

Figure S1. Genome completeness of *W. confusa* W1 and W2 analyzed by BUSCO

Table S1. Predicted virulence genes in VFDB database.

Genes	Function	W1 (No of genes)	W2 (No of genes)
<b>Antiphagocytic</b>			
<i>gnd</i>	6-phosphogluconate dehydrogenase, decarboxylating	1	1
<i>galE</i>	Polysaccharide capsule	1	1
<i>Tig/ropA</i>	Trigger factor	1	1
<i>ndk</i>	Nucleoside diphosphate kinase	1	1
<b>Adherence</b>			
<i>gap</i>	Glyceraldehyde-3-phosphate dehydrogenase	1	1

Table S2. Gene information involved in exopolysaccharide gene clusters

Strains	Gene name in sequences (prokka)	Gene name (uniprot)	Functions	Region	Functional category	Size (bp)
W1 (node 18)	Hypothetical protein	<i>RfbX</i>	Other Cellular Component	7,560 - > 6,076	other	1485
	Hypothetical protein	<i>FGL80_07090</i>	Glycosyltransferase	8,807 - > 7,680	synthesis	1128
	<i>tagG</i>	<i>tagG</i>	ABC-2 type transporter transmembrane domain-containing protein	9,648 - > 8,821	Export/import /regulation	828
	<i>btuD 3</i>	<i>btuD 3</i>	ABC type transporter	10,625 - > 9,654	Export/import /regulation	972
	Hypothetical protein	<i>H9L19_06025</i>	Glycosyltransferase family 2 protein	11,689 - > 10,802	synthesis	888
	putative glycosyltransferase	<i>IV68_GL000138</i>	Glycosyltransferase	12,731 - > 11,766	synthesis	966
	Hypothetical protein	<i>WOSG25_080230</i>	Glycosyltransferase RgtA/B/C/D-like domain-containing protein	14,536 - > 12,818	synthesis	1719
	Hypothetical protein	<i>E9934_11360</i>	Glycosyltransferase RgtA/B/C/D-like domain-containing protein	15,291 - > 14,590	synthesis	702
	Hypothetical protein	<i>lytG_2, QX99_01554</i>	Hydrolase activity, extracellular component	17,413 - > 15,476	cleavage	1938
	Hypothetical protein	<i>H9L19_07490</i>	Glycosyltransferase activity	19,499 - > 17,436	synthesis	2064
	Hypothetical protein	<i>WOSG25_080270</i>	Lipoprotein (other cellular component)	20,056 - > 19,541	other	516
	<i>glfC</i>	<i>glfC</i>	UDP-glucose 4-epimerase, exopolysaccharide (EPS) biosynthesis	21,362 - > 20,184	Synthesis	1179
	Hypothetical protein	<i>SAMN05216341_102152</i>	Predicted membrane protein (cellular component)	21,630 - > 22,985	other	1356
	Hypothetical protein	<i>FC34_GL001529</i>	GlsB/YeaQ/YmgE family stress response membrane protein (plasma membrane)	23,433 - > 23,185	other	249
	Hypothetical protein	<i>BN623_01340</i>	Acyltransferase 3 domain-containing protein	24,342 - > 23,509	modification	834
	Hypothetical protein	<i>PIROE2DRAFT_3857</i>	acyltransferase activity, (acyltransferases can be involved in the modification of EPS	24,548 - > 24,393	modification	156

			molecules by adding acyl groups, such as fatty acids, to the polysaccharide backbone)			
	<i>epsL</i>	<i>epsL</i>	Putative sugar transferase EpsL, chain length determination or regulation.	25,303 -> 24,674	synthesis	630
	Hypothetical protein	<i>QX99_01550</i>	Hypothetical protein	26,126 -> 25,356	other	771
	<i>map 2</i>	<i>map 2</i>	Methionine aminopeptidase	26,970 -> 26,188	cleavage	783
	<i>brp A</i>	<i>brp A</i>	Biofilm regulating protein	27,171 -> 28,064	regulation	894
	Hypothetical protein	<i>WOSG25_080290</i>	Teichoic acid glycosylation protein	28,541 -> 28,113	other	429
	Hypothetical protein	<i>DW717_02355</i>	PucR family transcriptional regulator, Sugar diacid utilization regulator	29,317 -> 28,598	Transcription/ regulation	720
	Hypothetical protein	<i>FPFC 1</i>	Transposases, DNA binding	29,621 -> 29,881	Transposases	261
	<i>ISWci2</i>	<i>ISWci2</i>	IS3 family transposase ISWci2	29,929 -> 30,636	Transposases	708
	Hypothetical protein	<i>HMPREF0877_1823</i>	Helix-turn-helix domain protein (DNA Binding)	31,141 -> 30,938	other	204
	Hypothetical protein	<i>QX99_01496</i>	Helix-turn-helix domain protein (DNA Binding)	32,538 -> 31,813	other	726
	Hypothetical protein	<i>QX99_01496</i>	Helix-turn-helix domain protein (DNA Binding)	33,074 -> 32,553	other	522
	<i>pepS</i>	<i>pepS</i>	Aminopeptidase, hydrolase activity	33,217 -> 34,455	cleavage	1239
	W2 (node 1)	<i>pepS</i>	<i>pepS</i>	Aminopeptidase, hydrolase activity	215,709 -> 214,477	cleavage
Hypothetical protein		<i>QX99_01496</i>	Helix-turn-helix domain protein	215,852 -> 217,114	other	1263
Hypothetical protein		<i>QX99_01498</i>	Helix-turn-helix domain protein	217,786 -> 218,559	other	774
Hypothetical protein		<i>QX99_01498</i>	Helix-turn-helix domain protein	218,549 -> 219,277	other	729

Hypothetical protein	<i>C1199_32025</i>	Transposase	219,371 -> 219,556	Transposases	186
<i>ISWci2</i>	<i>FPFC_120030</i>	IS3 family transposase ISWci2	220,546 -> 219,752	Transposases	795
Hypothetical protein	<i>FPFC_120020</i>	Transposase	220,854 -> 220,594	Transposases	261
Hypothetical protein	<i>DW717_02355</i>	PucR family transcriptional regulator	221,158 -> 221,877	Transcription/ regulation	720
Hypothetical protein	<i>WOSG25_080290</i>	Teichoic acid glycosylation protein	221,934 -> 222,362	other	429
<i>map 1</i>	<i>map 1</i>	Methionine aminopeptidase	222,586 -> 223,368	cleavage	783
Hypothetical protein	<i>FY536_01520</i>	DUF4422 domain- containing protein (unknown)	223,430 -> 224,200	other	771
<i>epsL</i>	<i>epsL</i>	Putative sugar transferase EpsL, chain length determination or regulation.	224,253 -> 224,882	synthesis	630
Hypothetical protein	<i>IRY55_04125</i>	GlsB/YeaQ/YmgE family stress response membrane protein	224,970 -> 225,218	other	249
Hypothetical protein	<i>LB941_12275</i>	ISL3 family transposase	226,206 -> 225,646	transposases	561
Hypothetical protein	<i>H9L19_07515</i>	CDP-glycerol glycerophosphotransferase family protein	227,100 -> 228,707	synthesis	1608
<i>tarD</i>	<i>C270_02975</i>	Glycerol-3-phosphate cytidyltransferase	228,725 -> 229,135	synthesis	411
putative glycosyltransferase	<i>H0267_10780</i>	Glycosyltransferase family 2 protein	229,266 -> 230,204	synthesis	939
Hypothetical protein	<i>HMPREF0877_1596</i>	Arylsulfatase (hydrolase)	230,207 -> 230,623	Modification (remove sulfate groups of precursors)	417
Hypothetical protein	<i>HMPREF0877_1596</i>	Arylsulfatase, 3.1.6.-	230,696 -> 231,241	Modification (remove sulfate groups of precursors)	546
Hypothetical protein	<i>QX99_01574</i>	Phosphoglycerol transferase, alkaline phosphatase superfamily	231,213 -> 232,694	other	1482
Hypothetical protein	<i>SAMN04488506_0470</i>	Uncharacterized membrane protein YfhO	233,078 -> 235,822	other	2745

<i>glf</i>	<i>glf</i>	Isomerase activity (UDP- galactopyranose mutase activity)	235,897 -> 237,075	synthesis	1179
<i>csbB</i>	<i>H9L19_07650</i>	Glycosyltransferase family 2 protein	237,182 -> 238,114	synthesis	933
Hypothetical protein	<i>WOSG25_080280</i>	Glycosyltransferase	238,212 -> 239,162	synthesis	951
Hypothetical protein	<i>WOSG25_080270</i>	lipoprotein	239,307 -> 239,780	other	474
Hypothetical protein	<i>WOSG25_080260</i>	Putative mannosyl- glycoprotein endo-beta-N- acetylglucosamidase	239,802 -> 241,985	other	2184
Hypothetical protein	<i>B5F53_04560</i>	Peptidase M23 domain- containing protein	242,019 -> 244,085	Cleavage	2067
Hypothetical protein	<i>FD46_GL000348</i>	Glycosyltransferase RgtA/B/C/D-like domain- containing protein	244,494 -> 246,380	synthesis	1887
<i>glfT1</i>	<i>glfT1(H9L19_06025)</i>	Glycosyltransferase family 2 protein	246,396 -> 247,280	synthesis	885
<i>btuD1</i>	<i>btuD1(H9L19_00885)</i>	ABC transporter ATP- binding protein	248,244 -> 249,215	Export/import /regulation	972
<i>tagG</i>	<i>tagG(IV73_GL000915)</i>	ABC-2 type transporter transmembrane domain- containing protein	249,221 -> 250,048	Export/import /regulation	828
Hypothetical protein	<i>FGL80_07090</i>	Glycosyltransferase	250,062 -> 251,189	synthesis	1128
Hypothetical protein	<i>rfbX, QX99_01555</i>	RfbX protein (membrane)	251,287 -> 252,771	other	1485

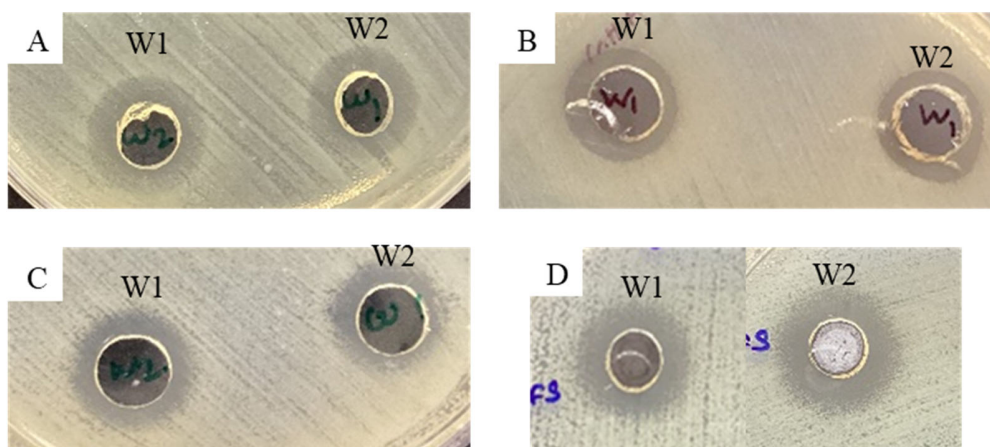


Figure S2. Antibacterial activity of CFS of *W. confusa* W1 and W2 strains against (A) *Salmonella enterica* serotype Typhi DMST 22842 (B) *Vibrio cholerae* DMST 2873 (C) Carbapenem-resistant *Acinetobacter baumannii* SK005 (D) *Stenotrophomonas maltophilia* DMST 19079 using agar-well diffusion method (Tests are done three independent times)