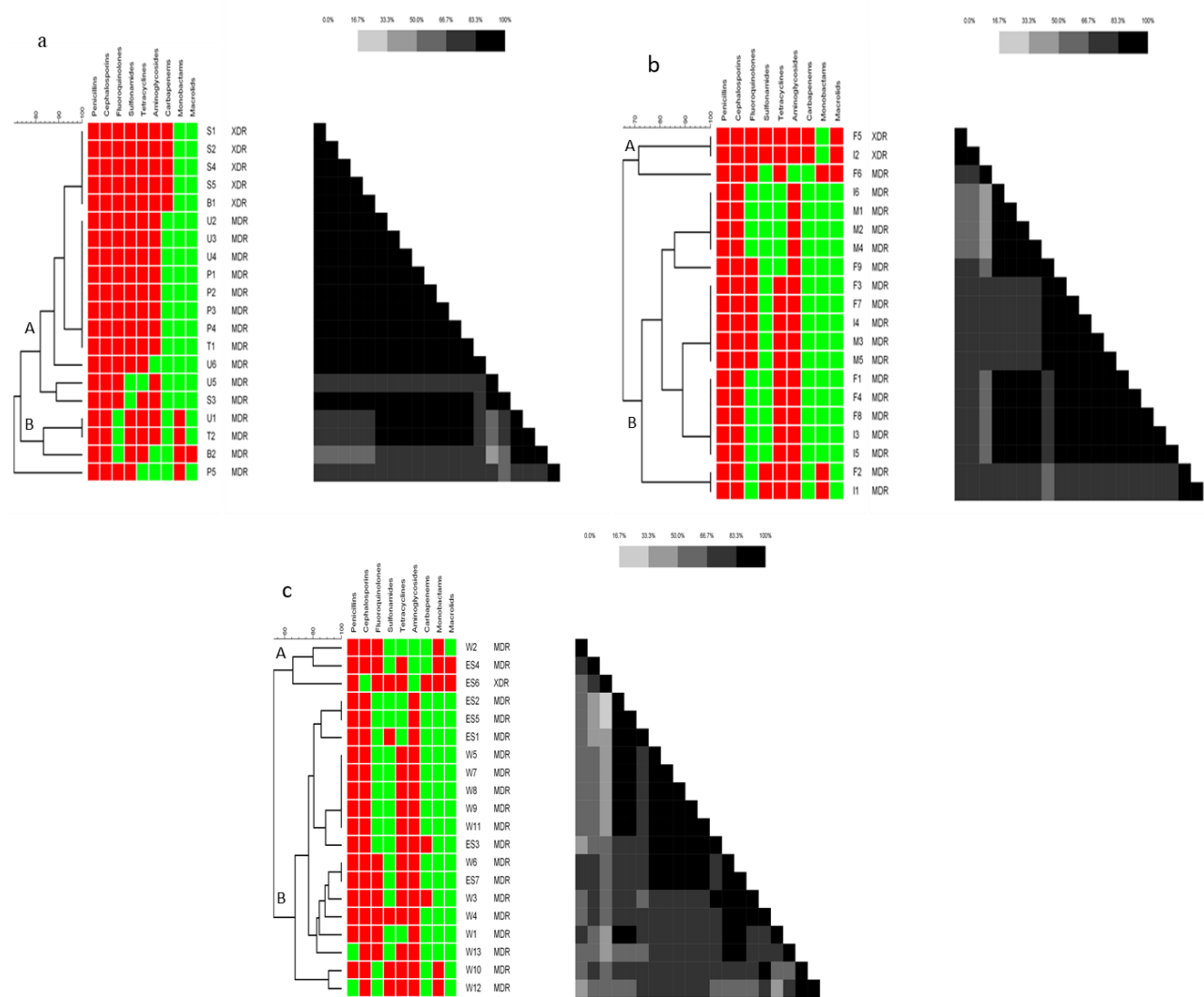


Figure S1: Clustering of *E. coli* strains from human (a), animal (b) and environmental (c) origins based on antimicrobial susceptibility patterns.

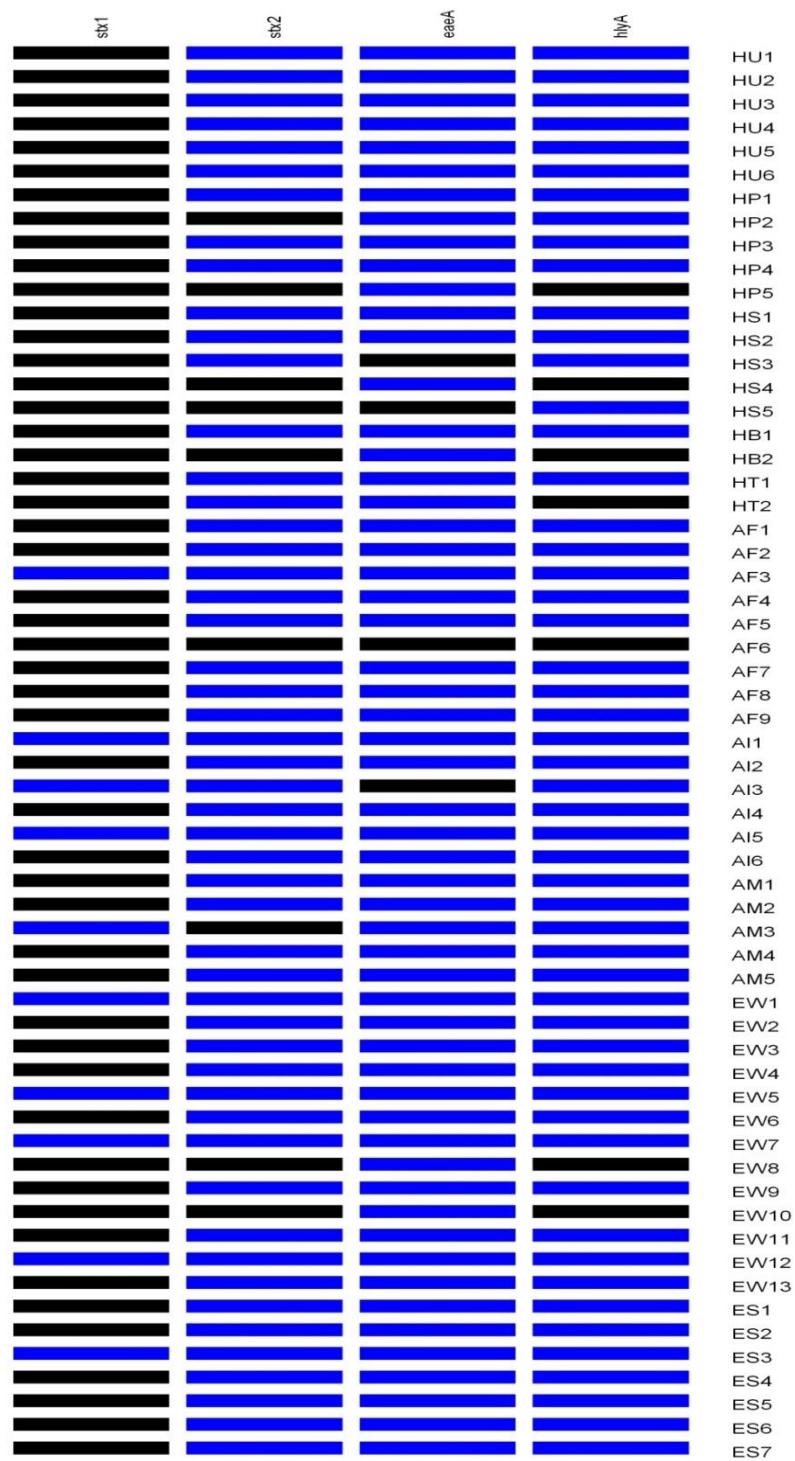


Figure S2. Heatmap showing the virulence genes profiles of all *E. coli* strains. Blue colour indicates the presence and while black colour indicates the absence of the gene. E letter is used for environment, A for animal and H for human origin.

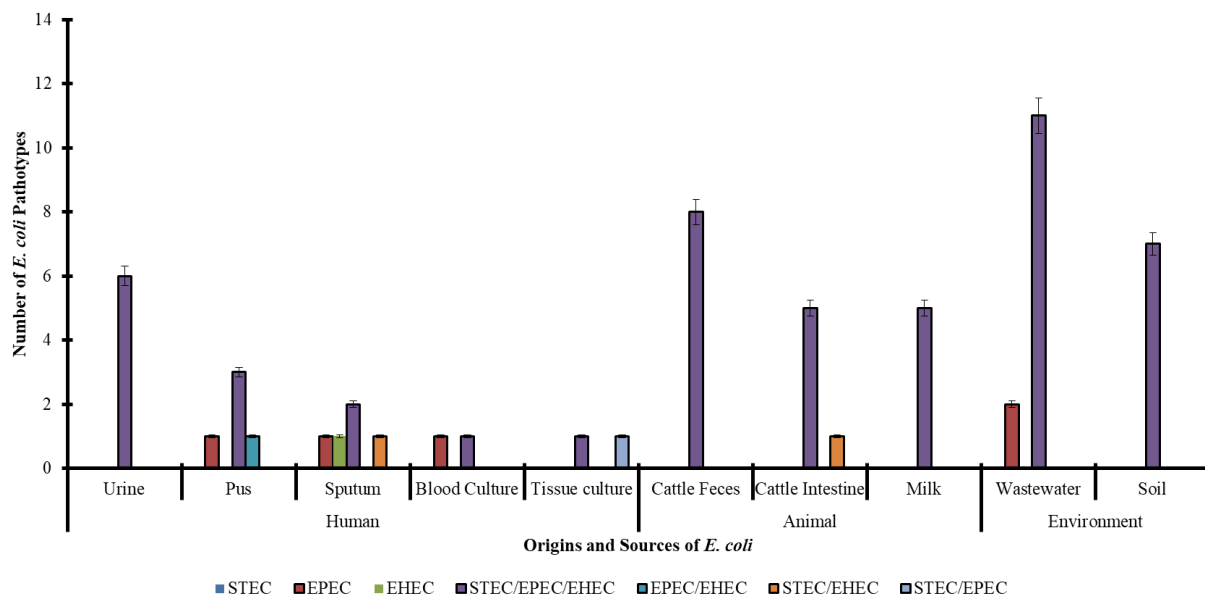


Figure S3: Distribution of *E. coli* pathotypes among human, animal and environmental origins and sources.

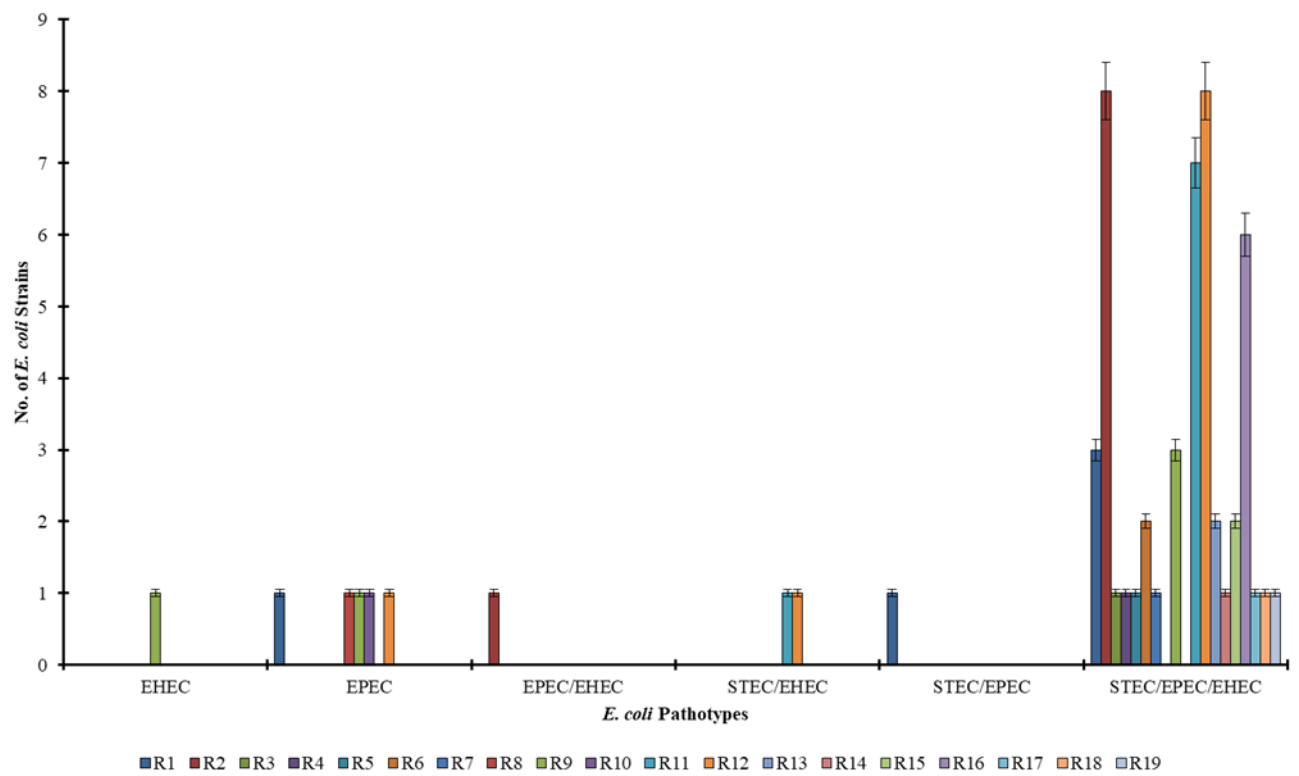


Figure S4: Association of pathotypes with antimicrobial resistance profiles (P -value 0.08).

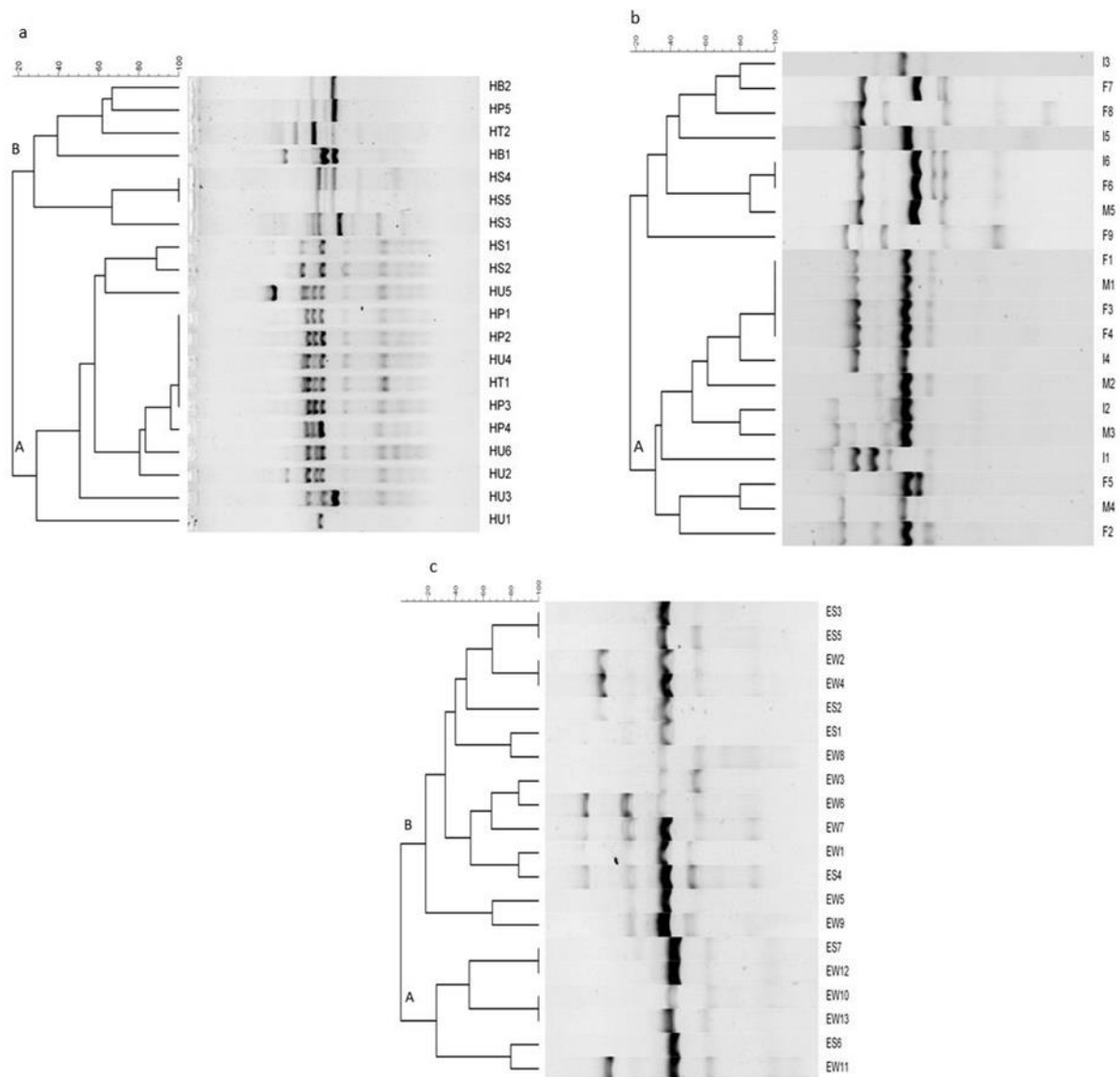


Figure S5: ERIC-PCR fingerprints based dendrograms of human (a), animal (b), environmental (c) strains based on Dice similarity coefficient UPGMA.