

## **Compare genomes of pathogenic *Listeria monocytogenes* and non-pathogenic *Listeria innocua***

### *Abstract*

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*Listeria monocytogenes* is a food-borne pathogen responsible for the disease listeriosis. *Listeria innocua* is a closely related non-pathogenic strain. Prokka was used for annotation. For comparison between genomes of the pathogenic and the non-pathogenic strain genes which are non-orthologous to each other were described with orthofinder.

*Listeria monocytogenes* with the accession number NC\_003210.1 from RefSeq and *listeria innocua* with the accession number of NZ\_CP045743.1 were used.

*Listeria monocytogenes* genome consists of 1 contig with 2944528 bases. Prokka version 1.14.6 describes 2875 coding regions, it finds 1 CRISPR region, 18 rRNAs and 67 tRNAs and 1 tmRNA. Diagnostic module *eautils* determined quality of the genome from a fastq file. Minimum phred score is 2 and a maximum value is 38. Their mean score is 29.1560 with a standard deviation of 13.5149.

*Listeria innocua* genome consists of 2 contigs, with 2922148 bases. There are 2879 coding regions, 18 rRNAs, 65 tRNAs and 1 tmRNA. Minimum phred score is 2 and maximum value is 38. Mean score is 29.1697 with a standard deviation of 13.5034.

OrthoFinder version 2.5.2 implements the bidirectional best blast searches for the identification of ortholog genes using the best mutual blast hits. All proteins are searched versus all other proteins. Then it analyzes these blast hits.

It found 2795 ortholog groups. Non homologous unassigned genes were 325. 146 genes occur only in *listeria monocytogenes* and 179 only in *listeria innocua*.

For lysis it is to be expected that the pathogenic strain has a thermoregulator though `-rfam` was not enabled with prokka. *Listeria innocua* may have other environmental specific proteins.

## Genomlist of listeria monocytogenes from unassignedGenes.tsv

locus_tag	length	gene	product
IHJOCPOM_00039	942	arcC1	Carbamate kinase 1
IHJOCPOM_00067	990	tri1	ADP-ribosylarginine hydrolase Tri1
IHJOCPOM_00199	954	plcA	1-phosphatidylinositol phosphodiesterase
IHJOCPOM_00200	1590	hly	Listeriolysin O
IHJOCPOM_00201	1533	mpl	COG3227 Zinc metalloproteinase
IHJOCPOM_00203	870	plcB	Phospholipase C
IHJOCPOM_00264	387	blaI	Penicillinase repressor
IHJOCPOM_00269	1179	rtcB	RNA-splicing ligase RtcB
IHJOCPOM_00433	555		Potassium channel
IHJOCPOM_00452	618	IntA	Listeria nuclear targeted protein A
IHJOCPOM_01105	561	rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase
IHJOCPOM_01158	309	yjcS_1	putative protein YjcS
IHJOCPOM_01470	1107	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin)
IHJOCPOM_01480	996	ispH	COG0761 4-hydroxy-3-methylbut-2-enyl diphosphate reductase
IHJOCPOM_01933	447	fhs1_1	Formate--tetrahydrofolate ligase 1
IHJOCPOM_02222	1902	yjcS_2	Putative alkyl/aryl-sulfatase YjcS
IHJOCPOM_02475	1227	yfeO	Putative ion-transport protein YfeO

Listeriolysin O is a hemolysin<sup>1</sup> and virulence factor. It is a thiol-activated<sup>2</sup> cholesterol dependent cytolysin. In a phagosome it gets activated at pH 5.5 and lyses it, the bacterium escapes into the cytosol without damaging the plasma membrane of the infected cell. LLO gets secreted combined with Phospholipase C and 1-phosphatidylinositol phosphodiesterase during lysis.

*Listeria m.* is so able to live intracellular, where they are protected from extracellular immune system factors.

*Listeria* nuclear targeted protein A is another virulence factor. It blocks<sup>3</sup> the recruitment of chromatin repressor BAH1, an epigenetic regulator<sup>4</sup> in the host cell nucleus which binds to interferon (IFN)-stimulated genes (ISGs). Therefore it represses the host cell immune response genes.

Metalloprotease has a proteolytic enzyme activity versus peptide bonds.

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1 [https://en.wikipedia.org/wiki/Listeriolysin\\_O](https://en.wikipedia.org/wiki/Listeriolysin_O)

2 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2173465/>

3 <https://liberumbio.com/recombinant/Listeria-nuclear-targeted-protein-A/IntA-1>

4 <https://www.rcsb.org/structure/2xl4>

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Genomlist of listeria innocua from unassignedGenes.tsv

locus_tag	length	gene	product
EOCLHOKO_00213	1095	comEC_1	ComE operon protein 3
EOCLHOKO_01237	639	ydeA	putative protease YdeA
EOCLHOKO_01270	6576	wapA	tRNA(Glu)-specific nuclease WapA
EOCLHOKO_01539	819	dppA	D-aminopeptidase
EOCLHOKO_02246	816	recT	Protein RecT
EOCLHOKO_02783	534	ywrO	General stress protein 14
EOCLHOKO_02928	2916	Tn3	family transposase
EOCLHOKO_02929	1161	mco	Multicopper oxidase mco
EOCLHOKO_02936	726	ISLre2	family transposase ISAot1