

Table S1. *Actinobacillus* species used in this study and their characteristics.

	Invasive/ non-invasive species	Species	Strain	GenBank Accession	Host	Source
1	Invasive species	<i>A. capsulatus</i>	DSM 19761	ARFN00000000.1	Rabbit	Joint
2		<i>A. equuli</i> subsp. <i>equuli</i>	ATCC 19392	NZ_CP007715.1	Horse	Unknown
3		<i>A. lignieresii</i>	NCTC4189	NZ_UFRM01000001	Cattle	Glands
4		<i>A. pleuropneumoniae</i>	NCTC10976	NZ_LR134515.1	Pig	Unknown
5		<i>A. seminis</i>	NCTC10851	NZ_UFSB01000001	Sheep	Semen
6		<i>A. suis</i>	ATCC33415	NZ_CP009159.1	Pig	Septicemia
7		<i>A. ureae</i>	NCTC10220	NZ_UFSD01000002.1	Human	Unknown
8	Non-invasive species	<i>A. delphinicola</i>	NCTC12871	NZ_LR134510.1	Porcine	Lung
9		<i>A. indolicus</i>	46K2C	NZ_CABFKH010000001.1	Pig	Upper respiratory tract
10		<i>A. minor</i>	NM305	ACQL00000000.1	Unknown	Unknown
11		<i>A. porcinus</i>	NM319	NZ_CABFKI010000029	Pig	Upper respiratory tract
12		<i>A. porcitonisillarum</i>	9953L55	NZ_CP029206.1	Pig	Unknown
13		<i>A. succinogenes</i>	GXAS137	NZ_NHRD000000000	Bovine	Rumen

Table S2. Shared and strain specific virulence-associated genes detected in *A. equuli* subsp. *equuli* 4524 and ATCC 19392 strains

<i>A. equuli</i> subsp. <i>equuli</i> strain 4524 (JAPHVQ000000000)				Homologue gene detected in <i>A. equuli</i> subsp. <i>equuli</i> ATCC 19392 (NZ_CP007715)	Shared genes/ Strain specific genes	Nucleotide Identity (%)	Amino acid Identity (%)	Comments
Virulence Factor	Gene	Start	End					
Iron acquisition	NA	NA	NA	<i>TonB-dependent siderophore receptor</i>		NA	NA	
	<i>TonB-dependent receptor plug domain protein</i>	15177	18164	NA	Strain specific genes	NA	NA	
	<i>FhuD</i>	127505	128386	NA		NA	NA	
	<i>FhuB</i>	128386	130335	NA		NA	NA	
	<i>mrp</i>	4188	5285	<i>apbC</i>		98.27	100	
	<i>fepD</i>	17374	18324	<i>fepD</i>		97.48	99.37	
	<i>hutW</i>	17463	19280	<i>hutW</i>		97.14	98.84	
	<i>Hemin receptor</i>	19211	21451	TonB-dependent receptor		98.53	99.46	
	<i>fbpB</i>	24003	26066	<i>fbpB</i>		98.64	99.56	
	<i>cirA</i>	45439	47415	<i>cirA</i>		98.99	99.09	
	<i>fhuC</i>	45811	46575	<i>ATP-binding cassette domain-containing protein</i>		99.48	100	
	<i>fepB</i>	46575	47528	<i>fepB</i>		98.64	99.06	
	<i>fepD</i>	47522	49468	<i>FhuB</i>		95.94	97.84	
	<i>petE</i>	49064	49495	<i>petE</i>		99.07	99.31	
	<i>znuA</i>	49397	50293	<i>znuA</i>		97.96	99.28	
	<i>Outer membrane ferric hydroxamate receptor</i>	49522	51609	<i>TonB-dependent siderophore receptor</i>	Shared genes	98.18	99.28	
	<i>fepD</i>	50288	51325	<i>fepD</i>		97.11	98.55	
	<i>znuC</i>	50295	51050	<i>znuC</i>		95.4	98.8	
	<i>erpA</i>	70275	70616	<i>erpA</i>		95.03	99.12	
	<i>iscC</i>	74520	75746	<i>iscS</i>		95.93	99.51	
	<i>iscU</i>	75879	76262	<i>iscU</i>		98.44	100	
	<i>iscA</i>	76403	76726	<i>iscA</i>		96.3	100	
	<i>fdx</i>	80441	80782	<i>fdx</i>		98.54	100	
	<i>iscX</i>	80782	80976	<i>iscX</i>		99.49	100	
	<i>TonB-dependent receptor</i>	81061	83778	<i>Lactoferrin/transferrin family TonB-dependent receptor</i>		99.68	99.78	

	<i>Iron-regulated protein FrpC</i>	100034	101014	<i>Hypothetical protein</i>		93.03	95.77
	<i>yddA</i>	105860	107644	<i>yddA</i>		95.19	97.48
	<i>fbpB</i>	110130	112130	<i>fbpB</i>		94	96.4
	<i>afuA</i>	112262	113293	<i>ABC transporter substrate-binding protein</i>		95.16	97.97
	<i>ceuD</i>	145185	145943	<i>ceuD</i>		97.1	98.81
	<i>ceuC</i>	145946	146893	<i>ceuC</i>		97.57	98.1
	<i>cirA</i>	146541	148835	<i>cirA</i>		98.95	98.95
	<i>ceuB</i>	146886	147782	<i>ceuB</i>		99.44	99.67
	<i>cysG</i>	188818	190278	<i>cysG</i>		95.62	97.54
	<i>efeB</i>	192983	194173	<i>efeB</i>		99.24	98.74
	<i>fur</i>	216404	216853	<i>fur</i>		99.56	100
	<i>cirA</i>	261290	263803	<i>cirA</i>		96.86	98.69
	<i>cyaA</i>	284521	284826	<i>cyaY</i>		99.67	100
	<i>cirA</i>	298547	301384	<i>cirA</i>		99.26	99.68
	<i>cirA</i>	305007	307307	<i>cirA</i>		99.46	99.59
	<i>znuB</i>	395938	396768	<i>znuB</i>		98.19	99.28
	<i>exbB</i>	474019	474471	<i>exbB</i>		94.92	100
	<i>exbD</i>	474516	474905	<i>exbD</i>		99.23	100
	<i>Protein TonB</i>	474915	475760	<i>Energy transducer TonB</i>		97.4	98.94
	NA	NA	NA	Wzz/FepE/Etk N-terminal domain-containing protein		NA	NA
	NA	NA	NA	<i>rfaJ</i>		NA	NA
	NA	NA	NA	<i>Glycosyltransferase family 4 protein</i>	Strain specific genes	NA	NA
	<i>glycosyltransferase family 2 protein</i>	23864	25705	NA		NA	NA
	<i>rfaF</i>	220335	221534	NA		NA	NA
	<i>fabZ</i>	154332	154796	<i>fabZ</i>		93.98	99.35
	<i>Udp-glcna--lipooligosaccharide n-acetylglucosaminyl glycosyltransferase</i>	463019	463717	<i>Glycosyltransferase family 25 protein</i>	Shared genes	94.42	100
	<i>glf</i>	61311	62462	<i>glf</i>		55.01	44.63

The nucleotide and amino acid sequences of *glf* gene of strain 4524 show 89.93% and 94% similarity, respectively, to that of

homologue gene in *A.*
pleuropneumoniae strain 3906

<i>glmU</i>	65991	67355	<i>glmU</i>	96.56	98.9
<i>kdsB1</i>	468431	469183	<i>kdsB</i>	96.55	99.2
<i>lptD</i>	55830	58160	<i>lptD</i>	90.87	96.39
<i>lptE</i>	107788	108282	<i>lptE</i>	95.76	98.78
<i>lptC</i>	174746	175369	<i>lptC</i>	99.68	99.51
<i>lptA</i>	175366	175866	<i>lptA</i>	95.32	97
<i>lptF</i>	265316	266419	<i>lptF</i>	93.3	99.18
<i>lptG</i>	266420	267502	<i>lptG</i>	95.94	99.72
<i>murG</i>	54675	55730	<i>murG</i>	98.2	99.14
<i>kdsC</i>	16446	16982	<i>kdsC</i>	97.21	98.88
<i>wbaP</i>	58126	59544	<i>wbaP</i>	65.04	63.58
<i>Pilin</i>					
<i>glycosyltransferase</i>	118954	119595	<i>Glycosyltransferase family 4 protein</i>	89.04	81.94
<i>erase</i>					
<i>Glycosyltransferase</i>	146773	147561	<i>Glycosyltransferase family 2 protein</i>	96.58	99.24
<i>erase</i>					
<i>Beta-galactoside</i>					
<i>alpha-2,3-sialyltransferase</i>	328450	329379	<i>Glycosyltransferase family 52</i>	99.03	99.35
<i>se</i>					
<i>Lipooligosaccharide N-acetylglucosamine glycosyltransferase</i>					
<i>wcaA</i>	329383	330153	<i>Glycosyltransferase family 25 protein</i>	94.03	94.94
<i>wcaA</i>	331344	332225	<i>wcaA</i>	98.53	97.95
<i>wcaA</i>	165271	166029	<i>wcaA</i>	97.63	99.2
<i>rfaF</i>	166998	168035	<i>rfaF</i>	96.24	99.71

The nucleotide and amino acid sequences of *wbaP* gene of strain 4524 show 96.83% and 94% similarity, respectively, to that of homologue gene of *A. suis* strains NCTC12996 and ATCC 33415

<i>Glycosyl transferase family protein</i>	179116	179904	<i>Glycosyltransferase family 8 protein</i>	85.62	88.21
<i>wcaA</i>	35490	36281	<i>Glycosyltransferase family 8 protein</i>	86.82	89.26
<i>rfaF</i>	220335	221534	<i>rfaF</i>	95.25	97.75
<i>rfaF</i>	306770	307816	<i>rfaF</i>	99.62	99.71
<i>Glyco-trans-2-like domain-containing protein</i>	385209	386027	<i>Glycosyltransferase family 2 protein</i>	89.01	91.94
<i>Udp-glcnaac--lipooligosacch aride n-acetylglucosa minyl glycosyltransfe rase</i>	463019	463717	<i>Udp-glcnaac--lipooligosaccharide n-acetylglucosaminyl glycosyltransferase</i>	94.42	95.27
<i>rfaJ</i>	299322	300164	<i>rfaJ</i>	89.21	90.03
<i>wcaA</i>	35490	36281	<i>wcaA</i>	89.55	92.04
<i>rfaJ</i>	345	1190	<i>rfaJ</i>	99.88	100
<i>glycosyltransfe rase family 2 protein</i>	23864	25705	<i>Glycosyltransferase family 2 protein</i>	37.49	20.22
<i>msrQ</i>	5298	5894	<i>msrQ</i>	99.33	98.995
<i>gmhA</i>	35386	35970	<i>gmhA/ipcA</i>	98.8	99.48
<i>kdtA</i>	298707	299987	<i>waaA</i>	91.65	95.08
<i>yciS</i>	128557	128847	<i>yciS</i>	93.47	98.96
<i>lapB</i>	128847	130034	<i>lapB</i>	97.81	98.99
<i>waaF</i>	78287	79324	<i>waaF</i>	94.99	96.53
<i>waaC</i>	79385	80359	<i>rfaC</i>	95.94	96.25
<i>rfbX</i>	327242	328450	<i>rfbX</i>	97.93	99.25
<i>rfbB</i>	56970	58043	<i>rfbB</i>	92.53	95.25
<i>glf</i>	61311	62462	<i>glf</i>	55	43.43

The amino acid sequence of glycosyltransferase family 2 protein was 99.35% identical to that of holomgue protein in *A. ureae*

The nucleotide and amino acid sequences of *glf* gene of strain 4524 showed 89.93% and 94% similarity, respectively, to that of homologue gene in *A. pleuropneumoniae* strain 3906

CPS	NA	NA	NA	<i>Glycosyl transferase</i>	NA	NA
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	<i>Putative glycosyltransferase YkoT</i>	65531	66496	NA	Strain specific genes	NA	NA
	<i>murB</i>	67774	68802	<i>murB</i>		99.03	98.83
	<i>murC</i>	53196	54623	<i>murC</i>		94.19	98.74
	<i>murD</i>	57061	58371	<i>murD</i>		94.51	98.17
	<i>murE</i>	61169	62674	<i>murE</i>		97.34	97.61
	<i>murF</i>	59650	61044	<i>murF</i>		96.77	98.71
	<i>wecC</i>	9986	11254	<i>wecC</i>		96.69	98.1
	<i>rimI</i>	9363	9986	<i>rffC</i>		95.99	96.63
	<i>cysA</i>	70739	71554	<i>elaA</i>		94.42	95.83
	<i>wecE</i>	8214	9347	<i>rffA</i>	Shared genes	98.41	98.94
	<i>rfbA</i>	56101	56973	<i>rfbA</i>		97.25	97.6
	<i>gutQ</i>	117062	117997	<i>gutQ</i>		88.68	94.23
	<i>Glycosyl transferase</i>	120713	121546	<i>Glycosyl transferase</i>		87.65	88.49
	<i>galE</i>	124052	125068	<i>galE</i>		90.86	98.52
	<i>murA</i>	141521	142798	<i>murA</i>		96.48	98.6
	<i>rpiR</i>	155869	156741	<i>rpiR</i>		97.59	100
	<i>nagC</i>	19616	20488	<i>nagC</i>		97.02	98.28
	<i>rfaF</i>	219155	220342	<i>rfaF</i>		94.11	96.71
	<i>wza</i>	116057	117214	<i>wza</i>		93.26	98.44
	NA	NA	NA	<i>ShlB/FhaC/HecB family hemolysin secretion/activation protein</i>	Strain specific genes	NA	NA
	NA	NA	NA	<i>ShlB/FhaC/HecB family hemolysin secretion/activation protein</i>		NA	NA
	<i>pgaC</i>	172303	173538	NA		NA	NA
	<i>dps</i>	96363	96932	<i>dps</i>		97.72	99.47
Miscellaneous	<i>UreD</i>	54034	54846	<i>UreD</i>		97.66	100
	<i>UreG</i>	55032	55667	<i>UreG</i>		94.81	99.53
	<i>UreF</i>	55688	56398	<i>UreF</i>		98.39	100
	<i>UreE</i>	56383	56946	<i>UreE</i>	Shared genes	99.47	100
	<i>UreA</i>	59925	60227	<i>UreA</i>		99.67	100
	<i>UreB</i>	59493	59798	<i>UreB</i>		100	100
	<i>UreC</i>	57763	59481	<i>UreC</i>		98.37	99.48
	<i>Recombination protein 2</i>	94843	97137	<i>DNA internalization-related competence protein ComEC/Rec2</i>		95.45	94.64

	<i>fhaC</i>	441089	442843	<i>fhaC</i>		91.69	95.72	
	<i>gstA</i>	219432	220058	<i>gstA</i>		92.66	99.04	
	<i>hypothetical protein</i>	57019	57306	<i>gstA</i>		97.92	98.96	
	<i>gstA</i>	19439	20056	<i>gstA</i>		98.38	99.51	
	<i>pgaB</i>	173552	175324	<i>pgaB</i>		98.93	99.32	
	<i>pgaA</i>	175338	177758	<i>pgaA</i>		94.63	96.9	
OMP	<i>ompC</i>	93317	94447	<i>ompC</i>		95.5	96.81	
	Outer membrane protein P2 (OMP P2)	169146	170249	Outer membrane protein P2 (OMP P2)	Shared genes	99.18	99.45	
	47 kDa outer membrane protein	72215	73555	Outer membrane protein transport protein (OMPP1/FadL/TodX)		94.77	93.88	
	<i>ompW</i>	250909	251562	<i>ompW</i>		99.24	100	
Salicylic acid	<i>nanE</i>	20498	21187	<i>nanE</i>	Shared genes	97.54	97.82	
	<i>nanA</i>	18717	19595	<i>nanA</i>		98.18	99.31	
RTX toxin	<i>apxIB</i>	31379	33502	<i>sunT</i>	Shared genes	64.78	64.55	The nucleotide and amino acid sequences of <i>apxIB</i> gene of strain 4524 showed 99.72% and 99.86% similarity, respectively, to <i>apxB</i> gene of <i>A. equuli</i> subsp. <i>haemolyticus</i> strain CCUG 19799
Auto-transporter	<i>Autotransporter adhesin</i>	74395	78480	YadA-like family protein	Shared genes	87.9	55.8	The nucleotide and amino acid sequences of <i>Autotransporter adhesin</i> gene of strain 4524 showed 95.25% and 96% similarity, respectively, to that of homologue gene in <i>A. suis</i> strain ATCC 33415