

Supplementary Data

Table S1. Enzymatic profile of *A. salmonicida* using the API ZYM system.

Enzyme Assayed for	J409	J410	J411	J223
Alkaline phosphatase	+	+	+	+
Esterase (C ₄)	+	-	-	-
Esterase lipase (C ₈)	+	+	+	+
Lipase (C ₁₄)	+	+	+	+
Leucine arylamidase	+	+	-	+
Valine arylamidase	-	+	-	-
Cystine arylamidase	+	-	+	-
Trypsin	+	+	+	-
α -Chymotrypsin	-	+	+	-
Acid Phosphatase	+	+	+	+
Naphthol-AS-BI-Phosphohydrolase	+	+	+	+
α -Galactosidase	-	-	-	-
β -Galactosidase	-	-	-	-
β -Glucuronidase	-	-	-	-
α -Glucosidase	-	-	-	-
β -Glucosidase	-	-	-	+
N-Acetyl- β -glucosaminidase	-	+	-	-
α -Mannosidase	-	-	-	-
α -Fucosidase	-	-	-	-

Table S2. Enzymatic profile of *A. salmonicida* using API20NE.

Enzyme Assayed for	J409	J410	J411	J223
Reduction of nitrates to nitrites	+	+	+	+
Indole production	-	-	-	-
Glucose fermentation	+	+	+	+
Urease	-	-	-	-
β -Galactosidase	+	+	+	-
Hydrolysis of:				
Arginine	+	+	+	+
Esculin	+	+	+	+
Gelatin	+	+	+	+
Assimilation of:				
D-Glucose	+	+	+	+
L-Arabinose	+	+	+	-
D-Mannose	+	+	+	+
D-Mannitol	+	+	+	+
N-acetyl-glucosamine	+	+	+	+
D-maltose	-	-	-	+
Potassium gluconate	+	+	+	-
Capric acid	+	+	+	-
Adipic acid	-	-	-	-
Malic acid	+	+	+	+
Trisodium citrate	+	+	+	-
Phenylacetic acid	-	-	-	-
Code	5577555	5577555	5577555	5554244

Table S3. Enzymatic profile of *A. salmonicida* using the API 20E.

Enzyme Assayed for	J409	J410	J411	J223
β -Galactosidase	+	+	+	-
Indole production	+	+	+	-
Acetoin production	+	+	+	-
Citrate utilization	-	-	-	-
H ₂ S production	-	-	-	-
Urease	-	-	-	-
Hydrolysis of:				
L-Arginine	+	+	+	+
L-Lysine	+	+	+	-
L-Ornithine	+	+	+	-
L-Tryptophane	-	-	-	-
Gelatinase	+	+	+	+
Assimilation of:				
D-Glucose	-	-	-	+
D-Mannitol	-	-	-	+
Inositol	-	-	-	-
D-Sorbitol	-	-	-	-
L-Rhamnose	-	-	-	-
D-Saccharose	+	+	+	-
D-Melibiose	-	-	-	-
D-Amygdaline	-	-	-	+
L-Arabinose	-	-	-	-

Table S4. *A. salmonicida* genomes used in this study.

Strain	Labels	Size (Mb)	Topology	RefSeq ID	INSDC identifier
J409	Chromosome	4.63	Circular	NZ_CP047374.1	CP047374.1
	p1AsJ409	0.1	Circular	NZ_CP047375.1	CP047375.1
J410	Chromosome	4.62	Circular	NZ_CP047376.1	CP047376.1
	p1AsJ410	0.072	Circular	NZ_CP047377.1	CP047377.1
J411	Chromosome	4.63	Circular	NZ_CP052034.1	CP052034.1
	p1AsJ411	0.084	Circular	NZ_CP052035.1	CP052035.1
J223	Chromosome	4.7	Circular	NZ_CP048223.1	CP048223.1
	pASal1	0.006	Circular	NZ_CP048225.1	CP048225.1
	pASal2	0.005	Circular	NZ_CP048226.1	CP048226.1
	pASal3	0.007	Circular	NZ_CP048227.1	CP048227.1
	pASal5	0.177	Circular	NZ_CP048224.1	CP048224.1

Table S5. Summary of the RAST annotation genome results.

Atypical <i>A. salmonicida</i> genome						
	J409		J410		J411	
	Chr	p1AsJ490	Chr	p1AsJ410	Chr	p1AsJ411
Genome size	4,632,948 bp	99,881 bp	4,617,865 bp	72,285 bp	4,631,770 bp	88,226 bp
G+C content	58.7 %	53.6%	58.7 %	54.8	58.7 %	54.3 %
N° of Subsystems	363	2	365	3	364	2
N° of CDS	4428	141	4395	104	4849	157
N° of RNAs	146	-	146	-	152	-
Typical <i>A. salmonicida</i> J223						
	Chr	pASal1	pASal2	pASal3	pASal5	
Genome size	4,702,618 bp	6,139 bp	5,247 bp	7,021 bp	176,655 bp	
G+C content	58.5 %	57.4%	52.2 %	55.3 %	54.8 %	
N° of Subsystems	344	-	-	1	5	
N° of CDS	4551	11	9	12	238	
N° of RNAs	144	-	-	-	-	

Table S6. Antibiotic resistance gene identification in atypical *A. salmonicida* strains.

RGI Criteria	ARO Term	SNP	Detection Criteria	AMR Gene Family	Drug Class	Resistance Mechanism	J409		J410		J411	
							% Identity	% Length	% Identity	% Length	% Identity	% Length
Strict	adeF	-	protein homolog model	resistance- nodulation-cell division (RND) antibiotic efflux pump	fluoroquinolone antibiotic, tetracycline antibiotic	antibiotic efflux	47.32	97.64	47.32	97.64	46.55	90.56
Strict	Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin	R234F	protein variant model	elfamycin resistant EF-Tu	elfamycin antibiotic	antibiotic target alteration	88.55	96.33	88.55	96.33	88.55	96.33
Gene description							J409	J410	J411			
Beta-lactamase							GO992_07995 *	GO994_16895	GO993_12435 *			
Subclass B2 metallo-beta-lactamase (<i>bla</i>)							GO992_09850 GO992_16415 *	GO994_031160 * GO994_18760	GO993_14300 * GO993_20940 *			
Class D beta- lactamase (<i>blaOXA</i>)							GO992_13085	GO994_22030	GO993_17570			

(*) Indicates a pseudo gene.

Table S7. Antibiotic resistance gene identification in typical *A. salmonicida*.

RGI Criteria	ARO Term	SNP	Detection Criteria	AMR Gene Family	Drug Class	Resistance Mechanism	<i>A. salmonicida</i> J223					
							CP048223.1	CP048225.1	CP048226.1	CP048227.1	CP048224.1	
						% Identity	% Length	-	-	-	-	
Strict	<i>adeF</i>		protein homolog model	resistance-nodulation-cell division (RND) antibiotic efflux pump	fluoroquinolone antibiotic, tetracycline antibiotic	antibiotic efflux	43.66	98.87	-	-	-	-
Strict	TRU-1		protein homolog model	TRU beta-lactamase	cephalosporin, penam	antibiotic inactivation	73.23	100.00	-	-	-	-
Strict	cphA5		protein homolog model	CphA beta-lactamase	carbapenem	antibiotic inactivation	98.8	99.61	-	-	-	-
Strict	<i>adeF</i>		protein homolog model	resistance-nodulation-cell division (RND) antibiotic efflux pump	fluoroquinolone antibiotic, tetracycline antibiotic	antibiotic efflux	47.32	97.64	-	-	-	-
Strict	Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin	R234F	protein variant model	elfamycin resistant EF-Tu	elfamycin antibiotic	antibiotic target alteration	88.55	96.33	-	-	-	-
				Gene description			CP048223.1	CP048225.1	CP048226.1	CP048227.1	CP048224.1	
				<i>ampC</i>			AXA69_001940	-	-	-	-	
				Class D beta- lactamase (<i>blaOXA</i>)			AXA69_007990 *	-	-	-	-	
				CphA family subclass B2 metallo-beta-lactamase			AXA69_11710	-	-	-	-	

(*) Indicates a pseudo gene.

Table S8. Insertion sequence abundance in typical and atypical *A. salmonicida* genomes.

Insertion Sequences Families	<i>A. salmonicida</i> J409		<i>A. salmonicida</i> J410		<i>A. salmonicida</i> J411		<i>A. salmonicida</i> J223				
	Chrom.	p1AsJ409	Chrom.	p1AsJ410	Chrom.	p1AsJ411	Chrom.	pAsal1	pAsal2	pAsal3	pAsal5
IS1											
ISAs8	1		1		1		1				
Unknown	2		2		2		2				
IS110											
Unknown		2		1		1					3
IS256											
ISAs3	9	3	9	1	9	1	9				4
IS3											
ISAs32	1		1		1		1				
ISAs33							1				
ISAs5							15				2
ISAs6	1		1		1		2				
Unknown	9		9		8		6				3
IS4											
Unknown	2		2		2						1
IS481											
ISAs19							1				
IS5											
ISAs4	174	11	174	8	174	4					
ISAs34							1				
Unknown	3	6	3	2	4	1					2
IS5/IS182											
Unknown	5	1	5	1	6	3					
IS21											
ISAs29/ <i>istB</i>		1		1			8				4
Unknown		1		1			8				3
IS30											
Unknown		1		1		1					4
Tn3											
Unknown		1		1							2
ISAs1											
Unknown	47		46		47						
IS630											
Unknown	23	1	23	1	23	3	35				3

(*) N° of copies identified for each ISs. (Data accessed Nov. 09th, 2021)