

Supplementary material:

Table 1: Genome annotation statistics. The overall statistical prediction shows the nucleotidic composition of the genes and the pseudomolecule built for the annotation process. A total of 1,204 genes were predicted, with an average length of 1,037 nt.

Genome annotation statistics		
	Genes predicted (1204)	Pseudomolecule
Number of bases	1249098	2467130
A composition	29.58%	29.39%
C composition	20.39%	20.92%
G composition	22.90%	19.73%
T composition	27.11%	29.64%
N composition	0.00%	0.29%
GC percentage	43.30%	40.65%
Gene density in pseudomolecule	0.488 genes per kb	
Average gene length	1037	

Table 2: Functional annotation of *Avibacterium paragallinarum*. This table shows 8 major categories and 49 sub-categories assigned to the annotated genes. These categories correspond to the general Cluster of Orthologous Genes functional categories.

Functional annotation of <i>Avibacterium paragallinarum</i>			
Major Functions	Categories by Gene Ontology	Number of sequences	
Biological process	metabolic process	585	
	cellular process	557	
	localization	126	
	response to stimulus	58	
	cellular component organization or biogenesis	59	
	biological regulation	85	
	carbon utilization	3	
	signaling	4	
	multi-organism process	3	
	developmental process	14	
	biological adhesion	1	
	Cellular process	metabolic phosphorus metabolic process	59
		heterocycle metabolic process	120
generation of precursor metabolites and energy		33	
cofactor metabolic process		50	
cellular aromatic compound metabolic process		35	
sulfur compound metabolic process		13	
photosynthesis		2	
peptide metabolic process		3	
Metabolic process		primary metabolic process	475
		oxidation-reduction process	103
	macromolecule metabolic process	282	
	biosynthetic process	294	
	small molecule metabolic process	276	
	nitrogen compound metabolic process	340	

	catabolic process	78
	organophosphate metabolic process	14
Cellular amino acid metabolic process	glutamine family amino acid metabolic process	18
	branched chain family amino acid metabolic process	8
	aspartate family amino acid metabolic process	12
	histidine family amino acid metabolic process	10
	amino acid activation	13
	serine family amino acid metabolic process	5
	cellular modified amino acid metabolic process	7
tRNA aminoacylation for protein translation	aspartyl-tRNA aminoacylation	3
	phenylalanyl-tRNA aminoacylation	2
	lysyl-tRNA aminoacylation	2
	glutamyl-tRNA aminoacylation	1
	glutamyl-tRNA aminoacylation	1
	arginyl-tRNA aminoacylation	1
	asparaginyl-tRNA aminoacylation	1
Transport	organic substance transport	40
	ion transport	29
	nitrogen compound transport	10
	cofactor transport	3
	secretion	4
Nucleotide metabolic process	ribonucleotide metabolic process	43
Amino acid transport	aromatic amino acid transport	3
	branched-chain aliphatic amino acid transport	1

Table 3: Virulence factors of *Avibacterium paragallinarum*. Full list of virulence factors (103) found in *Avibacterium paragallinarum*, with at least 60% of identity with VFDB. A short description of their functions is provided, according the information obtained by the annotation process.

Virulence factors of *Avibacterium paragallinarum*

Virulence Factor	Short Description
algU	alginate biosynthesis protein AlgZ/FimS
bexA	ATP-dependent polysaccharide export protein
bexB	Capsular polysaccharide export protein
bexC	Capsular polysaccharide export protein
bexD	Capsular polysaccharide export protein
clpE	ATP-dependent protease
clpP	ATP-dependent Clp protease proteolytic subunit
clpV1	Required for secretion of hcp1 probably by providing the energy source for its translocation
comE/pilQ	competence protein E, type IV pilus secretin PilQ
cpsG	phosphomannomutase
csrA	Binds to mRNA to regulate post-transcriptional activity. Regulates glycogen synthesis and cell size and surface properties
ctrB	Membrane fusion protein, capsular polysaccharide export
ctrC	capsule polysaccharide export inner-membrane protein
ctrD	capsule polysaccharide export ATP-binding protein
cyaB	Involved in the export of calmodulin-sensitive adenylate cyclase-hemolysin (cyclolysin)
eno	phosphopyruvate hydratase, putative enolase
fcl	putative fucose synthetase
fur	transcriptional repressor of iron-responsive genes (Fur family) (ferric uptake regulator)
galE	UDP-glucose 4-epimerase

galU	UTP--glucose-1-phosphate uridylyltransferase, carbon storage regulator, argininosuccinate lyase
glnA1	glutamine synthetase
gmd	GDP-D-mannose dehydratase
gmhA/lpcA	phosphoheptose isomerase
hasB	UDP-glucose 6-dehydrogenase
hemA	glutamyl-tRNA reductase
hemB	porphobilinogen synthase
hemC	hydroxymethylbilane synthase, porphobilinogen deaminase
hemE	uroporphyrinogen decarboxylase
hemH	ferrochelatase
hemL	glutamate-1-semialdehyde-2,1-aminomutase, aminotransferase
hemN	oxygen-independent coproporphyrinogen III oxidase
hemX	phosphate-starvation-inducible protein PsiE, putative uroporphyrin-III C-methyltransferase
hemY	porphyrin biosynthesis protein
hlyB	hemolysin transport-secretion protein, alpha-hemolysin translocation ATP-binding protein
hlyD	HlyD protein
hscA	Transport of secretory b polysaccharide accors the outer membrane
hscB	Transport of secretory b polysaccharide accors the outer membrane
htpB	Hsp60, 60kDa heat shock protein, chaperonin
htrB	lipid A biosynthesis lauroyl acyltransferase
hxC	heme-hemopexin utilization protein C
iga	IgA1 protease, specific serine endopeptidase, specific metalloendopeptidase
intT1	Tn21 integrase IntI1
IS1016	Insertion sequence
kdsA	2-dehydro-3-deoxyphosphooctonate aldolase
kdtA	3-deoxy-D-manno-octulosonic-acid transferase
kdtB	lipopolysaccharide core biosynthesis protein
kfiD	putative UDP-glucose 6-dehydrogenase
kpsF	arabinose-5-phosphate isomerase
lap	alcohol-acetaldehyde dehydrogenase
lgtF	UDP-glucose--lipooligosaccharide glucosyltransferase
lipA	capsule polysaccharide modification protein LipA
lipB	capsule polysaccharide modification protein
lpxA	acyl-(acyl-carrier-protein)--UDP-N-acetylglucosamine O-acyltransferase
lpxB	lipid-A-disaccharide synthase
lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase
lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
lpxH	UDP-2,3-diacetylglucosamine hydrolase
lsgF	putative UDP-galactose--lipooligosaccharide galactosyltransferase
manA	mannose-6-phosphate isomerase
mrsA/glmM	phosphoglucosamine mutase
msbA	lipid A, export ABC transporter ATP-binding protein
msbB	lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase
mutS	methyl-directed mismatch repair, recognize exocyclic adducts of guanosine
nanE	Sialic acid catabolism, which confers advantage in mucus intestine
neuB	N-acetyl neuramic acid synthetase
oapA	opacity associated protein
ompA/ompP5	major outer membrane protein homolog, OmpA2, hemagglutinin antigen
opsX/rfaC	ADP-heptose--lipooligosaccharide heptosyltransferase 1
orf 4 E. coli 536	Involved in horizontal gene transfer
orf 7 E. coli 536	Involved in horizontal gene transfer
orf16 E. coli 536	Putative F17-like fimbrial isher
orf17 S. flexneri R27	methyltransferase homologue to ybeA/ydjA
orf18 S. flexneri R27	transcriptional regulator, homologue to ybdA/yeaA
orf45 E. coli 536	putative lysil-tRNA synthetase LysU
orf70 E. coli 536	Involved in horizontal gene transfer
orfM	non-canonical purine NTP pyrophosphatase, rdgB/HAM1 family
pgi	glucose-6-phosphate isomerase
pilB	putative type IV fimbrial biogenesis secretion protein
radC	DNA repair protein RadC

relA	GTP pyrophosphokinase
rfaD	ADP-L-glycero-D-mannoheptose-6-epimerase
rfaE	ADP-heptose synthase, bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenylyltransferase
rfaF	ADP-heptose-LPS heptosyltransferase II
rtxB	RTX toxin transporter, ABC-type bacteriocin/lantibiotic exporter
sigA	Mycobacterium tuberculosis H37Rv
sitA	Sallmonella iron transporter fur regulated
sitB	Sallmonella iron transporter fur regulated
sitC	Sallmonella iron transporter fur regulated
ssb	ssDNA-binding protein controls activity of RecBCD nuclease
tetA(B)	tetracycline resistance protein TetA(B)
tetC	putative transcriptional regulator
tetD	putative transcriptional regulator
tetR	tet repressor
tuf	elongation factor Tu
VC1777	sialic acid-specific subfamily of TRAP transporters
VC1779	sialic acid-specific subfamily of TRAP transporters
waaC	heptosyltransferase I
wbfV/wcvB	Predicted UDP-glucose 6-dehydrogenase
wecA	PII uridylyl-transferase, undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase
y1079	DNA-polymerase repair proteins
ybeB/ydjA	Ribosomal silencing factor RsfS
ybfA/ydhA	sodium/glutamate symporter
yhxB/manB	phosphomannomutase
