

**Supplementary table:** Antimicrobial resistance pattern and genotype of all isolates.

<i>Isolate</i>	<i>Estimate</i>	<i>Subspecies</i>	<i>Serotype</i>	<i>AMR phenotype</i>	<i>AMR genotype</i>	<i>Replicon profile</i>	<i>Class 1 Integrase</i>
10.1	E10	<i>diarizonae</i>	38:z10:z53	-	-	-	-
10.2	E10	<i>diarizonae</i>	38:z10:z53	STR-SUL-TRS	-	-	-
10.3	E10	<i>diarizonae</i>	38:z10:z53	STR-SUL-(GEN-NEO)	-	-	-
10.4	E10	<i>diarizonae</i>	38:z10:z53	STR-SUL-(NEO)	-	-	-
10.5	E10	<i>enterica</i>	Enteriditis 9,12:g,m:-	NAL-(ENR)	<i>gyrA</i> <sub>(D87Y)</sub>	-	-
10.6	E10	<i>enterica</i>	Enteriditis 9,12:g,m:-	(SUL)	-	-	-
10.7	E10	<i>enterica</i>	Enteriditis 9,12:g,m:-	NAL-(ENRO)	<i>gyrA</i> <sub>(D87Y)</sub>	-	-
2.1	E2	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	STR-SUL	-	-	-
2.2	E2	<i>salamae</i>	4,12:b:-	(STR)	-	-	-
1.1	E1	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	DOX-TET	<i>strA-strB</i>	-	-
1.2	E1	<i>salamae</i>	4,12:b:-	(NEO-STR)	-	-	-
1.3	E1	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	SUL-(STR)	<i>sul1</i>	-	-
1.4	E1	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	SUL-(STR)	<i>sul1</i>	-	-
1.5	E1	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	NEO-SUL-(STR)	-	-	-
1.6	E1	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	SUL-(STR)	<i>sul1</i>	-	-
1.7	E1	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	STR-(NEO)	-	-	-
1.8	E1	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	SUL-(STR)	<i>sul1</i>	-	-
1.9	E1	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	(STR)	-	-	-
1.10	E1	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	SUL-(NEO-STR)	-	-	-
3.1	E3	<i>enterica</i>	Choleraesuis 6,7:c:1,5 (v.Krf)	NAL-STR-(ENR)	<i>gyrA</i> <sub>(D87N)</sub>	-	-
3.2	E3	<i>enterica</i>	Typhimurium 1,4,5,12:i:1,2	AMP-CHL-SUL- (TET)	<i>blaPSE-aadA1- sul1</i>	-	+
3.3	E3	<i>enterica</i>	Bredeney 4,12:1,v:1,7	AMP-CHL-CTA- CTF-DOX-STR- SUL-TET-TRS	<i>aadA1-strA-strB- sul1-sul2</i>	-	+

(---) Antimicrobial intermediate sensitivity // (v. Krf) Kunzendorf variant.

**Supplementary table (cont-1):** Antimicrobial resistance pattern and genotype of all isolates.

<i>Isolate</i>	<i>Estimate</i>	<i>Subspecies</i>	<i>Serotype</i>	<i>AMR phenotype</i>	<i>AMR genotype</i>	<i>Replicon profile</i>	<i>Class 1 integrase</i>
3.4	E3	<i>diarizonae</i>	38:z10:z53	SUL-(STR)	-	FIIA-HI1-HI2-K/B	-
3.5	E3	<i>enterica</i>	Typhimurium 1,4,5,12:i:1,2	AMP-DOX-STR- SUL-TET	<i>blaTEM-strA-strB-sul2-tetB</i>	-	-
6.1	E6	<i>enterica</i>	Hessarek 4,12:a:1,5	SUL	-	-	-
6.2	E6	<i>enterica</i>	Typhimurium monofásica 4,5,12:i : -	AMP-DOX-STR- SUL-TET-TRS- (NEO)	<i>blaTEM-strA-strB-sul2-tetB</i>	-	-
6.3	E6	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	NAL-STR-(ENR- TET)	<i>sul1-gyrA<sub>(D87N)</sub></i>	-	-
8.1	E8	<i>salamae</i>	50:b:z6	-	-	-	-
8.2	E8	<i>salamae</i>	50:b:z7	(NEO)	-	-	-
26.1	E26	<i>enterica</i>	Enteriditis 9,12:g,m:-	-	-	-	-
26.2	E26	<i>enterica</i>	Lille 6,7:z38:-	-	-	FIC-I1	-
26.3	E26	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	NAL-STR-SUL- (ENR)	<i>gyrA<sub>(D87N)</sub></i>	-	-
26.4	E26	<i>enterica</i>	Enteriditis 9,12:g,m:-	SUL-(NEO)	<i>sul3</i>	HI1	-
17.1	E17	<i>enterica</i>	Hessarek 4,12:a:1,5	NEO-(CTA-CTF)	-	-	-
17.2	E17	<i>diarizonae</i>	48:i:z53	STR-SUL-TRS	-	-	-
17.3	E17	<i>enterica</i>	Typhimurium 1,4,12:i:1,2	SUL	-	-	-
9.1	E9	<i>houtenae</i>	45:z4,z23:-	-	-	-	-
9.2	E9	<i>diarizonae</i>	48:i:z	(STR)	<i>sul2</i>	-	-
9.3	E9	<i>enterica</i>	Choleraesuis 6,7:c:1,5 (v.Krf)	DOX-STR-SUL- TET	<i>strA-strB-sul1-sul2-tetA-tetB</i>	FIIA	-
9.4	E9	<i>diarizonae</i>	47:1,v:z53	STR-SUL	-	-	-
9.5	E9	<i>enterica</i>	Choleraesuis 6,7:c:1,5 (v.Krf)	STR-SUL-TET	<i>strA-strB-tetA</i>	FIIA-HI1	-
9.6	E9	<i>diarizonae</i>	48:k:1,5,7	(STR)	-	-	-
12.1	E12	<i>enterica</i>	Mikawasima 6,7:y:e,n,z15	(DOX)	-	I1	-

(---) Antimicrobial intermediate sensitivity // (v. Krf) Kunzendorf variant.

**Supplementary table (cont-2):** Antimicrobial resistance pattern and genotype of all isolates.

<i>Isolate</i>	<i>Est</i>	<i>Subspecies</i>	<i>Serotype</i>	<i>AMR phenotype</i>	<i>AMR genotype</i>	<i>Replicon profile</i>	<i>Class 1 integrase</i>
12.2	E12	<i>enterica</i>	Bardo 8:e,h:1,2	SUL-TRS	-	HI1	-
12.3	E12	<i>enterica</i>	Bardo 8:e,h:1,2	AMP-SUL-TRS	-	HI1	-
12.4	E12	<i>enterica</i>	Newport 6,8:e,h:1,2	SUL-TRS	-	HI1	-
12.5	E12	<i>diarizonae</i>	61:k:1,5,7	SUL-TRS	-	HI1	-
12.6	E12	<i>diarizonae</i>	61:k:1,5,8	SUL-TRS	<i>tetB</i>	FIA-HI1-K/B-W	-
12.7	E12	<i>enterica</i>	Bardo 8:e,h:1,2	SUL-TRS	-	HI1	-
12.8	E12	<i>diarizonae</i>	48:k:1,5,7	SUL-TRS-(STR)	-	HI1	-
12.9	E12	<i>diarizonae</i>	48:k:1,5,8	SUL-(NEO-STR)	-	-	-
12.10	E12	<i>enterica</i>	Newport 6,8:e,h:1,2	SUL-TRS-(NEO)	-	HI1	-
12.11	E12	<i>enterica</i>	Newport 6,8:e,h:1,2	SUL-TRS	-	-	-
12.12	E12	<i>diarizonae</i>	16: 1,v: 1,5,7	-	<i>sul2</i>	-	-
12.13	E12	<i>enterica</i>	Newport 6,8:e,h:1,2	(TET)	-	-	-
20.1	E20	<i>enterica</i>	Welikade 16:1v:1,7	(STR)	-	-	-
20.2	E20	<i>enterica</i>	Welikade 16:1v:1,8	(NEO-STR)	-	FIA	-
20.3	E20	<i>enterica</i>	Typhimurium 4,5,12:i:1,2	AMP-CHL-DOX-STR-SUL-TET-TRS-(NEO)	<i>blaTEM-dhfrA1-aadA1-sul1-sul3</i>	HI1	+
20.4	E20	<i>enterica</i>	Welikade 16:1v:1,8	STR-SUL	-	FIA-HI1	-
20.5	E20	<i>enterica</i>	Hessarek 4,12:a:1,5	-	-	HI1-I1	-
15.1	E15	<i>diarizonae</i>	35:r.z35	-	-	FIIA	-
15.2	E15	<i>diarizonae</i>	48:k:1,5,7	SUL-TRS-(NEO-STR)	-	-	-
15.3	E15	<i>diarizonae</i>	48:k:1,5,7	SUL-(NEO-STR)	-	FIA-HI1-K/B-W	-
4.1	E4	<i>enterica</i>	Choleraesuis 6,7:c:1,5 (v.Krf)	DOX-STR-SUL-TET	<i>aadA1-strA-strB-sul1-sul2-tetA</i>	-	-

(---) Antimicrobial intermediate sensitivity // (v. Krf) Kunzendorf variant.

**Supplementary table (cont-3):** Antimicrobial resistance pattern and genotype of all isolates.

<i>Isolate</i>	<i>Estimate</i>	<i>Subspecies</i>	<i>Serotype</i>	<i>AMR phenotype</i>	<i>AMR genotype</i>	<i>Replicon profile</i>	<i>Class 1 integrase</i>
4.2	E4	<i>enterica</i>	Choleraesuis 6,7:c:1,5 (v.Krf)	STR-SUL-TET-(DOX)	<i>strA-strB-sul1-sul2-tetA-tetB</i>	-	-
4.3	E4	<i>salamae</i>	13,22: k:-	(STR)	-	-	-
4.4	E4	<i>enterica</i>	Choleraesuis 6,7:c:1,5	DOX-STR-SUL-TET-(CTA)	<i>sul1</i>	-	-
4.5	E4	<i>enterica</i>	Newport 6,8:e,h:1,2	SUL-(NEO)	-	-	-
4.6	E4	<i>diarizonae</i>	48:z10:e,n,x,z15	SUL-(STR)	<i>strA</i>	-	-
4.7	E4	<i>diarizonae</i>	38:z10:z53	SUL-(NEO-STR)	-	-	-
4.8	E4	<i>diarizonae</i>	61:1,v:1,5,7	(STR)	-	-	-
4.9	E4	<i>salamae</i>	13,22:k:-	AMP-NAL-TET-(DOX-ENR-NEO)	<i>blaTEM-strA-strB-sul1-sul2-sul3-tetA</i>	HI1	+
4.10	E4	<i>salamae</i>	4,12,27: g,s,t:-	AMP-(STR)	<i>blaTEM</i>	-	-
4.11	E4	<i>salamae</i>	4,12,27: g,s,t:-	AMP-SUL-TRS-(STR)	<i>blaTEM</i>	FIA-HI1	-
4.12	E4	<i>enterica</i>	Choleraesuis 6,7:c:1,5	DOX-STR-SUL-TET	<i>strA-strB-sul2-tetA</i>	B/O-FIIA-HI1-I1	-
4.13	E4	<i>enterica</i>	Choleraesuis 6,7:c:1,6	DOX-STR-SUL-TET	<i>strA-strB-sul2-tetA</i>	-	-
4.14	E4	<i>enterica</i>	Hessarek 4,12:a:1,5	SUL-(NEO)	-	-	-
4.15	E4	<i>salamae</i>	13,23:z29:e,n,x	AMP-STR-SUL	<i>blaTEM</i>	-	-
4.16	E4	<i>salamae</i>	13,23:z29:e,n,x	AMP-SUL-(NEO-STR)	<i>blaTEM-aadA1-tetB</i>	-	+
4.17	E4	<i>diarizonae</i>	48:i:z53	STR-(TET)	-	-	-
4.18	E4	<i>diarizonae</i>	47:1,v:z53	STR-(TET)	-	-	-
4.19	E4	<i>diarizonae</i>	38:z10:z53	(STR)	-	Y	-
4.20	E4	<i>diarizonae</i>	38:z10:z53	(STR-TET)	-	-	-
4.21	E4	<i>diarizonae</i>	38:z10:z53	(STR)	-	-	-
4.22	E4	<i>diarizonae</i>	16:1,v:1,5,7	SUL-TRS-(STR)	-	-	-
23.1	E23	<i>enterica</i>	Lille 6,7:z38:-	(STR)	<i>sul1-sul2</i>	-	-

(---) Antimicrobial intermediate sensitivity // (v. Krf) Kunzendorf variant.

**Supplementary table (cont-4):** Antimicrobial resistance pattern and genotype of all isolates.

<i>Isolate</i>	<i>Estimate</i>	<i>Subspecies</i>	<i>Serotype</i>	<i>AMR phenotype</i>	<i>AMR genotype</i>	<i>Replicon profile</i>	<i>Class 1 integrase</i>
23.2	E23	<i>enterica</i>	Muenchen 6,8:d:1,2	SUL-(NEO-STR)	<i>aadA1</i>	-	-
23.3	E23	<i>enterica</i>	Lille 6,7:z38:-	SUL-(STR)	-	-	-
23.4	E23	<i>salamae</i>	4,12:b:-	SUL-TRS-(STR)	-	-	-
23.5	E23	<i>salamae</i>	4,12:b:-	SUL-TRS-(NEO-STR)	-	-	-
23.6	E23	<i>salamae</i>	4,12:b:-	SUL-TRS-(STR)-	-	-	-
23.7	E23	<i>salamae</i>	4,12:b:-	SUL-(STR)	-	FIIA	-
22.1	E22	<i>salamae</i>	42:b:e,n,x,z,15	-	<i>sul2</i>	B/O-HI1	-
22.2	E22	<i>salamae</i>	42:b:e,n,x,z,15	SUL-TRS-(NEO)	-	-	-
22.3	E22	<i>salamae</i>	42:b:e,n,x,z,15	-	-	B/O-HI1-	-
13.1	E13	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	-	-	A/C-B/O- FIC-HI1- K/B	-
5.1	E5	<i>diarizonae</i>	48:i:z53	SUL-TRS	-	-	-
5.2	E5	<i>diarizonae</i>	47:1,v:z53	SUL-TRS-(NEO-STR)	-	FIA-FIB - HI1-I1	-
5.3	E5	<i>diarizonae</i>	47:1,v:z53	SUL-TRS-(STR)	-	HI1-HI2	-
5.4	E5	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	(STR)	<i>sul1</i>	FIB-HI1	-
7.1	E7	<i>enterica</i>	Rissen 6,7:f,g:-	AMP-CHL-DOX- SUL-TET-(STR)	<i>aadA1-sul3-tetA</i>	HI1	+
7.2	E7	<i>enterica</i>	Brandenburg 4,12:1,v:e,n,z15	SUL-(STR)	-	HI1	-
7.3	E7	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	STR-SUL	-	FIIA-HI1	-
7.4	E7	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	STR-SUL	<i>sul1</i>	FIIA	-
7.5	E7	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	CHL-STR-SUL	-	HI1	-
29.1	E29	<i>diarizonae</i>	48:i:z53	STR-SUL-TRS	-	-	-
14.1	E14	<i>enterica</i>	Choleraesuis 6,7:- :1,5 (v.Krf)	NAL-STR-(ENR- TET)	-	-	-

(---) Antimicrobial intermediate sensitivity // (v. Krf) Kunzendorf variant.

**Supplementary table (cont-5):** Antimicrobial resistance pattern and genotype of all isolates.

<i>Isolate</i>	<i>Estate</i>	<i>Subspecies</i>	<i>Serotype</i>	<i>AMR phenotype</i>	<i>AMR genotype</i>	<i>Replicon profile</i>	<i>Class 1 integrase</i>
14.2	E14	<i>enterica</i>	Thompson 6,7:k:1,5	AMP-CHL-DOX-STR-SUL-TET-TRS	<i>blaTEM-dhfrA1-aadA1-sul1-sul3</i>	HI2-N	+
14.3	E14	<i>diarizonae</i>	48:i:z53	STR-SUL-TRS	-	-	-
38.1	E38	<i>enterica</i>	Choleraesuis 6,7:-:1,5 (v.Krf)	STR-SUL	<i>sul1</i>	FIIA-HI1	-
38.2	E38	<i>enterica</i>	Typhimurium monofásica 4,12:i:-	AMP-DOX-STR-SUL-TET-TRS	<i>strA-strB-tetB</i>	HI1	-
38.3	E38	<i>enterica</i>	Choleraesuis 6,7:c:1,5 (v.Krf)	AMP-STR-SUL-TET-TRS	<i>blaTEM-aadA1-sul1-sul3-tetA</i>	-	-
35.1	E35	<i>diarizonae</i>	47:1,v:z53	STR	-	FIB	-
36.1	E36	<i>diarizonae</i>	50:z52:1,5,7	-	-	FIIA-FIB	-
37.1	E37	<i>enterica</i>	Choleraesuis 6,7:c:1,5	DOX-STR-SUL-TET	<i>strA-strB-sul1-tetA</i>	FIIA-HI1	-
37.2	E37	<i>diarizonae</i>	65:k:HM III	DOX-STR-SUL-TET	<i>strA-strB-tetA</i>	FIIA-HI1	-
37.3	E37	<i>enterica</i>	Choleraesuis 6,7:c:1,5	SUL-(STR)	<i>sul1</i>	-	-
37.4	E37	<i>enterica</i>	Typhimurium monofásica 4,12:i:-	AMP-DOX-STR-SUL-TET	<i>strA-strB-sul2-tetB</i>	Y	-
37.5	E37	<i>enterica</i>	Choleraesuis 6,7:c:1,5	DOX-STR-SUL-TET-(CTA)	<i>strA-strB-sul1-sul2-tetA</i>	FIIA-HI1	-
37.6	E37	<i>enterica</i>	Choleraesuis 6,7:c:1,5	DOX-STR-SUL-TET	<i>strA-strB-sul2-tetA</i>	FIIA-HI1	-
37.8	E37	<i>enterica</i>	Choleraesuis 6,7:c:1,5	DOX-STR-SUL-TET	<i>strA-strB-sul2-tetA</i>	FIIA-HI2	-

(---) Antimicrobial intermediate sensitivity // (v. Krf) Kunzendorf variant.