Table S1. PCR primer used for the identification of different foodborne pathogens.

Pathogen	Target gene	Primer sequence	Amplicon size	PCR conditions	Reference
E. coli O157:H7	O157	RfbF: GTGTCCATTTATACGGACATCCATG RfbR: CCTATAACGTCATGCCAATATTGCC	292	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 30s, 59°C for 60s, and 72°C for 60s; and one final cycle of 72°C for 7 min	(Hu et al., 1999)
	H7	FLICh7: FGCGCTGTCGAGTTCTATCGAGC FLICh7-RCAACGGTGACTTATCGCCATTCC	625	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 30s, 59°C for 60s, and 72°C for 60s; and one final cycle of 72°C for 7 min	(Hu et al., 1999)
	Intimin	IntF : GACTGTCGATGCATCAGGCAAAG IntR : TTGGAGTATTAACATTAACCCCAGG	368	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 30s, 59°C for 60s, and 72°C for 60s; and one final cycle of 72°C for 7 min	(Hu et al., 1999)
	SLT-I	SLT-IF: TGTAACTGGAAAGGTGGAGTATAC SLT-IR: GCTATTCTGAGTCAACGAAAAATAAC	210	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 30s, 59°C for 60s, and 72°C for 60s; and one final cycle of 72°C for 7 min	(Hu et al., 1999)
	SLT-II	SLT-IIF: GTTTTTCTTCGGTATCCTATTCCG SLT-IIR: GATGCATCTCTGGTCATTGTATTAC	483	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 30s, 59°C for 60s, and 72°C for 60s; and one final cycle of 72°C for 7 min	(Hu et al., 1999)
Salmonella	*invA*	S139F: GTGAAATTATCGCCACGTTCGGGCAA S141R: TCATCGCACCGTCAAAGGAACC	284	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 1min, 53°C for 2min, and 72°C for min; and one final cycle of 72°C for 7 min	(Rahn et al., 1992)
Listeria monocytogenes	*Imo0737*	F: AGGGCTTCAAGGACTTACCC R: ACGATTTCTGCTTGCCATTC	691	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 24s, 53°C for 69s, and 72°C for 69s; and one final cycle of 72°C for 7 min	(Doumith et al., 2004)
	Imo1118	F: AGGGGTCTTAAATCCTGGAA R: CGGCTTGTTCGGCATACTTA	906	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 24s, 53°C for 69s, and 72°C for 69s; and one final cycle of 72°C for 7 min	(Doumith et al., 2004)
	ORF2819	F: AGCAAAATGCCAAAACTCGT R: CATCACTAAAGCCTCCCATTG	471	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 24s, 53°C for 69s, and 72°C for 69s; and one final cycle of 72°C for 7 min	(Doumith et al., 2004)

	ORF2110	F: AGTGGACAATTGATTGGTGAA R: CATCCATCCCTTACTTTGGAC	597	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 24s, 53°C for 69s, and 72°C for 69s; and one final cycle of 72°C for 7 min	(Doumith et al., 2004)
	hylA	F: CCTAACATATCCAGGTGCTCTC R: CTGATTGCGCCGAAGTTTAC	350	Initial denaturation step at 94°C for 3 min; 35 cycles of 94°C for 24s, 53°C for 69s, and 72°C for 69s; and one final cycle of 72°C for 7 min	(Doumith et al., 2004)
Campylobacter spp.	16s rRNA	C412F: GGATGACACTTTTCGGAGC C1228R: CATTGTAGCACGTGTGTC	816	Initial denaturation step at 94°C for 15 min; 25 cycles of 95°C for 30s, 58°C for 90s, and 72°C for 60s; and one final cycle of 72°C for 7 min	(Yamazaki-Matsune et al., 2007)

Table S2: Interpretive Criteria for Minimum Inhibitory Concentrations

Bacteria	Antimicrobial class	Mode of action	Antimicrobial Agents	Minimum Inhibitory Concertation interpretive criteria (µg/mL) *			Reference
				S	I	R	
E. coli O157	Aminoglycosides	Inhibit protein synthesis	Streptomycin	≤32	-	≥64	(NARMS, 2019)
			Kanamycin	≤16	32	≥64	(CLSI, 2015)
			Gentamycin	≤4	8	≥16	(CLSI, 2015)
	β–lactam	Inhibit cell wall synthesis	Amoxicillin	≤8	16	≥32	(NARMS, 2019)
	Quinolones	Inhibit the bacterial DNA gyrase enzyme, and replication	Nalidixic acid	≤16	-	≥32	(NARMS, 2019)
			Ciprofloxacin	≤1	2	≥4	(CLSI, 2015)
	Phenicols	Inhibit protein synthesis	Chloramphenicol	8	16	32	(CLSI, 2015)
	Tetracyclines	Inhibit protein synthesis	Tetracycline	≤4	8	≥16	(CLSI, 2015)
	Cephems	Inhibit cell wall synthesis	Ceftriaxone	≤1	2	≥4	(NARMS, 2019)
			Cefoxitin	≤8	16	≥32	(NARMS, 2019)
	Macrolides	Inhibit protein synthesis	Azithromycin	≤16	-	≥32	(NARMS, 2019)
	Folate pathway antagonists	Inhibit folate action	Sulfisoxazole	≤256	-	≥512	(NARMS, 2019)
			Trimethoprim sulfamethoxazole	≤2	-	≥4	(NARMS, 2019)
	Penicillin	Inhibit cell wall synthesis	Ampicillin	≤8	16	≥32	(CLSI, 2015)
	Penems	Inhibit cell wall synthesis	Meropenem	≤1	2	≥4	(NARMS, 2019)
	Polymyxins	Disrupt cell wall integrity	Colistin	≤2	-	≥2	(Matuschek et al., 2018)
Salmonella	Aminoglycosides	Inhibit protein synthesis	Streptomycin	≤32	-	≥64	(NARMS, 2019)
			Kanamycin	≤16	32	≥64	(CLSI, 2015)
			Gentamycin	≤4	8	≥16	(CLSI, 2015)
	β–lactam	Inhibit cell wall synthesis	Amoxicillin	≤8	16	≥32	(NARMS, 2019)
	Quinolones	Inhibit the bacterial DNA gyrase enzyme, and replication	Ciprofloxacin	≤0.06	0.12-0.5	≥1	(CLSI, 2015)
			Nalidixic acid	≤16	-	≥32	(NARMS, 2019)
	Phenicols	Inhibit protein synthesis	Chloramphenicol	≤8	16	≥32	(CLSI, 2015)
	Tetracyclines	Inhibit protein synthesis	Tetracycline	≤4	8	≥16	(CLSI, 2015)
	Cephems	Inhibit cell wall synthesis	Ceftriaxone	≤1	2	≥4	(NARMS, 2019)
			Cefoxitin	≤8	16	≥32	(NARMS, 2019)
	Macrolides	Inhibit protein synthesis	Azithromycin	≤16	-	≥32	(NARMS, 2019)

	Folate pathway antagonists	Inhibit folate action	Sulfisoxazole	≤256	-	≥512	(NARMS, 2019)
			Trimethoprim sulfamethoxazole	≤2	-	≥4	(NARMS, 2019)
	Penicillin	Inhibit cell wall synthesis	Ampicillin	≤8	16	≥32	(CLSI, 2015)
	Penem	Inhibit cell wall synthesis	Meropenem	≤1	2	≥4	(NARMS, 2019)
	Polymyxins	Disruption of cell wall integrity	Colistin	≤2	-	≥2	(Matuschek et al., 2018)
L. monocytogenes	Penicillin	Inhibit cell wall synthesis	Ampicillin	≤1	-	≥1	(EUCAST, 2018)
			Penicillin G	≤1	-	≥1	(EUCAST, 2018)
	Phenicol	Inhibit protein synthesis	Chloramphenicol	≤8	16	≥32	(Ruiz-Bolivar et al., 2011)
	Quinolones	Inhibit the bacterial DNA gyrase enzyme, and replication	Ciprofloxacin	≤1	2	≥4	(Ruiz-Bolivar et al., 2011)
			Nalidixic acid	≤8	-	≥16	(Ruiz-Bolivar et al., 2011)
	Aminoglycosides	Inhibit protein synthesis	Kanamycin	≤16	32	≥64	(CLSI, 2015)
			Gentamycin	≤4	8	≥16	(CLSI, 2015)
			Streptomycin	≤8	-	≥16	(CLSI, 2015)
	Macrolides	Inhibit protein synthesis	Erythromycin	≤0.5	1-4	≥8	(Ruiz-Bolivar et al., 2011)
			Azithromycin	≤0.06	-	≥1	(Madeo et al., 2015)
	Tetracyclines	Inhibit protein synthesis	Tetracycline	≤4	8	≥16	(Ruiz-Bolivar et al., 2011)
	Cephems	Inhibit cell wall synthesis	Ceftriaxone	≤4	-	≥8	((Madeo et al., 2015)
			Cefoxitin	≤4	-	≥8	(Chen et al., 2018)
	Lincomycin	Inhibit protein synthesis	Clindamycin	≤0.06	-	2	(Madeo et al., 2015)
	Folate pathway antagonists	Inhibit folate action	Trimethoprim sulfamethoxazole	≤0.06	-	≥0.06	(EUCAST, 2020)
	Nitrofuran	Inactivate ribosomal protein	Nitrofurantoin	≤32	64	≥128	(Chen et al., 2018)
	Glycopeptide	Inhibit cell wall synthesis	Vancomycin	≤0.125	-	2	((Granier et al., 2011)
	Fluoroquinolone	Inhibit DNA synthesis	Levofloxacin	≤0.06	-	2	(Madeo et al., 2015)
	Oxazolidinone	Inhibit protein synthesis	Linezolid	≤0.5	-	4	(Granier et al., 2011)
	Penem	Inhibit cell wall synthesis	Meropenem	≤0.25	-	≥0.25	(EUCAST, 2020)
	Antimycobacterial	Inhibition of RNA synthesis	Rifampicin	<0.25	-	0.5	(Granier et al., 2011)

Campylobacter	Penicillin	Inhibit cell wall synthesis	Ampicillin	≤8	16	≥32	(Kashoma et al., 2015)
			Penicillin	≤1	-	≥64	(Haruna et al., 2012)
	Phenicol	Inhibit protein synthesis	Chloramphenicol	≤16	-	≥32	(NARMS, 2019)
			Florfenicol	≤4		≥8	(NARMS, 2019)
	Quinolones	Inhibit the bacterial DNA gyrase enzyme, and replication	Ciprofloxacin	≤0.5	-	≥1	(NARMS, 2019)
			Nalidixic acid	≤16		≥32	(NARMS, 2019)
	Aminoglycosides	Inhibit protein synthesis	Streptomycin	≤2	4	≥8	(Kashoma et al., 2015)
			Gentamycin	≤2	-	≥4	(NARMS, 2019)
			Kanamycin	≤16	32	≥64	(CLSI, 2015)
	Macrolides	Inhibit protein synthesis	Erythromycin	≤4	-	≥8	(NARMS, 2019)
			Azithromycin	≤0.25		≥0.5	(NARMS, 2019)
	Tetracyclines	Inhibit protein synthesis	Tetracycline	≤1	-	≥2	(NARMS, 2019)
	ketolides	Inhibit protein synthesis	Telithromycin	≤4		≥8	(NARMS, 2019)
	Lincomycin	Inhibit protein synthesis	Clindamycin	≤0.5		≥1	(NARMS, 2019)

*S: Susceptible, I: Intermediate, R: Resistance

Table S3: Antimicrobial resistance gene primers used for the detection of antimicrobial resistance genes in *E. coli* O157, *Salmonella* *L. monocytogenes* and *Campylobacter*

Foodborne pathogen	**Antimicrobial agent**	**Resistant gene**	**Primer[a]: Nucleotide sequence**	**Resistance mechanism**	**Annealing Temp (°C)**	**Fragment length (bp)**	**References**
E. coli O157	Tetracycline	*tet(A)*	F: GCTACATCCTGCTTGCCTTC R: CATAGATCGCCGTGAAGAGG	Efflux pump	50	210	(Bryan et al., 2004)
	Gentamicin	*aac(3)-IV*	F: CTTCAGGATGGCAAGTTGGT R: TCATCTCGTTCTCCGCTCAT	Aminoglycoside acetyltransferase	50	286	(Saenz et al., 2004)
	Streptomycin	*aadA*	F: GCAGCGCAATGACATTCTTG R: ATCCTTCGGCGCGATTTTG	Aminoglycoside adenyltransferase	50	282	(Saenz et al., 2004)
	Kanamycin	*aphA1*	F: ATGGGCTCGCGATAATGTC R: CTCACCGAGGCAGTTCCAT	Aminoglycoside phosphoryltranferase	50	600	(Rosengren et al., 2009)
	Trimethoprim-sulfamethoxazole	*sulII*	F: CGGCATCGTCAACATAACCT R: TGTGCGGATGAAGTCAGCTC	Target modification	52	721	(Srinivasan et al., 2005)
	Azithromycin	*mph(A)*	F: GTGAGGAGGAGCTTCGCGAG R: TGCCGCAGGACTCGGAGGTC	Target modification	59	403	(Cho et al., 2019)
Salmonella	Ampicillin	bla_{TEM-1}	F: CAGCGGTAAGATCCTTGAGA R: ACTCCCCGTCGTGTAGATAA	β – Lactamase	49	643	(Chen et al., 2004)
	Streptomycin	*strA*	F: CTTGGTGATAACGGCAATTC R: CCAATCGCAGATAGAAGGC	Aminoglycoside phosphoryltranferase	47	548	(Gebreyes and Altier, 2002)
	Tetracycline	*tet(B)*	F: TTGGTTAGGGGCAAGTTTTG R: GTAATGGGCCAATAACACCG	Efflux pump	48.5	659	(Chen et al., 2004)
	Gentamicin	*aac(3)-IVa*	F: GATGGGCCACCTGGACTGAT R: GCGCTCACAGCAGTGGTCAT	Aminoglycoside acetyltransferase	54.5	462	(Chen et al., 2004)
	Trimethoprim sulfamethoxazole	*sulII*	F: CCTGTTTCGTCCGACACAGA R: GAAGCGCAGCCGCAATTCAT	Target modification	55	435	(Chen et al., 2004)
	Azithromycin	*ermB*	F: GAAAAAGTACTCAACCAAATA	Target modification	45	639	(Mąka et al., 2015)

			R: AATTTAAGTACCGTTACT				
L. monocytogen	Ampicillin	*ampC*	F: TTCTATCAAMACTGGCARC R: CCYTTTTATGTACCCAYGA	β – Lactamase	45	550	(Srinivasan et al., 2005)
	Ciprofloxacin	*Lde*	F: ATCGTGAACTTAATGGTGG R: ATCCTCATATAACTCAAGCG	Efflux pump	45	1518	(Godreuil et al., 2003)
	Erythromycin	*ermB*	F: GAAAAGGTACTCAACCAAATA R: AGTAACGGTACTTAAATTGTTTAC	Target modification	46	639	(Srinivasan et al., 2005)
	Tetracycline	*Tet(O)*	F: AATGAAGATTCCGACAATTTR R: CTCATGCGTTGTAGTATTCCA	Efflux pump	45	781	(Li et al., 2007)
	Gentamicin	*aadB*	F: GAGCGAAATCTGCCGCTCTTG R: CTGTTACAACGGACTGGCCGC	Aminoglycoside adenyltransferase	54	310	(Srinivasan et al., 2005)
	Penicillin G	*penA*	F: ATCGAACAGGCGACGATGTC R: GATTAAGACGGTGTTTTACGG	Transpeptidases	46	500	(Srinivasan et al., 2005)
	Cefoxitin	*cfxA*	F: GCTCAAACAGATAGTTTTAT R: GGCAACATTGTGAGCTG	β – Lactamase	50	333	(Maung et al., 2019)
	Clindamycin	*mefA*	F: AGTATCATTAATCACTAGTGC R: TTCTTCTGGTACTAAAAGTGG	Target modification	50	345	(Maung et al., 2019)
	Trimethoprim-sulfamethazole	*sulI*	F: CGGCGTGGGCTACCTGAACG R: GCCGATCGCGTGAAGTTCCG	Target modification	50	433	(Iwu and Okoh, 2019)
Campylobacter	Ampicillin	*blaOXA-61*	F: AGAGTATAATACAAGCG R: TAGTGAGTTGTCAAGCC	β - Lactamase	45	372	(Obeng et al., 2012)
	Streptomycin	*aadE*	F: GAACAGGATGAACGTATTCG R: GCATATGTGCTATCCAGG	Aminoglycoside phosphoryltranferase	45	837	(Obeng et al., 2012)
	Tetracycline	*tet(O)*	F: GCGTTTTGTTTATGTGCG R: ATGGACAACCCGACAGAAG	Antibiotic target protection	49	559	(Obeng et al., 2012)
	Gentamycin	*aph-3-1*	F: TGCGTAAAAGATACGGAAG R: CAATCAGGCTTGATCCCC	Aminoglycoside adenyltransferase	49	701	(Obeng et al., 2012)

[a] F, forward primer; R, reverse primer

Table S4: Antimicrobial resistance profile of the *E. coli* O157 isolates according to manure amendment type and the source of the isolates**.**

Antimicrobial agents	**Source of isolate and number of resistant isolates (%)**											
	Dairy cattle (n=13)			**Poultry (n=2)**			**Manure (n= 11)**			**Soil (n=4)**		
	R No. (%)	**I No. (%)**	**S No. (%)**	**R No. (%)**	**I No. (%)**	**S No. (%)**	**R No. (%)**	**I No. (%)**	**S No. (%)**	**R No. (%)**	**I No. (%)**	**S No. (%)**
Amp	4 (30.7)	0	9 (69.3)	2 (100)	0	0	4 (36.3)	0	7 (63.6)	2 (50)	0	2 (50)
Chl	0	0	13 (100)	0	0	2 (100)	0	0	11 (100)	0	0	4 (100)
Cip	0	4 (30.7)	9 (69.3)	0	1 (50)	1 (50)	0	4(36.3)	7 (63.6)	0	1 (25)	3 (75)
Kan	8 (61.5)	0	5 (39.5)	1 (50)	1 (50)	0	7(63.3)	0	4(36.3)	2 (50)	1 (25)	1 (25)
Nal	0	0	13 (100)	0	0	2 (100)	0	0	11 (100)	0	0	4 (100)
Str	6 (46.2)	0	7 (53.8)	2 (100)	0	0	6(54.5)	0	5 (45.4)	2 (50)	0	2 (50)
Tet	1 (7)	1 (7)	11 (84.6)	1 (50)	1 (50)	0	1 (9)	1 (9)	9 (82)	1 (25)	1 (25)	2 (50)
Gen	11 (84.6)	1 (7.7)	1 (7.7)	2 (100)	0	0	10(91)	1 (9)	0	3 (75)	0	1 (25)
Amo	1 (7.7)	0	12 (82.3)	0	0	2 (100)	1(9)	0	10 (91)	0	0	4 (100)
Cefo	1 (7.7)	0	12 (82.3)	0	0	2 (100)	1(9)	0	10 (91)	0	0	4 (100)
Ceft	0	0	13 (100)	0	0	2 (100)	0	0	11 (100)	0	0	4(100)
Sul	13 (100)	0	0	2 (100)	0	0	11(100)	0	0	4 (100)	0	0
Tri	13 (100)	0	0	2 (100)	0	0	11(100)	0	0	4 (100)	0	0
Azi	11 (84.6)	0	2 (14)	0	0	2 (100)	9(81.8)	0	2 (18.2)	2 (50)	0	2 (50)
Mer	0	0	13 (100)	0	0	2 (100)	0	0	11 (100)	0	0	4 (100)
Col	1 (7.7)	0	12 (82.3)	0	0	2 (100)	0	0	11 (100)	1 (25)	0	3 (75)

S, susceptible; I, intermediate; R, resistance

The antimicrobial resistance was determined using the broth microdilution method. Results are shown as number of isolates with the percentage given in parentheses. Amp; ampicillin, Cip; ciprofloxacin, Gen; gentamicin, Str; streptomycin, Tet; tetracycline, Nal; nalidixic acid, Kan; kanamycin, Chl; chloramphenicol, Amo; amoxicillin, Cefo; cefoxitin, Ceft; ceftriaxone, Sul; sulfisoxazole, Tri; Trimethoprim, Azi; azithromycin, Mer: Meropenem, Col: Colistin

Table S5: Antimicrobial resistance profile of the *Salmonella* isolates according to manure amendment type and the source of the isolates**.**

Antimicrobial agents	**Source of isolate and number of resistant isolates (%)**											
	Dairy cattle (n=6)			**Poultry (n=7)**			**Manure (n= 12)**			**Soil (n=1)**		
	R No. (%)	**I No. (%)**	**S No. (%)**	**R No. (%)**	**I No. (%)**	**S No. (%)**	**R No. (%)**	**I No. (%)**	**S No. (%)**	**R No. (%)**	**I No. (%)**	**S No. (%)**
Amp	5 (83.3)	0	1 (16.7)	1 (14.2)	2 (28)	4 (57)	6 (50)	2 (17.3)	4 (33.3)	0	0	1 (100)
Chl	1 (16.7)	0	5 (83.3)	0	0	7 (100)	1 (8.3)	0	11 (91.7)	0	0	1 (100)
Cip	0	4 (66.6)	2 (33.3)	3 (42.8)	1 (14.2)	3 (42.8)	1 (8.3)	7 (58.3)	4 (33.3)	0	0	1 (100)
Kan	2 (33.3)	2 (33.3)	2 (33.3)	4 (57)	0	3 (43)	6 (50)	2 (17.3)	4 (33.3)	0	0	1 (100)
Nal	2 (33.3)	0	4 (66.6)	5 (71.4)	1 (14.2)	1 (14.2)	7 (58.3)	1(8.3)	4 (33.3)	0	0	1 (100)
Str	5 (83.3)	0	1 (16.7)	6 (85.7)	0	1 (14.2)	10 (83.3)	0	2 (16.7)	1 (100)	0	0
Tet	1 (16.7)	1 (16.7)	4 (66.6)	2 (28.5)	0	5 (71.4)	3 (25)	2 (16.6)	7 (58.3)	0	0	1 (100)
Gen	3 (50)	1 (16.7)	2 (33.3)	7 (100)	0	0	9 (75)	1 (8.3)	2 (17.3)	1(100)	0	0
Amo	1 (16.7)	0	5 (83.3)	0	0	7 (100)	1 (8.3)	0	11 (91.7)	0	0	1 (100)
Cefo	1 (16.7)	1 (16.7)	4 (66.6)	0	0	7 (100)	1 (8.3)	1 (8.3)	10 (83.3)	0	0	1 (100)
Ceft	1 (16.7)	0	5 (83.3)	0	0	7 (100)	1 (8.3)	0	11 (91.7)	0	0	1 (100)
Sul	6 (100)	0	0	7 (100)	0	0	12 (100)	0	0	1 (100)	0	0
Tri	6 (100)	0	0	7 (100)	0	0	12 (100)	0	0	1 (100)	0	0
Azi	3 (50)	0	3 (50)	7 (100)	0	0	9 (75)	0	3 (25)	1 (100)	0	0
Mer	0	0	6 (100)	0	0	7 (100)	0	0	12 (100)	0	0	1 (100)
Col	0	0	6 (100)	2 (28.5)	0	5 (71.5)	1 (8.3)	0	11 (91.7)	1 (100)	0	0

S, susceptible; I, intermediate; R, resistance

The antimicrobial resistance was determined using the broth microdilution method. Results are shown as number of isolates with the percentage given in parentheses. Amp; ampicillin, Cip; ciprofloxacin, Gen; gentamicin, Str; streptomycin, Tet; tetracycline, Nal; nalidixic acid, Kan; kanamycin, Chl; chloramphenicol, Amo; amoxicillin, Cefo; cefoxitin, Ceft; ceftriaxone, Sul; sulfisoxazole, Tri; Trimethoprim, Azi; azithromycin, Mer: Meropenem, Col: Colistin

Table S6: Antimicrobial resistance profile of the *L. monocytogens* isolates according to manure amendment type and the source of the isolates**.**

Antimicrobial agents	**Source of isolate and number of resistant isolates (%)**											
	Dairy cattle (n=58)			**Poultry (n=9)**			**Manure (n= 47)**			**Soil (n=20)**		
	R No. (%)	**I No. (%)**	**S No. (%)**	**R No. (%)**	**I No. (%)**	**S No. (%)**	**R No. (%)**	**I No. (%)**	**S No. (%)**	**R No. (%)**	**I No. (%)**	**S No. (%)**
Amp	52 (89.6)	0	6 (8.9)	8 (88.8)	0	1 (11.1)	42(89.3)	0	5 (10.7)	18 (90)	0	2 (10)
Chl	15 (25.6)	7 (12)	36 (62)	2 (22.2)	1 (11.1)	6 (66.6)	14(29.7)	6 (12.7)	27 (57.4)	3 (15)	2 (10)	15 (75)
Cip	46 (79.2)	1 (1.7)	11 (16.4)	7 (77.7)	0	2 (22.2)	38(80.8)	1 (2.1)	8 (17)	15 (75)	0	5 (25)
Kan	50 (86)	0	8 (84)	9 (100)	0	0	42(89.3)	0	5 (10.7)	17 (85)	0	3 (15)
Nal	55 (94.8)	0	3 (95.2)	9 (100)	0	0	44(93.6)	0	3 (6.3)	20 (100)	0	0
Str	58 (100)	0	0	8 (88.8)	0	1 (11.1)	47(100)	0	0	19 (95)	0	1 (10)
Tet	20 (34)	0	38(66)	3 (33.3)	0	6 (66.6)	15(31.9)	0	32 (68)	8 (40)	0	12 (60)
Gen	44 (75.8)	0	14 (24.2)	8 (88.8)	0	1 (11.1)	36(76.6)	0	11 (23.3)	16 (80)	0	4 (20)
Pen	28 (48.3)	0	30 (51.7)	4 (44.4)	0	5 (55.5)	24(51)	0	23 (49)	8 (40)	0	12 (60)
Ery	22 (37.9)	0	36 (62.1)	3 (33.3)	0	6 (66.6)	24(51)	0	23 (49)	1 (5)	0	19 (95)
Ceft	58 (100)	0	0	9 (100)	0	0	47(100)	0	0	20 (100)	0	0
Cli	58 (100)	0	0	9 (100)	0	0	47(100)	0	0	20 (100)	0	0
Lev	52(89.6)	6 (8.9)	0	9 (100)	0	0	42(89.3)	5 (10.7)	0	19 (95)	1 (5)	0
Rif	58 (100)	0	0	9 (100)	0	0	47(100)	0	0	20 (100)	0	0
Tri	58 (100)	0	0	9 (100)	0	0	47(100)	0	0	20 (100)	0	0
Van	39(67)	19(33)	0	6 (66.6)	3 (33.3)	0	31(65.9)	16 (34)	0	14 (70)	6 (30)	0
Mer	58(100)	0	0	9 (100)	0	0	47(100)	0	0	20 (100)	0	0
Lin	36(62)	22 (38)	0	3 (33.3)	6 (66.6)	0	29(62)	18 (38)	0	10 (50)	10 (50)	0
Nit	6 (8.9)	50 (86)	2 (3.6)	0	9 (100)	0	4(8.5)	41 (87)	2 (4.2)	2 (10)	18 (90)	0
Azi	58 (100)	0	0	9 (100)	0	0	47(100)	0	0	20 (100)	0	0
Cefo	58 (100)	0	0	9 (100)	0	0	47(100)	0	0	20 (100)	0	0

S, susceptible; I, intermediate; R, resistance

The antimicrobial resistance was determined using the broth microdilution method. Results are shown as number of isolates with the percentage given in parentheses. Amp; ampicillin, Cip; ciprofloxacin, Gen; gentamicin, Str; streptomycin, Tet; tetracycline, Nal; nalidixic acid, Kan; kanamycin, Chl; chloramphenicol, Cefo: Cefoxitin, Azi: Azithromycin, Nit: Nitrofurantoin, Lin: Linezolid, Mer: Meropenem, Van: Vancomycin, Tri: Trimethoprim, Rif: Rifampicin, Lev: Levofloxacin, Cli: Clindamycin, Ceft: Ceftriaxone, Ery: Erythromycin, Pen: Penicillin G

Table S7: Antimicrobial resistance profile of the *Campylobacter* isolates according to manure amendment type and the source of the isolates.

Antimicrobial agents	Source of isolate and number of resistant isolates (%)											
	Dairy cattle (n=66)			Poultry (n=2)			Manure (n= 67)			Soil (n=1)		
	R No. (%)	I No. (%)	S No. (%)	R No. (%)	I No. (%)	S No. (%)	R No. (%)	I No. (%)	S No. (%)	R No. (%)	I No. (%)	S No. (%)
Amp	61(92.4)	0	5 (7.6)	2 (100)	0	0	63 (94)	0	4 (6)	0	0	1 (100)
Chl	6(9)	0	60 (91)	0	0	2 (100)	6(8.9)	0	61 (91.1)	0	0	1 (100)
Cip	62(93.9)	0	4 (6.1)	0	0	2 (100)	62(92.5)	0	5(7.5)	0	0	1 (100)
Ery	66(100)	0	0	1 (50)	0	1(50)	67(100)	0	0	0	0	1 (100)
Kan	32 (48.4)	3	31 (46.9)	1 (50)	0	1(50)	32(47.7)	3 (4.4)	32 (47.7)	1 (100)	0	0
Nal	21(31.8)	0	45 (68.1)	2 (100)	0	0	23(34.3)	0	44 (65.7)	0	0	1 (100)
Str	15(22.7)	12 (18.1)	39 (59)	0	0	2 (100)	15(22.2)	12 (19.7)	40 (59.7)	0	0	1 (100)
Tet	43(65)	0	23 (35)	0	0	2 (100)	43(64)	0	24 (36)	0	0	1 (100)
Gen	16(24)	0	50 (76)	1 (50)	0	1 (50)	17(25.3)	0	50 (74.6)	0	0	1 (100)
Pen	66(100)	0	0	2 (100)	0	0	67(100)	0	0	1(100)	0	0
Tel	4(6)	0	62 (94)	0	0	2 (100)	4(5.9)	0	63 (94.1)	0	0	1 (100)
Cli	58(87.8)	0	8 (12.2)	0	0	2 (100)	58 (86.5)	0	9(13.4)	0	0	1 (100)
Azi	6(9)	0	60 (91)	0	0	2 (100)	6(8.9)	0	61 (91.1)	0	0	1 (100)
Flo	2(3)	0	64 (97)	0	0	2 (100)	2(2.9)	0	65 (97.1)	0	0	1 (100)

S, susceptible; I, intermediate; R, resistance

The antimicrobial resistance was determined using the broth microdilution method. Results are shown as number of isolates with the percentage given in parentheses. Amp; ampicillin, Cip; ciprofloxacin, Gen; gentamicin, Str; streptomycin, Tet; tetracycline, Nal; nalidixic acid, Kan; kanamycin, Chl; chloramphenicol, Pen: Penicillin G, Ery: Erythromycin, Tel: Telithromycin, Cli: Clindamycin, Azi: Azithromycin, Flo: Florfenicol

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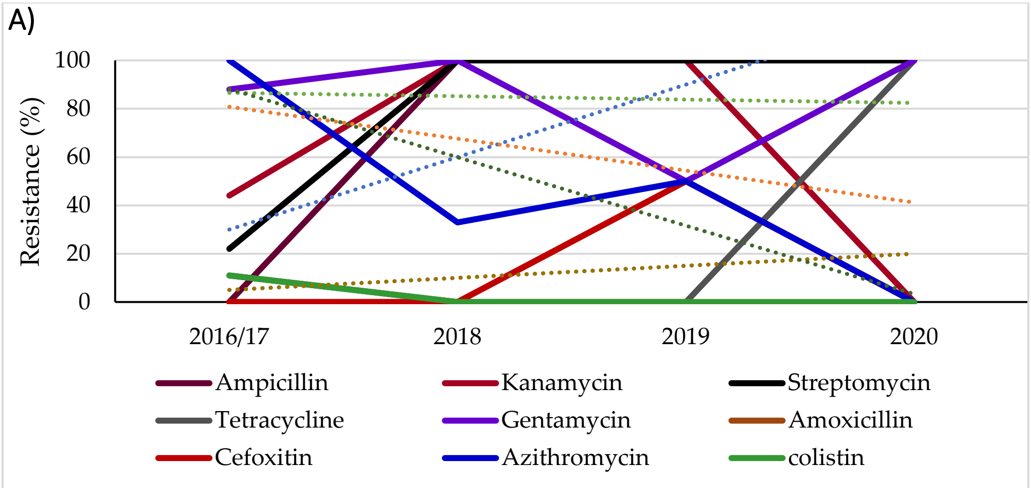
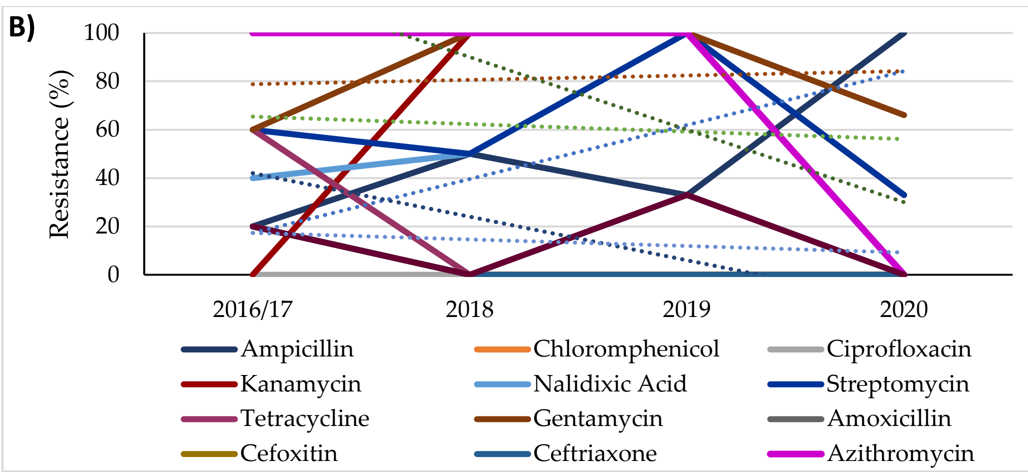
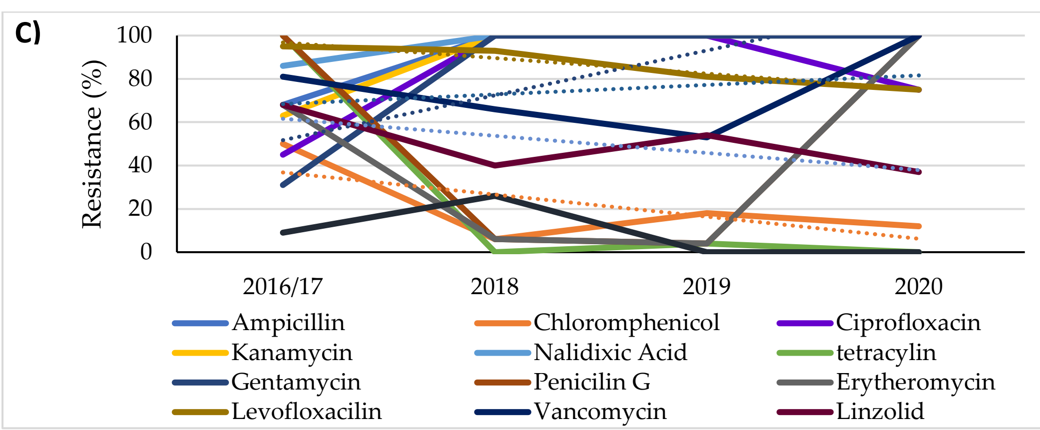

A)
Resistance (%)
100
80
60
40
20
0
2016/17
2018
2019
2020
Ampicillin
Kanamycin
Streptomycin
Tetracycline
Gentamycin
Amoxicillin
Cefoxitin
Azithromycin
colistin


B)
Resistance (%)
100
80
60
40
20
0
2016/17
2018
2019
2020
Ampicillin
Chloromphenicol
Ciprofloxacin
Kanamycin
Nalidixic Acid
Streptomycin
Tetracycline
Gentamycin
Amoxicillin
Cefoxitin
Ceftriaxone
Azithromycin


C)
Resistance (%)
100
80
60
40
20
0
2016/17
2018
2019
2020
Ampicillin
Chloromphenicol
Ciprofloxacin
Kanamycin
Nalidixic Acid
tetracylin
Gentamycin
Penicilin G
Erytheromycin
Levofloxacilin
Vancomycin
Linzolid

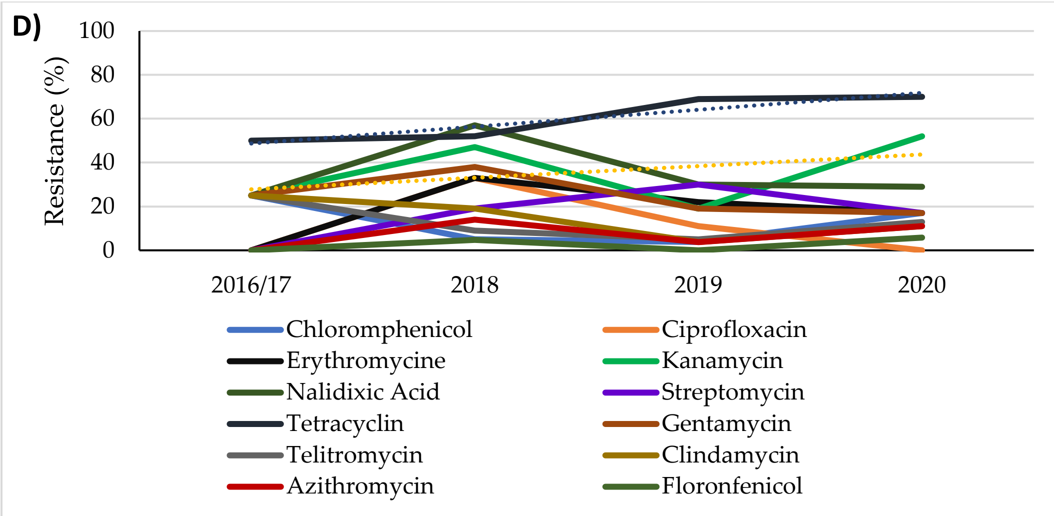
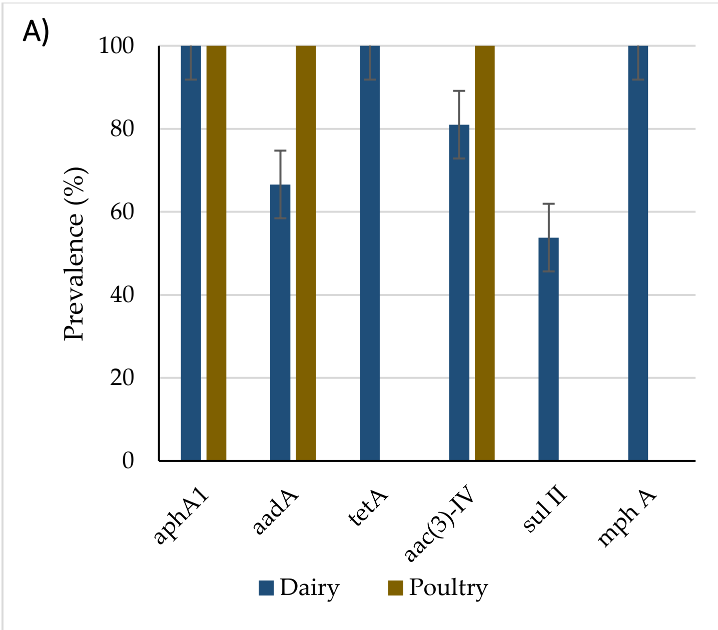
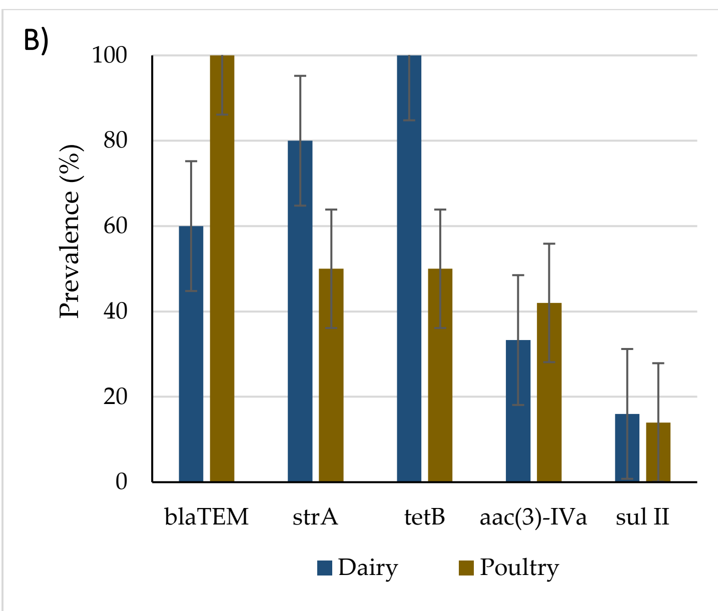
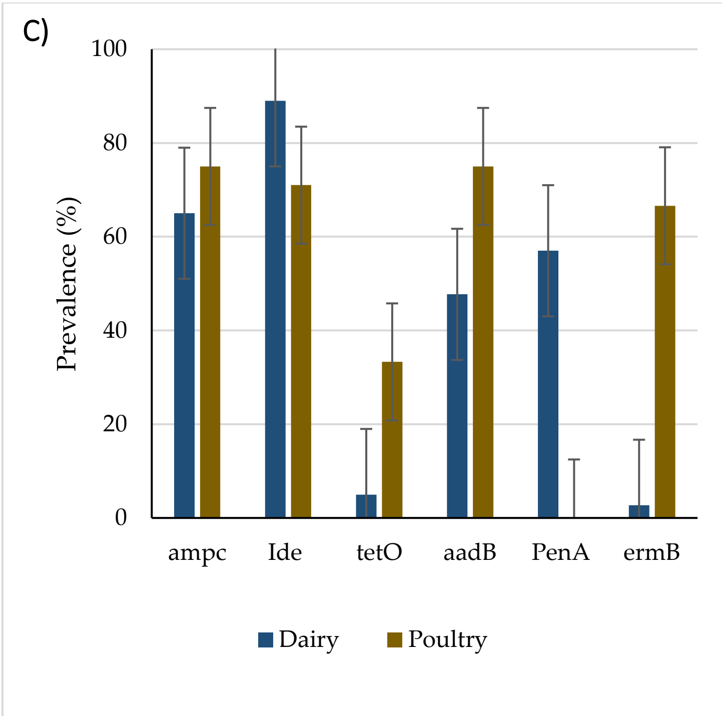


Figure S1. Antimicrobial resistance trend in different foodborne pathogens between 2016 and 2020.


A)
100
80
60
40
20
0
Prevalence (%)
aphA1
aadA
tetA
aac(3)-IV
sul II
mph A
Dairy
Poultry


B)
100
80
60
40
20
0
Prevalence (%)
blaTEM
strA
tetB
aac(3)-IVa
sul II
Dairy
Poultry



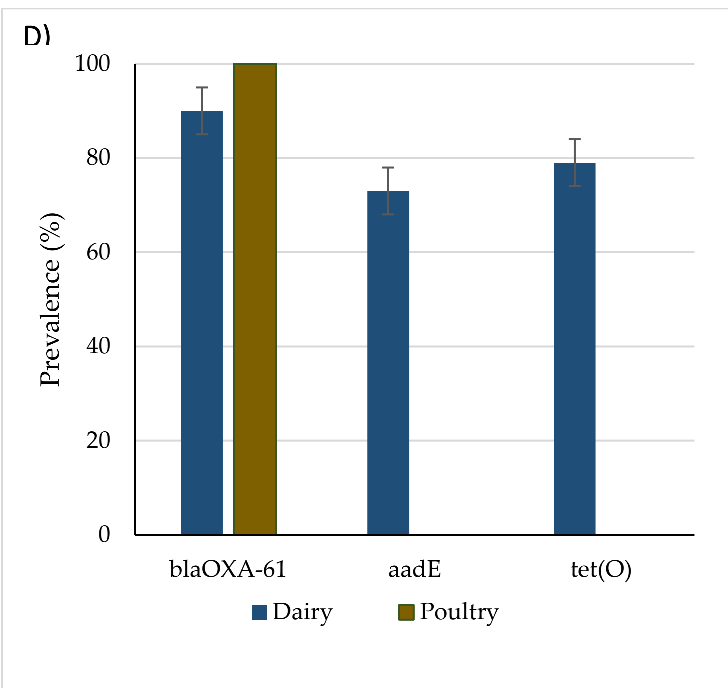


Figure S2. Antimicrobial resistance genes of; **A)** *E. coli O157* **B)** *Salmonella* **C)** *L. monocytogenes* **D)** *Campylobacter* recovered from different manure type.