Salmonella enterica SRR1427104

Salmonella functional genotyping report

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Date:	2020-05-18
Name:	Salmonella enterica SRR1427104
run accession:	SRR1427104
organism:	Salmonella enterica subsp. enterica
serotype:	Amsterdam
antigenic profile:	3,10:g,m,s:-
acquired resistance:	gentamicin (a)
mutational resistance:	nalidixic acid ciprofloxacin
acquired virulence:	secretion system adherence immune evasion magnesium uptake peptide resistance
virulence/pathogenicity islands:	SPI-4 SPI-5 SPI-6 SPI-1 SPI-2 CS54 island SPI-8 SPI-3 SPI-9 SPI-12 SPI-11
full phages:	Unidentified Siphoviridae I

Details

Serotype

Serotype: Amsterdam
Antigenic profile: 3,10:g,m,s:-

Details
O antigen: O-3,10
H1 antigen (fliC): g,m,s
H2 antigen (fljB): -

Acquired Resistance

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
gentamicin (a)	**aac(6')-Iaa**	100.00	97.72	154940..154503	NC_003197
class: aminoglycoside					

Mutational Resistance

Trait	Locus	Position	Reference	Mutation	Requirements
nalidixic acid	**gyrA**	87	D	Y	
No requirements					
ciprofloxacin	**gyrA**	87	D	Y	
No requirements					

Acquired Virulence

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
secretion system	**avrA**	100.00	99.01	1423415..1424323	NP_461786
description: type III secretion system effector AvrA, acetyltransferease					
adherence	**bcfA**	100.00	99.63	1812447..1811905	NP_459026
description: fimbrial subunit					
adherence	**bcfB**	100.00	99.85	1811804..1811118	NP_459027
description: fimbrial chaperone					
adherence	**bcfC**	100.00	99.28	1811113..1808492	NP_459028
description: fimbrial usher					
adherence	**bcfD**	100.00	98.81	1808491..1807484	NP_459029
description: fimbrial adhesin protein					
adherence	**bcfE**	100.00	97.99	1807483..1806938	NP_459030
description: fimbrial subunit					
adherence	**bcfF**	100.00	100.00	1806922..1806404	NP_459031
description: fimbrial subunit					
adherence	**bcfG**	100.00	98.77	1806438..1805707	NP_459032
description: fimbrial chaperone					
adherence	**csgA**	100.00	99.12	676232..675777	NP_460115
description: curlin major subunit CsgA					
adherence	**csgB**	100.00	99.78	676729..676274	NP_460114
description: minor curlin subunit precursor, curli nucleator protein CsgB					
adherence	**csgC**	100.00	99.69	675715..675389	NP_460116

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
description:	curli assembly protein CsgC				
adherence	**csgD**	100.00	99.39	677484..678134	NP_460113
description:	DNA-binding transcriptional regulator CsgD				
adherence	**csgE**	100.00	100.00	678139..678534	NP_460112
description:	curli production assembly/transport protein CsgE				
adherence	**csgF**	100.00	100.00	678561..678977	NP_460111
description:	curli production assembly/transport protein CsgF				
adherence	**csgG**	100.00	99.16	679004..679837	NP_460110
description:	curli production assembly/transport protein CsgG				
secretion system	**fimC**	100.00	98.99	3331909..3332601	NP_459540
description:	chaperone protein FimC				
immune evasion	**fimD**	100.00	98.97	3332632..3335244	NP_459541
description:	usher protein FimD				
adherence	**fimF**	100.00	98.84	3336276..3336794	NP_459543
description:	type I fimbriae adaptor protein FimF				
adherence	**fimH**	100.00	98.71	3335259..3336266	NP_459542
description:	type I fimbriae minor fimbrial subunit FimH, adhesin				
adherence	**fimI**	100.00	98.88	3331332..3331865	NP_459539
description:	fimbrial protein internal segment				
secretion system	**invA**	100.00	99.17	1393755..1395812	NP_461817
description:	type III secretion system major export apparatus protein InvA				
secretion system	**invB**	100.00	99.02	1395836..1396243	NP_461816
description:	type III secretion system protein InvB				
secretion system	**invC**	100.00	99.15	1396240..1397535	NP_461815
description:	type III secretion system ATPase InvC				
secretion system	**invE**	100.00	99.55	1392612..1393730	NP_461818
description:	type III secretion system gatekeeper invE				
secretion system	**invF**	100.00	99.69	1390280..1390930	NP_461820
description:	type III secretion system regulatory protein InvF				
secretion system	**invG**	100.00	99.70	1390927..1392615	NP_461819
description:	type III secretion system secretin invG				
secretion system	**invH**	100.00	99.32	1389824..1389381	NP_461821
description:	type III secretion system pilotin invG				
secretion system	**invI**	100.00	99.55	1397513..1397956	NP_461814
description:	type III secretion system stalk protein InvI				
secretion system	**invJ**	100.00	99.21	1397956..1398966	NP_461813
description:	type III secretion system needle length regulator InvJ				
magnesium uptake	**mgtB**	100.00	98.90	4166221..4168947	NP_462662
description:	Mg2+ transport protein				
magnesium uptake	**mgtC**	100.00	98.56	4165306..4166001	NP_462663
description:	Mg2+ transport protein				
peptide resistance	**mig-14**	100.00	97.77	1504363..1503467	NP_461708
description:	antimicrobial peptide resistance protein Mig-14				
adherence	**misL**	99.44	97.73	4175714..4172862	NP_462656
description:	putative autotransporter				
secretion system	**orgA**	100.00	99.33	1419187..1419786	NP_461791
description:	type III secretion system accessory cytosolic protein OrgA				
secretion system	**orgB**	97.65	99.10	1419743..1420407	NP_461790

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
description: type III secretion system stator OrgB					
secretion system	**orgC**	100.00	98.68	1420430..1420882	NP_461789
description: type III secretion system effector OrgC					
secretion system	**pipB**	100.00	99.09	2341495..2342370	NP_460061
description: type III secretion system effector PipB					
secretion system	**pipB2**	100.00	94.11	1506104..1507156	NP_461706
description: type III secretion system effector PipB3					
secretion system	**prgH**	100.00	99.41	1416691..1417869	NP_461795
description: type III secretion system outer MS ring protein PrgH					
secretion system	**prgI**	100.00	98.35	1417894..1418136	NP_461794
description: type III secretion system needle filament protein PrgI					
secretion system	**prgJ**	100.00	99.02	1418155..1418460	NP_461793
description: type III secretion system inner rod protein PrgJ					
secretion system	**prgK**	100.00	99.74	1418457..1419215	NP_461792
description: type III secretion system inner MS ring protein PrgK					
secretion system	**sicA**	100.00	98.80	1402817..1403314	NP_461807
description: chaperone for SipC and SipB					
secretion system	**sicP**	100.00	99.24	1410131..1410523	NP_461800
description: chaperone for SptP					
secretion system	**sifA**	100.00	95.85	598342..599352	NP_460194
description: type III secretion system effector SifA, N-terminal SKIP-binding domain, C-term					
secretion system	**sifB**	100.00	96.32	170118..169168	NP_460561
description: type III secretion system effector SifB					
adherence	**sinH**	99.95	95.81	2689158..2691350	NP_461452
description: intimin-like protein					
secretion system	**sipA/sspA**	100.00	98.49	1407476..1409533	NP_461803
description: type III secretion system effector SipA, actin polymerizing activity					
secretion system	**sipB/sspB**	100.00	99.38	1403317..1405098	NP_461806
description: type III secretion system hydrophilic translocator, pore protein SipB					
secretion system	**sipC/sspC**	100.00	99.43	1405126..1406355	NP_461805
description: type III secretion system hydrophilic translocator, pore protein SipC					
secretion system	**sipD**	100.00	99.03	1406426..1407457	NP_461804
description: type III secretion system hydrophilic translocator, needle tip protein SipD					
secretion system	**slrP**	98.69	95.34	2557249..2554982	NP_459778
description: type III secretion system effector SlrP, E3 ubiquitin ligase					
secretion system	**sopA**	100.00	97.96	765896..768244	NP_461011
description: type III secretion system effector SopA, E3 ubiquitin ligase					
secretion system	**sopB/sigD**	100.00	98.22	2338475..2340160	NP_460064
description: type III secretion system effector SopB, phosphoinositide phosphatase					
secretion system	**sopD**	99.37	98.73	1346957..1346010	NP_461866
description: type III secretion system effector SopD					
secretion system	**sopD2**	100.00	97.50	2415139..2414180	NP_459947
description: type III secretion system effector SopD2					
secretion system	**sopE2**	100.00	97.51	3871636..3870914	NP_460811
description: type III secretion system effector SopE2, guanine nucleotide exchange factor					
secretion system	**spaO**	100.00	99.56	1398966..1399877	NP_461812
description: type III secretion system C ring protein SpaO					
secretion system	**spaP**	100.00	99.26	1399867..1400541	NP_461811

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
description: type III secretion system minor export apparatus protein SpaP					
secretion system	**spaQ**	100.00	100.00	1400567..1400827	NP_461810
description: type III secretion system minor export apparatus protein SpaQ					
secretion system	**spaR**	100.00	99.62	1400831..1401622	NP_461809
description: type III secretion system minor export apparatus protein SpaR					
secretion system	**spaS**	100.00	98.69	1401609..1402679	NP_461808
description: type III secretion system export apparatus switch protein SpaS					
secretion system	**spiC/ssaB**	100.00	99.75	382365..381964	NP_460358
description: type III secretion system protein SsaB					
secretion system	**sptP**	100.00	99.20	1410510..1412141	NP_461799
description: type III secretion system effector SptP, tyrosine phosphatase and GTPase-activa					
secretion system	**ssaC**	100.00	98.39	381962..380469	NP_460359
description: type III secretion system secretin SsaC					
secretion system	**ssaD**	100.00	98.43	380488..379277	NP_460360
description: type III secretion system outer MS ring protein SsaD					
secretion system	**ssaE**	100.00	98.35	379269..379027	NP_460361
description: chaperone for sseB					
secretion system	**ssaG**	100.00	98.61	372827..372612	NP_460371
description: type III secretion system needle filament protein SsaG					
secretion system	**ssaH**	100.00	98.25	372571..372344	NP_460372
description: type III secretion system protein SsaH					
secretion system	**ssaI**	100.00	98.39	372332..372084	NP_460373
description: type III secretion system inner rod protein SsaI					
secretion system	**ssaJ**	100.00	98.67	372087..371338	NP_460374
description: type III secretion system inner MS ring protein SsaJ					
secretion system	**ssaK**	100.00	98.81	370775..370101	NP_460376
description: type III secretion system stator SsaK					
secretion system	**ssaL**	100.00	99.12	370135..369119	NP_460377
description: type III secretion system gatekeeper SsaL					
secretion system	**ssaM**	100.00	97.29	369061..368693	NP_460378
description: type III secretion system protein SsaM					
secretion system	**ssaN**	100.00	98.69	366673..365372	NP_460380
description: type III secretion system ATPase SsaN					
secretion system	**ssaO**	100.00	99.47	365369..364992	NP_460381
description: type III secretion system stalk protein SsaO					
secretion system	**ssaP**	100.00	98.13	365011..364637	NP_460382
description: type III secretion system needle length regulator SsaP					
secretion system	**ssaQ**	100.00	98.14	364656..363688	NP_460383
description: type III secretion system C ring protein SsaQ					
secretion system	**ssaR**	100.00	99.07	363620..362973	NP_460384
description: type III secretion system minor export apparatus protein SsaR					
secretion system	**ssaS**	100.00	100.00	362976..362710	NP_460385
description: type III secretion system minor export apparatus protein SsaS					
secretion system	**ssaT**	100.00	98.08	362709..361930	NP_460386
description: type III secretion system minor export apparatus protein SsaT					
secretion system	**ssaU**	100.00	99.24	361933..360875	NP_460387
description: type III secretion system export apparatus switch protein SsaU					
secretion system	**ssaV**	100.00	99.36	368708..366663	NP_460379

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
description: type III secretion system major export apparatus protein ssaV					
secretion system	**sscA**	100.00	97.05	377843..377370	NP_460364
description: chaperone for sseC					
secretion system	**sscB**	100.00	98.16	374839..374405	NP_460368
description: chaperone for sseF					
secretion system	**sseA**	100.00	99.08	378763..378437	NP_460362
description: chaperone for sseB and sseD					
secretion system	**sseB**	100.00	97.63	378430..377840	NP_460363
description: type III secretion system effector SseB					
secretion system	**sseC**	100.00	95.81	377367..375913	NP_460365
description: type III secretion system hydrophilic translocator, pore protein SseC					
secretion system	**sseD**	100.00	98.13	375897..375310	NP_460366
description: type III secretion system hydrophilic translocator, pore protein SseD					
secretion system	**sseE**	100.00	99.04	375307..374891	NP_460367
description: type III secretion system effector SseE					
secretion system	**sseF**	100.00	98.21	374389..373607	NP_460369
description: type III secretion system effector SseF					
secretion system	**sseG**	100.00	97.97	373610..372921	NP_460370
description: type III secretion system effector SseG					
secretion system	**sseJ**	100.00	98.45	140997..139771	NP_460590
description: type III secretion system effector SseJ, glycerophospholipid:cholesterol acyltr					
secretion system	**sseK1**	100.00	98.32	4416755..4415745	NP_463026
description: type III secretion system effector SseK1					
secretion system	**sseK2**	100.00	98.19	852600..853646	NP_461081
description: type III secretion system effector SseK2					
secretion system	**sseL**	100.00	94.97	2930841..2929888	NP_461229
description: type III secretion system effector SseL, deubiquitinase					
secretion system	**sspH1**	100.00	98.34	3911669..3909558	AAD40326
description: type III secretion system effector SspH1, E3 ubiquitin ligase					
secretion system	**steA**	100.00	98.26	192158..192790	NP_460542
description: type III secretion system effector SteA					
secretion system	**steB**	100.00	98.26	142669..142268	AAL20547
description: type III secretion system effector SteB					
secretion system	**steC**	100.00	96.58	61727..63100	NP_460656
description: type III secretion system effector SteC					

Virulence/Pathogenicity Islands

Island	Loci Found	Loci Known	Found (%)	Loci Spread (bp)
SPI-4	11	11	100.00	227.82
Loci: siiA, siiB, siiC, siiD, siiE, siiF, soxR, soxS, ssb, yjcB, yjcC				
SPI-5	8	8	100.00	82.00
Loci: STM1089, copR, copS, pipA, pipB, pipC, pipD, sopB				
SPI-6	5	15	33.33	517263.20
Loci: safB, safC, safD, sinR, yqgA				
SPI-1	39	41	95.12	266.31
Loci: avrA, fhlA, hilA, hilC, hilD, iacP, iagB, invA, invB, invE, invF, invG, invH, invI, invJ, mutS, orgA, orgC, prgH, prgI, prgJ, prgK, sicA, sicP, sipA, sipB, sipC, sipD, sitA, sitB, sitC, sitD, spaO, spaP, spaQ, spaR, spaS, sprB, sptP				
SPI-2	41	44	93.18	75.36

Island	Loci Found	Loci Known	Found (%)	Loci Spread (bp)
Loci: orf242, orf245, orf319, orf32, orf408, orf48, orf78, pykF, spiC, ssaC, ssaD, ssaE, ssaG, ssaH, ssaI, ssaJ, ssaL, ssaM, ssaN, ssaO, ssaQ, ssaR, ssaS, ssaT, ssaU, ssaV, sscA, sscB, sseA, sseB, sseC, sseD, sseE, sseF, sseG, ssrA, ssrB, ttrA, ttrB, ttrC, ttrR				
CS54 island	3	8	37.50	7500.33
Loci: sinH, xseA, yfgK				
SPI-8	2	16	12.50	26.00
Loci: STY3291, STY3292				
SPI-3	9	17	52.94	263.22
Loci: cigR, fidL, marT, mgtB, mgtC, misL, rhuM, rmbA, slsA				
SPI-9	4	4	100.00	24.75
Loci: STY2875, STY2876, STY2877, STY2878				
SPI-12	5	7	71.43	594.40
Loci: ccmE, ccmF, ccmG, msgA, narP				
SPI-11	8	9	88.89	846.38
Loci: cspH, envE, envF, icdA, msgA, pagC, pagD, ysdB				

Full Phages

Trait	Locus	Coverage (%)	Identity (%)	Accession
Unidentified Siphoviridae I	**Salmonella phage vB_SosS_Oslo**	52.98	90.83	JQ806764.1
Position: 479135..477832, 477600..475383, 474778..472347, 472193..468965, 465523..465441, 464971..464851, 462238..461242, 460950..459058, 458338..453870, 452748..450514, 496352..496318, 495018..494852, 494858..494729, 494151..491521, 491262..491211, 485199..484664, 484660..484566, 484313..483732, 483743..483372, 482472..481376, 481280..479846				

Info

Acquired Resistance

Search for known resistance, based on locus presence

Analysis Date:	2020-04-03 17:05:43
Plugin version:	1.1
Knowledgebase name:	salmo_acquired_resistance_kb.zip
Knowledgebase version:	1.0
Acquired resistance experiment (loci):	Acquired_Resistance_loci_identity
Acquired resistance experiment (traits):	Acquired_Resistance_traits_identity
Combine fragments:	True
Minimum coverage (%):	90.0
Minimum percent identity (%):	90.0
Sequence experiment:	denovo

Acquired Virulence

Search for known virulence factors, based on locus presence

Analysis Date:	2020-04-03 17:05:47
Plugin version:	1.1
Knowledgebase name:	salmo_acquired_virulence_kb.zip
Knowledgebase version:	1.0
Acquired virulence experiment (loci):	Acquired_Virulence_loci_identity
Acquired virulence experiment (traits):	Acquired_Virulence_traits_identity
Combine fragments:	True
Minimum coverage (%):	90.0
Minimum percent identity (%):	90.0
Sequence experiment:	denovo

Full Phage Detection

Search for known full phages, based on sequence similarity to known phages

Analysis Date:	2020-04-03 17:05:50
Plugin version:	1.1
Knowledgebase name:	salmo_phage_kb.zip
Knowledgebase version:	1.0
Combine fragments:	True
Full phage experiment:	Phage_Full_coverage
Minimum coverage (%):	20.0
Minimum percent identity (%):	80.0
Sequence experiment:	denovo

Mutational Resistance

Search for known resistances, based on mutations

Analysis Date:	2020-04-03 17:05:45
Plugin version:	1.1
Knowledgebase name:	salmo_mutational_resistance_kb.zip
Knowledgebase version:	1.0

Combine fragments:	True
Minimum coverage (%):	90.0
Minimum percent identity (%):	95.0
Mutational resistance experiment (identifiers):	Mutational_Resistance_identifiers
Mutational resistance experiment (traits):	Mutational_Resistance_traits
Sequence experiment:	denovo

Serotype

Detection of Salmonalla serotypes using SeqSero 1.0 on the calculation environment (CE). Results are automatically processed upon retrieving the job. Running this feature without posting a new job reprocesses the previous results.

Analysis Date:	2020-04-03 17:05:48
Plugin version:	1.1
Knowledgebase name:	Unknown
Knowledgebase version:	Unknown

Antigenic profile infofield:	Profile_reads
Sequence experiment:	n/a
Sequence/Reads experiment:	wgs
Sequence/Reads type:	paired_end_seperated
Serotype infofield:	Serotype_reads

Virulence Islands

Search for virulence islands, cataloging loci presence

Analysis Date:	2020-04-03 17:05:48
Plugin version:	1.1
Knowledgebase name:	salmo_virulence_islands_kb.zip
Knowledgebase version:	1.0

Combine fragments:	True
Island counts experiment:	Island_Counts
Island percentages experiment:	Island_Percentages
Minimum coverage (%):	90.0
Minimum loci (%):	0.0
Minimum percent identity (%):	90.0
Sequence experiment:	denovo
Total islands infofield:	Total Islands

Disclaimer

The contents of this report are for research purposes only and not intended for clinical decision making.