

Supplementary Table S4: Reference sequences and description of virulence-associated genes, capsular and lipopolysaccharide biosynthesis genes that were used for *in silico* screening of *P. multocida* ST122^{RIRDC} genomes

Gene category and name	Description	GenBank accession no. of reference sequence	Reference strain
Biosynthesis of capsule			
<i>hyaD-hyaC</i>	Specific genes of capsular type A	CP003022.1:910400- 914575	<i>Pm</i> 36950
<i>bcbD</i>	Specific genes of capsular type B	AF169324.1:17690-16422	M-1404
<i>dcbF</i>	Specific genes of capsular type D	AF302465.1:2892-4397	P934
<i>ecbJ</i>	Specific genes of capsular type E	AF302466.1:3246-5363	P1234
<i>fcB</i>	Specific genes of capsular type F	AY604234.1:1-3156	J-4103
Biosynthesis of LPS			
locus_tag "NCTC10382_00021"	LPS genotype 1 (carboxylate/amino acid/amine transporter)	LS483473.1:16183-17091	NCTC 10382
locus_tag "NCTC10323_00016"	LPS genotype 2 (Glycosyl transferase family 2)	LR134532.1:12164-13006	NCTC 10323
locus_tag "ATO47_06115"	LPS genotype 3 (beta-1,4 galactosyltransferase)	CP013291.1:1387020-1386238	ATO47_06115
<i>latB</i>	LPS genotype 4 (putative acyltransferase 3)	KM670447.1:3565-1715	P2192
<i>rmlC</i>	LPS genotype 5 (putative dTDP-4-dehydrorhamnose 3,5-epimerase)	JN571483.1:13180-13722	P2095
<i>nctB</i>	LPS genotype 6 (putative beta-1,3 N-acetyl-glucosyltransferase)	KJ689443.1:4447-3443	P1573
<i>ppgB</i>	LPS genotype 7 (biosynthesis of 1[(4 aminobutyl)amino]-3-hydroxy-1-oxopropan-2-yl hydrogen phosphate"	JX987238.1:3739-4788	P1591
<i>natF</i>	LPS genotype 8 (predicted1,4 N acetyl galactosamine transferase)	KM670448.1:4920-5795	P2723
Adhesins/Colonization factors			
<i>ptfA</i>	Type 4 fimbriae	KP726888.1:1-435	P-1059 (ATCC 15742)
<i>fimA</i>	Fimbriae (from Pm70)	KP660167.1:1-1125	UNMSM
<i>hsf-1</i>	Autotransporter adhesion (from Pm70)	AE004439.1: 840331-832193	Pm70
<i>hsf-2</i>	Autotransporter adhesion (from Pm70)	AE004439.1:1775628-1779527	Pm70
<i>pfhB-igB</i>	Filamentous hemagglutinin and putative immunoglobulin binding protein	AY035342.1:9393-11444	232
<i>pfhB1</i>	Filamentous hemagglutinin (FhaB) protein	AE004439.1:64167-72014	Pm70

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<i>pflB2</i>	Filamentous hemagglutinin (FhaB) protein	ALBZ01000007.1:1250-5997	P52VAC
<i>tad</i> locus (<i>flp1-flp2-tadV-rcpCAB-tadZABCDEFG</i>)	Non-specific tight adherence protein locus (colonization island)	CP003328.1:946117-957784	PmHB03
Toxin			
<i>toxA</i>	G-protein deamidating <i>P. multocida</i> toxin	AY864768.1:22-3879	<i>Pm</i> clone HN-13
Iron regulation/acquisition			
<i>afuCBA</i>	Afu iron transport system	AE004439.1:1124243-1130644	Pm70
<i>ccmABCDE</i>	Proteins involved in posttranslational attachment of heme	AE004439.1:5567-10363	Pm70
<i>exbB</i>	Accessory protein Ton-dependent transport of iron compound	AF468825.1:531-989	PM25
<i>exbD</i>	Accessory protein Ton-dependent transport of iron compound	AF468825.1:998-1387	PM25
<i>tonB</i>	Proteins forming the TonB-dependent transporter	AF468825.1:1384-2154	PM25
<i>fecB</i>	Iron-dicitrate transporter substrate-binding subunit	CP014618.1:1113112-1114008	Pm-3
<i>fecC</i>	Iron-dicitrate transporter permease subunit	CP014618.1:1114008-1114991	Pm-3
<i>fecD</i>	Iron-dicitrate transporter subunit FecD	CP014618.1:1114991-1115983	Pm-3
<i>fecE</i>	Ferric citrate ABC transporter ATP-binding protein	CP014618.1:1115983-1116756	Pm-3
<i>fbpABC</i>	Ferric binding proteins	AE004439.1:52929-56773	Pm70
<i>fur</i>	Ferric uptake regulation protein	KP659942.1:1-441	UNMSM
<i>hgbA</i>	Putative TonB-dependent receptor	AF237932.1:1-2904	Not specified
<i>hgbB</i>	Putative hemoglobin-iron uptake protein	KX832982.1:1-755	Pm04
<i>thpA</i>	Transferrin-binding protein A	DQ782801.1:1-2334	Pm D:1
Extracellular enzymes			
<i>nanB</i>	Sialidase NanB	AF274868.1:77-3289	86-1913
<i>nanH</i>	Sialidase NanH	AF274869.1:90-2333	86-1913
<i>neuA</i>	CMP-sialic acid synthetase	AE004439.1:209243-209914	Pm70
<i>nanATEK</i>	Structural proteins involved in sialic acid catabolism	CP008918.1:655947-659112	ATCC 43137
<i>nanR</i>	Regulatory protein involved in sialic acid catabolism	UGSY01000001.1:313035-314003	<i>P. testudinis</i> NCTX 12150
<i>pmHAS</i>	Hyaluronan synthase	AF036004.2:1-2919	P-1059 (ATCC 15742)

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<i>siaPT-nanM</i>	Proteins that form the TRAP system required for sialic acid uptake; NanM: N-acetylneuraminate epimerase	CP008918.1:660846-665052	ATCC 43137
Oxidative stress			
<i>sodA</i>	Superoxide dismutase A	AE004439.1:185-829	Pm70
<i>sodC</i>	Superoxide dismutase C	AE004439.1:2190308-2190868	Pm70
Secretion systems			
locus_tag "DR93_1687"	Type II secretion system	NZ_CP008918.1:1761952-1761098	ATCC 43137
locus_tag "DR93_1692"	Type II and type III secretion system	NZ_CP008918.1:1767124-1765769	ATCC 43137
Outer membrane proteins/protectins			
<i>ompA</i>	Outer membrane protein A	KU342632.1:1-1077	768
<i>ompH</i>	Outer membrane protein H	JX473022.1:1-1023	XJNKY-12-YF1
<i>oma87</i>	Outer membrane protein 87	U60439.1:345-2714	PBA100
<i>plpB</i>	Pasteurella lipoprotein B	KP659994.1:1-831	UNMSM