

SRR1378346

Listeria functional genotyping report

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Date: 2020-05-18

Name: SRR1378346

serovar: III (4a, 4c)

serogroup: IVa

acquired resistance: heavy metals
fosfomycin
teichoic acid biosynthesis

acquired virulence: motility
regulation
adhesion
invasion
survival in GI
stress response
cold adaptation
iron aquisition
toxin
intracellular growth
immune modulator
phagosomal escape
immune evasion

virulence/pathogenicity islands: internalin
LIPI-3
LIPI-1

full phages: SiphoviridaeIVa

Details

Serotype

Serovar: III (4a, 4c)

Serogroup: IVa

Marker	Coverage (%)	Identity (%)
prs	100.00	98.60
plcA	100.00	97.53

Details

No further details

Acquired Resistance

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
heavy metals	copA	100.00	93.32	77593..75380	NC_003210.1
<i>description:</i> heavy metal transporter					
fosfomycin	fosX	99.75	92.56	1256415..1256014	AL591981
<i>description:</i> fosX					
teichoic acid biosynthesis	gltA	99.98	95.41	1292273..1287681	NZ_CBXR000000000
<i>description:</i> Glutamate synthase, large subunit A					
teichoic acid biosynthesis	gltB	100.00	96.33	1287666..1286197	NZ_CBXR000000000
<i>description:</i> Glutamate synthase, large subunit B					
teichoic acid biosynthesis	tagB	100.00	98.71	1566577..1567737	NC_003210.1
<i>description:</i> Teichoic acid biosynthesis protein B precursor					

Acquired Virulence

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
motility	actA	100.00	99.34	2580871..2579057	gi:226222833
<i>description:</i> actin-assembly inducing protein precursor					
regulation	agrA	100.00	98.90	1543854..1544582	gi:16802099
<i>description:</i> hypothetical protein					
regulation	agrC	100.00	99.69	1542540..1543835	gi:46906281
<i>description:</i> accessory gene regulator protein C					
adhesion	ami	98.97	99.57	2820785..2820045, 2843059..2842121, 2456251..2455611	gi:404287930
<i>description:</i> N-acetylmuramoyl-L-alanine amidase Ami, family 2/autolysin (GW motif), C-termin					
invasion	aut	96.66	97.22	2764183..2765658	gi:386046738

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
<i>description:</i> N-acetylmuramoyl-L-alanine amidase family protein					
survival in GI	brtA	100.00	90.09	14497..13610	NC_003210.1
<i>description:</i> Bile-regulated transcription factor A					
survival in GI	bsh	100.00	97.75	1444552..1445529	gi:16804106
<i>description:</i> bile salt hydrolase					
invasion	cheA	100.00	95.85	2373252..2371396	gi:16802734
<i>description:</i> two-component sensor histidine kinase CheA					
invasion	cheR	100.00	96.45	1947221..1948009	gi:16802725
<i>description:</i> hypothetical protein					
invasion	cheY	100.00	96.94	2373631..2373272	gi:16802733
<i>description:</i> Chemotaxis response regulator CheY					
stress response	clpB	99.96	92.58	1392028..1394628	NC_003210.1
<i>description:</i> stress reponse protein					
stress response	clpC	100.00	94.07	1937458..1934996	gi:16802278
<i>description:</i> endopeptidase Clp ATP-binding chain C					
stress response	clpE	99.72	93.61	2198167..2195999	gi:16803037
<i>description:</i> ATP-dependent protease					
cold adaptation	cspA	100.00	100.00	1777695..1777489	X91789.1
<i>description:</i> cold shock protein					
cold adaptation	cspB	100.00	99.50	2898168..2897968	NC_003210.1
<i>description:</i> cold shock protein					
cold adaptation	cspD	100.00	98.01	100096..100296	NC_003210.1
<i>description:</i> cold shock protein					
adhesion	dlfA	100.00	96.02	1674565..1676097	gi:16803014
<i>description:</i> D-alanine--poly(phosphoribitol) ligase subunit 1					
adhesion	fbpA	100.00	91.83	50734..52446	gi:16803869
<i>description:</i> fibronectin-binding protein					
invasion	flaA	100.00	98.15	2374769..2373906	gi:16802732
<i>description:</i> flagellin					
invasion	flgB	100.00	95.02	2357087..2356686	gi:16802752
<i>description:</i> flagellar basal body rod protein FlgB					
invasion	flgC	100.00	91.73	2356674..2356264	gi:16802753
<i>description:</i> flagellar basal body rod protein FlgC					
invasion	flgD	100.00	94.56	2369591..2369169	gi:16802738
<i>description:</i> flagellar basal body rod modification protein					
invasion	flgE	100.00	94.01	2369149..2367914	gi:16802739
<i>description:</i> flagellar hook protein FlgE					
invasion	flgG	100.00	95.90	1946413..1947192	gi:16802724
<i>description:</i> flagellar basal body rod protein FlgG					

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
invasion	flgK	99.93	91.79	2361474..2359954	gi:16802747
<i>description:</i>	flagellar hook-associated protein FlgK				
invasion	flgL	100.00	93.15	2359942..2359067	gi:16802748
<i>description:</i>	flagellar hook-associated protein FlgL				
invasion	flhA	100.00	93.21	1943096..1945171	gi:16802722
<i>description:</i>	flagellar biosynthesis protein FlhA				
invasion	flhB	100.00	94.27	1942003..1943049	gi:16802721
<i>description:</i>	flagellar biosynthesis protein FlhB				
invasion	flhF	100.00	94.04	1945193..1946416	gi:16802723
<i>description:</i>	flagellar biosynthesis regulator FlhF				
invasion	fliD	100.00	94.57	2359055..2357766	gi:16802749
<i>description:</i>	flagellar capping protein				
invasion	fliE	100.00	97.98	2356247..2355951	gi:16802754
<i>description:</i>	flagellar hook-basal body protein FliE				
invasion	fliF	99.88	94.49	2355883..2354233	gi:16802755
<i>description:</i>	flagellar MS-ring protein				
invasion	fliG	100.00	96.39	2354228..2353122	gi:16802756
<i>description:</i>	flagellar motor switch protein G				
invasion	fliH	100.00	94.37	2353135..2352443	gi:16802757
<i>description:</i>	flagellar assembly protein H				
invasion	fliI	100.00	95.93	2352446..2351145	gi:16802758
<i>description:</i>	flagellum-specific ATP synthase				
invasion	fliM	100.00	94.56	2367643..2366651	gi:16802741
<i>description:</i>	flagellar motor switch protein FliM				
invasion	fliP	100.00	96.88	1940171..1940938	gi:16802718
<i>description:</i>	flagellar biosynthesis protein FliP				
invasion	fliQ	100.00	98.53	1940951..1941223	gi:16802719
<i>description:</i>	flagellar biosynthesis protein FliQ				
invasion	fliR	100.00	93.96	1941226..1941987	gi:16802720
<i>description:</i>	flagellar biosynthesis protein FliR				
invasion	fliS	100.00	97.16	2357747..2357361	gi:16802750
<i>description:</i>	hypothetical protein				
invasion	fliY	100.00	92.05	2366648..2365101	gi:16802742
<i>description:</i>	flagellar motor switch protein				
iron aquisition	fur	100.00	96.25	184077..183625	NC_003210.1
<i>description:</i>	Transcriptional regulator (Fur family)				
stress response	gbuA	100.00	96.73	2739173..2737980	NC_003210.1
<i>description:</i>	glycine betaine transporter				
iron aquisition	hbp2	100.00	93.57	266488..264779	gi:16804224
<i>description:</i>	hemin/hemoglobin-binding protein 2				
iron aquisition	hdp1	100.00	90.27	267127..266501	gi:16804225
<i>description:</i>	Haemoglobin binding protein 1				
toxin	hly	100.00	97.30	2584527..2582938	gi:386052479

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
<i>description:</i> listeriolysin O					
intracellular growth	hpt	100.00	99.59	2075741..2074512	gi:424713716
<i>description:</i> Hexose phosphate transport protein					
invasion	iap/cwhA	99.38	96.35	285154..286596	gi:16802625
<i>description:</i> P60 extracellular protein, invasion associated protein iap					
invasion	inIA	100.00	99.79	1956039..1953637	gi:404279991
<i>description:</i> internalin A					
immune modulator	inIC	100.00	97.19	2398290..2397400	gi:16803826
<i>description:</i> internalin C					
invasion	inIF	100.00	99.68	1978509..1976038	gi:386731175
<i>description:</i> internalin, peptidoglycan bound protein (LPXTG motif)					
invasion	inIH	99.94	91.57	1413551..1411905	NC_003210.1
<i>description:</i> internalin H					
adhesion	inIJ	100.00	99.64	648549..651299	gi:46909010
<i>description:</i> cell wall surface anchor family protein					
immune modulator	inIK	97.81	89.42	2611348..2611627, 2531450..2532220, 2532274..2532952	gi:470207056
<i>description:</i> Internalin-I					
adhesion	iap	100.00	97.23	1060914..1058314	gi:16803674
<i>description:</i> Listeria adhesion protein Lap					
adhesion	iapB	100.00	92.79	2272563..2277707	gi:284802058
<i>description:</i> peptidoglycan linked protein (LPXTG)					
intracellular growth	igt	100.00	96.64	1169988..1169155	gi:16804520
<i>description:</i> hypothetical protein					
stress response	lisK	100.00	95.87	1761477..1760026	gi:16803418
<i>description:</i> two-component sensor histidine kinase					
stress response	lisR	100.00	97.94	1762154..1761474	gi:16803417
<i>description:</i> two-component response regulator					
toxin	lIsY	99.67	96.01	2371383..2371084	gi:16802735
<i>description:</i> flagellar motor switch protein					
immune modulator	IntA	100.00	97.26	1618564..1618432, 1618389..1618091, 1618061..1617947	gi:470206109
<i>description:</i> Listeria nuclear targeted protein A					
immune modulator	IntA	98.40	90.58	1618563..1617947	gi:405754537
<i>description:</i> hypothetical protein					
invasion	lpeA	100.00	96.68	71338..70406	gi:16803887
<i>description:</i> lipoprotein promoting cell invasion					

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
intracellular growth	lplA1	91.37	92.97	2530467..2531376	gi:16802971
<i>description:</i> lipoate protein ligase					
phagosomal escape	lspA	100.00	97.42	67481..67017	gi:16803884
<i>description:</i> signal peptidase II					
survival in GI	mdrM	100.00	93.54	1077396..1078865	NC_003210.1
<i>description:</i> Multidrug resistance efflux pump					
survival in GI	mdrT	100.00	94.40	13509..12028	NC_003210.1
<i>description:</i> Cholic acid efflux pump					
phagosomal escape	mpl	100.00	94.52	2582603..2581071	gi:16802249
<i>description:</i> Zinc metalloproteinase precursor					
immune evasion	oatA	100.00	93.64	2534871..2532985	gi:16803331
<i>description:</i> peptidoglycan O-acetyltransferase					
cold adaptation	oppA	100.00	99.88	2118170..2119846	gi:226224804
<i>description:</i> pheromone ABC transporter (binding protein)					
immune evasion	pdgA	100.00	99.92	1970484..1969252	gi:405751639
<i>description:</i> polysaccharide deacetylase family protein					
phagosomal escape	plcA	100.00	97.69	2584770..2585723	gi:16802247
<i>description:</i> phosphatidylinositol-specific phospholipase c					
phagosomal escape	plcB	99.89	95.51	2579020..2578152	gi:16802251
<i>description:</i> phospholipase C					
regulation	prfA	100.00	97.48	2585996..2586709	gi:16802246
<i>description:</i> listeriolysin positive regulatory protein					
intracellular growth	prsA2	100.00	96.26	1382351..1381470	gi:16804258
<i>description:</i> post translocation chaperone PrsA2					
intracellular growth	purQ	100.00	96.04	1330744..1328525	NC_003210.1
<i>description:</i> phosphoribosylformylglycinamideine synthase II					
stress response	rsbV	100.00	96.81	1654659..1655003	AM773838.1
<i>description:</i> Anti-anti-sigma factor (antagonist of RsbW)					
regulation	sigB	100.00	96.67	1655438..1656217	NC_003210.1
<i>description:</i> RNA polymerase sigma-37 factor (sigma-B)					
invasion	srtA	100.00	94.47	2528931..2529599	gi:16802969
<i>description:</i> hypothetical protein					
invasion	srtB	100.00	95.28	262077..261337	gi:16804220
<i>description:</i> hypothetical protein					

Trait	Locus	Coverage (%)	Identity (%)	Position	Accession
immune evasion	stp	100.00	95.92	42801..42043	gi:16803861
<i>description:</i> hypothetical protein					
invasion	vip	91.15	89.46	975770..974709	gi:386045959
<i>description:</i> peptidoglycan bound protein					
regulation	virR	100.00	99.85	1302504..1301827	gi:46907975
<i>description:</i> DNA-binding response regulator					
regulation	virS	100.00	95.87	1298622..1297582	gi:16803781
<i>description:</i> hypothetical protein					

Virulence/Pathogenicity Islands

Island	Loci Found	Loci Known	Found (%)	Loci Spread (bp)
internalin	3	4	75.00	474269.33
<i>Loci:</i> inIA, inIC, inIH				
LIPI-3	1	8	12.50	
<i>Loci:</i> IIsY				
LIPI-1	8	8	100.00	129285.00
<i>Loci:</i> actA, agrA, hly, lmo0206, mpl, plcA, plcB, prfA				

Full Phages

Trait	Locus	Coverage (%)	Identity (%)	Accession
SiphoviridaeIVa	Listeria phage A118	57.90	88.93	AJ242593.1
<i>Position:</i> 2473082..2480834, 2481083..2483191, 2483435..2491174, 2492351..2492608, 16555..16128, 2457833..2459795, 2460107..2460545, 2467836..2468177, 2468344..2470200, 2470215..2471019, 2471555..2471590				

Info

Acquired Resistance

Search for known resistance, based on locus presence

Analysis Date: 2020-05-18 11:09:05
Plugin version: 1.1
Knowledgebase name: listeria_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 (%): 85.0
Sequence experiment: denovo

Acquired Virulence

Search for known virulence factors, based on locus presence

Analysis Date: 2020-05-18 11:09:06
Plugin version: 1.1
Knowledgebase name: listeria_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 (%): 85.0
Sequence experiment: denovo

Full Phage Detection

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

Analysis Date: 2020-05-18 11:09:09
Plugin version: 1.1
Knowledgebase name: listeria_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

Serotype

Detect Listeria serotypes, based on combinations of presence and absence of markers

Analysis Date: 2020-05-18 11:09:08

Plugin version: 1.1
Knowledgebase name: listeria_serotype_kb.zip
Knowledgebase version: 1.0

Combine fragments: True
Minimum coverage (%): 90.0
Minimum percent identity (%): 90.0
Sequence experiment: denovo
Serogroup infofield: Serogroup
Serovar infofield: Serovar_gt

Virulence Islands

Search for virulence islands, cataloging loci presence

Analysis Date: 2020-05-18 11:09:07
Plugin version: 1.1
Knowledgebase name: listeria_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 (%): 85.0
Sequence experiment: denovo
Total islands infofield: Total Islands

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