

Supplementary material

# Incidence and genomic background of antibiotic resistance in food-borne and clinical isolates of *Salmonella enterica* serovar Derby from Spain

**Table S1.** Primers used for detection of resistance genes, amplification conditions and size of expected amplicons.

Target	Sequence 5'-3'	Tm	Amplicon (bp)	Reference
<i>aadA1</i> -like	GTGGATGGCGGCCTGAAGCC/ ATTGCCCAGTCGGCAGCG	70	526	[62]
<i>aadA2</i>	TGTTGGTTACTGTGGCCGTA/ GATCTCGCCTTTCACAAAGC	56	623	[63]
<i>strA</i>	CTTGGTGATAACGGCAATTC/ CCAATCGCAGATAGAAGGC	60	669	[64]
<i>strB</i>	ATCGTCAAGGGATTGAAACC/ GGATCGTAGAACATATTGGC	60	509	[64]
<i>bla</i> <sub>TEM-1</sub> -like	TTGGGTGCACGAGTGGGT/ TAATTGTTGCCGGGAAGC	55	503	[65]
<i>bla</i> <sub>OXA-1</sub> -like	AGCAGCGCCAGTGCATCA/ ATTCGACCCCAAGTTTCC	60	708	[28]
<i>bla</i> <sub>PSE-1</sub>	CGCTTCCCGTTAACAAGTAC/ CTGGTTCATTTCAGATAGCG	65	419	[62]
<i>fosA7</i>	CAGTCGGGATGCTAAATCTC/ GATACTGGCGCTTACCTTAC	58	267	This study
<i>sul1</i>	CTTCGATGAGAGCCGGCGGC/ GCAAGGCGGAAACCCGCGCC	65	436	[62]

<i>sul2</i>	TCAACATAACCTCGGACAGT/ GATGAAGTCAGCTCCACCT	55	707	[66]
<i>sul3</i>	GAGCAAGATTTTTGGAATCG/ CTAACCTAGGGCTTTGGA	50	773	[30]
<i>tet(A)</i>	GCTACATCCTGCTTGCCTTC/ CATAGATCGCCGTGAAGAGG	55	210	[67]
<i>tet(B)</i>	TTGGTTAGGGGCAAGTTTTG/ GTAATGGGCCAATAACACCG	55	659	[67]
<i>tet(C)</i>	CTTGAGAGCCTTCAACCCAG/ ATGGTCGTCATCTACCTGCC	55	428	[67]
<i>tet(G)</i>	GCTCGGTGGTATCTCTGC/ AGCAACAGAATCGGGAAC	55	500	[28]
<i>tet(M)</i>	GTGGACAAAGGTACAACGAG/ CGGTAAAGTTCGTCACACAC	57	406	[29]



**Table S2.** Accession numbers of *Salmonella enterica* serovar Derby isolates obtained from food and clinical samples in Spain, and parameters related to the quality of the assemblies.

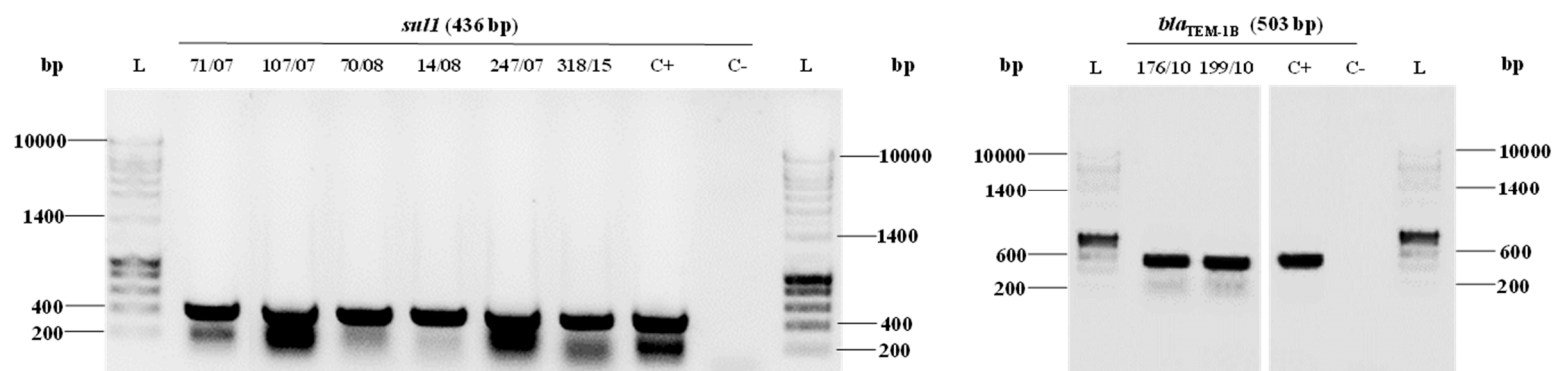
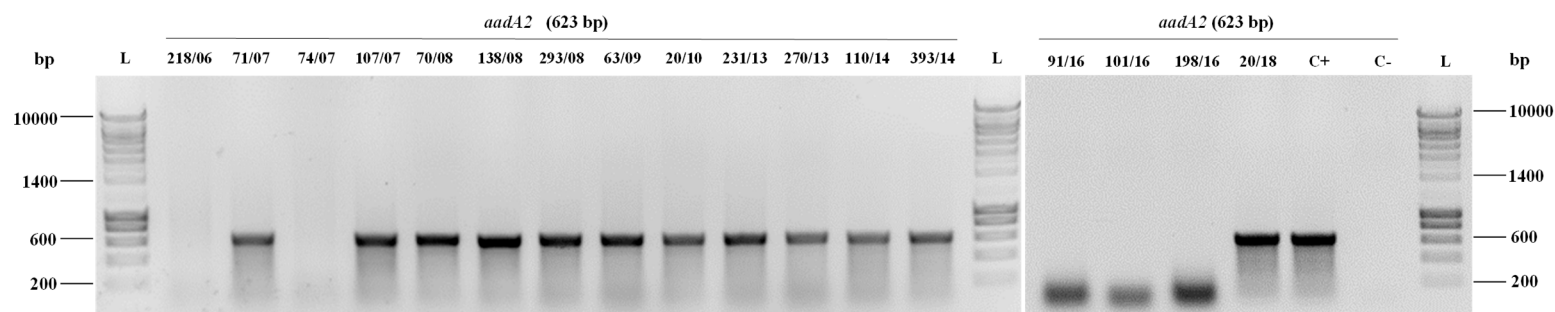
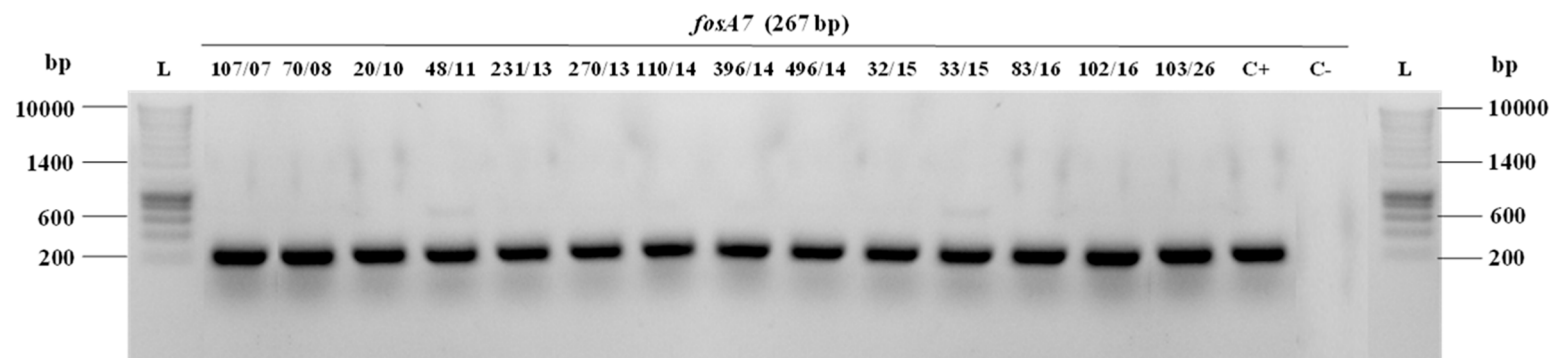
Isolate <sup>a</sup>	Kmer	Contigs	N50	Longest contig (bp)	Total bp in contigs	Contigs > 1 kb	GenBank accession number
LSP 218/06	127	93	397161	685719	4979598	39	JAPWTI000000000
LSP 71/07	127	85	473222	1641246	4834536	29	JAPWTA000000000
LSP 247/07	127	83	473406	1480285	4835929	25	JAPWTF000000000
LSP 14/08	127	101	375436	897376	4843242	36	JAPWSX000000000
LSP 138/08	127	124	487459	1641081	4855858	35	JAPWTD000000000
LSP 63/09	127	103	414700	952109	4914147	34	JAPWSZ000000000
LSP 217/09	127	111	165660	707665	5076596	53	JASTWD000000000
LSP 293/09	127	77	473422	860081	4834348	24	JAPWTG000000000
LSP 176/10	127	88	317905	317905	4951122	31	JAPWTE000000000
LSP 199/10	127	85	409282	1200751	4973614	33	JASNGD000000000
LSP 73/12	127	233	76664	214620	4907238	147	JAPWGG000000000
LSP 217/12	127	236	60780	272135	4878792	164	JAPWGB000000000
LSP 393/13	127	78	473343	860016	4843491	28	JASJEL000000000
LSP 123/15	127	83	457230	457230	4825116	28	JAPWTC000000000
LSP 318/15	127	87	462555	1541386	4921753	30	JAPWTH000000000
LSP 25/16	127	81	326393	605518	4805373	31	JAPWSY000000000
LSP 82/16	127	233	64096	242078	4769093	157	JAPWGF000000000
LSP 91/16	127	272	59058	244242	4756890	185	JAPWGE000000000
LSP 101/16	127	111	537578	1477530	4904217	35	JAPWTB000000000
LSP 198/16	127	243	75300	241746	4768307	163	JAPWGC000000000
LSP 356/16	127	84	276140	599614	4832529	31	JASIRX000000000
LSP 20/18	127	71	473481	1641750	4840526	23	JASIRW000000000

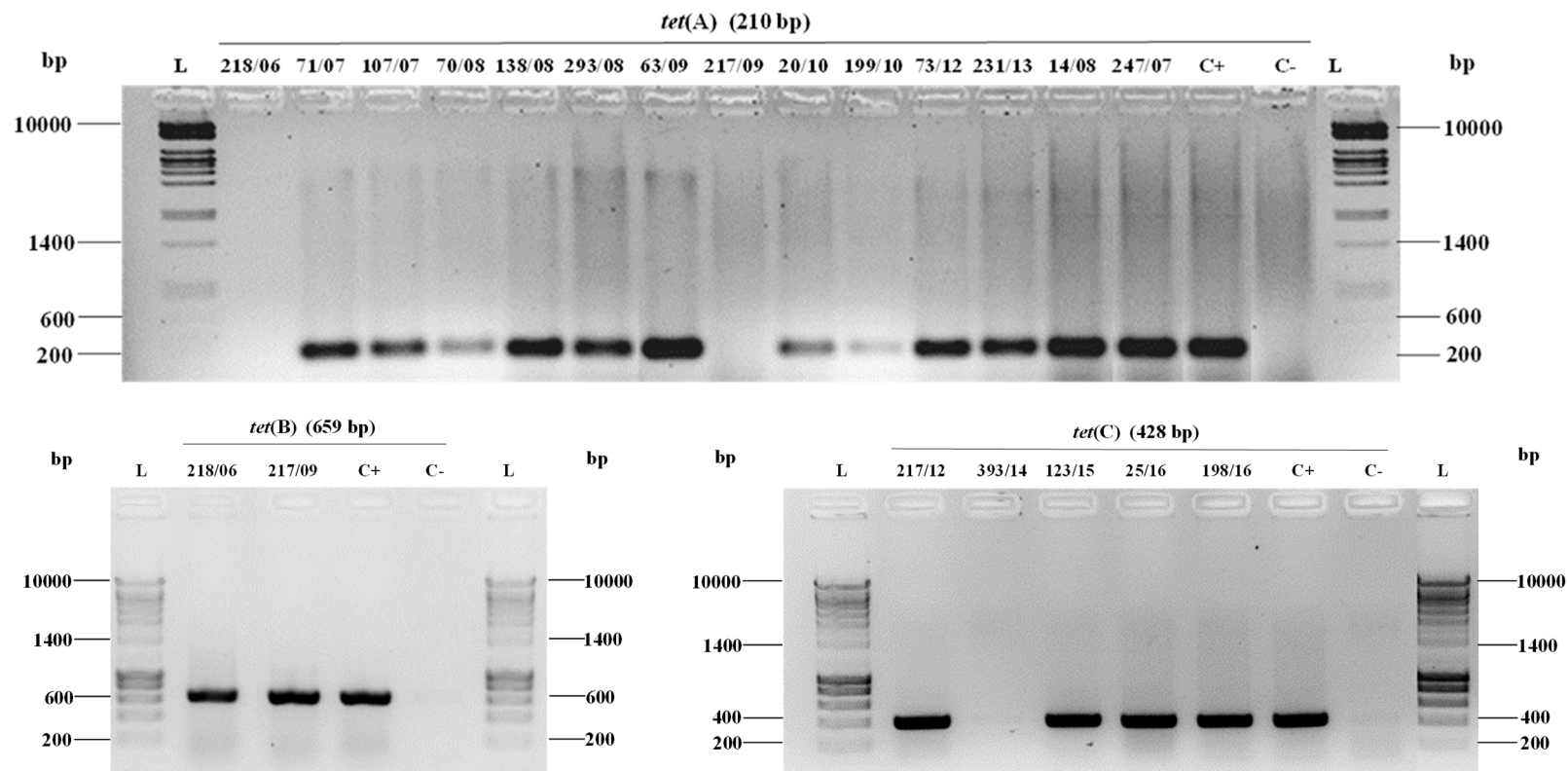
<sup>a</sup>, LSP, “Laboratorio de Salud Pública”, Asturias, Spain.

**Table S3.** Pairwise distance matrix calculated from SNP in the genomes of *Salmonella enterica* serovar Derby isolates obtained from food and clinical samples in Spain.

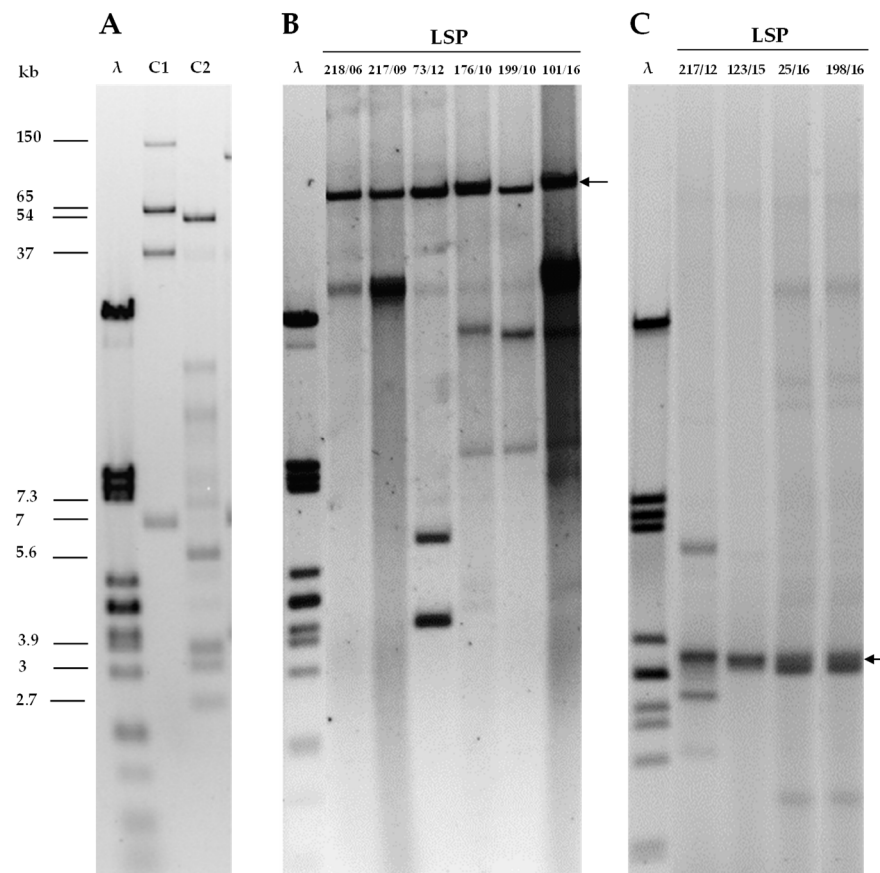
	LSP 101/16	LSP 123/15	LSP 138/08	LSP 14/08	LSP 176/10	LSP 198/16	LSP 199/10	LSP 20/18	LSP 217/09	LSP 217/12	LSP 218/06	LSP 247/07	LSP 25/16	LSP 293/08	LSP 318/15	LSP 393/14	LSP 536/16	LSP 63/09	LSP 71/07	LSP 73/12	LSP 82/16	LSP 91/16
LSP 101/16	0	161	237	236	93	120	93	263	214	102	220	251	150	247	253	245	115	246	238	248	2	12
LSP 123/15	161	0	264	263	170	195	170	290	241	179	247	278	55	274	280	272	192	273	265	275	163	173
LSP 138/08	237	264	0	35	246	267	246	62	109	253	115	50	253	46	42	44	266	45	37	37	239	249
LSP 14/08	236	263	35	0	243	266	243	57	108	250	114	45	252	41	51	39	265	40	36	46	238	248
LSP 176/10	93	170	246	243	0	129	2	272	223	21	229	260	159	256	262	254	124	255	247	257	95	105
LSP 198/16	120	195	267	266	129	0	129	293	244	138	250	281	184	277	283	275	103	276	268	278	122	130
LSP 199/10	93	170	246	243	2	129	0	272	223	21	229	260	159	256	262	254	124	255	247	257	95	105
LSP 20/18	263	290	62	57	272	293	272	0	135	279	141	58	279	54	78	52	292	43	63	73	265	275
LSP 217/09	214	241	109	108	223	244	223	135	0	230	40	123	230	119	125	117	243	118	110	120	216	226
LSP 217/12	102	179	253	250	21	138	21	279	230	0	236	267	168	263	269	261	133	262	254	264	104	114
LSP 218/06	220	247	115	114	229	250	229	141	40	236	0	129	236	125	131	123	249	124	116	126	222	232
LSP 247/07	251	278	50	45	260	281	260	58	123	267	129	0	267	10	66	40	280	41	51	61	253	263
LSP 25/16	150	55	253	252	159	184	159	279	230	168	236	267	0	263	269	261	181	262	254	264	152	162
LSP 293/08	247	274	46	41	256	277	256	54	119	263	125	10	263	0	62	36	276	37	47	57	249	259
LSP 318/15	253	280	42	51	262	283	262	78	125	269	131	66	269	62	0	60	282	61	53	37	255	265
LSP 393/14	245	272	44	39	254	275	254	52	117	261	123	40	261	36	60	0	274	35	45	55	247	257
LSP 536/16	115	192	266	265	124	103	124	292	243	133	249	280	181	276	282	274	0	275	267	277	117	125
LSP 63/09	246	273	45	40	255	276	255	43	118	262	124	41	262	37	61	35	275	0	46	56	248	258
LSP 71/07	238	265	37	36	247	268	247	63	110	254	116	51	254	47	53	45	267	46	0	48	240	250
LSP 73/12	248	275	37	46	257	278	257	73	120	264	126	61	264	57	37	55	277	56	48	0	250	260
LSP 82/16	2	163	239	238	95	122	95	265	216	104	222	253	152	249	255	247	117	248	240	250	0	14
LSP 91/16	12	173	249	248	105	130	105	275	226	114	232	263	162	259	265	257	125	258	250	260	14	0

min: 2 max: 293; SNP, Single Nucleotide Polymorphism; LSP, "Laboratorio de Salud Pública", Asturias, Spain.





**Figure S1.** Agarose gels showing examples of PCR fragments amplified with primer pairs specific for the following resistance genes: *fosA7*, *aadA2*, *bla<sub>TEM-1</sub>*-like, *sul1*, *tet(A)*, *tet(B)* and *tet(C)*, with the size of the expected amplicons shown in parenthesis. The fragments were visualized in agarose gels (1% in TAE running buffer consisting of 40 mM Tris-acetate pH 8.6, 1 mM EDTA. Lane L, 200 bp ladder (NZYDNA Ladder III, NZYTech, Lisboa, Portugal) used as size marker. Numbers in the other lanes correspond to LSP (“Laboratorio de Salud Pública”; Asturias, Spain) isolates (see Tables 1 and 2 for details); C+, positive control; C-, negative control.



**Figure S2.** Plasmid profiles of *Salmonella enterica* serovar Derby isolates harboring resistance genes of plasmid location. Plasmids were extracted with the Kado and Liu method [70] and visualized on agarose gels (0.6% in TAE buffer; see legend to Figure S1). **A.** Size standards. Lane  $\lambda$ , lambda phage DNA digested with PstI, included for comparison. Lanes C1 and C2, plasmids extracted from *Escherichia coli* strains 39R861 and V517 [68–70], used as size references for undigested plasmid DNA. **B.** Isolates carrying IncI1-I( $\alpha$ ) plasmids (indicated with an arrow). **C.** Isolates carrying pSC101-like plasmids (indicated with an arrow). Other lanes in **B** and **C** correspond to LSP (“Laboratorio de Salud Pública”, Asturias, Spain) isolates. Please note that not all plasmids experimentally detected in the isolates were necessarily identified by PlasmidFinder (see Table 2 for comparison).



## References

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