

Supplementary

# Discovery of Novel Resistance Mechanisms of *Vibrio parahaemolyticus* Biofilm against Aminoglycoside Antibiotics

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**Table S1** The OD<sub>600</sub> value of *V. parahaemolyticus* biofilm

	OD	OD <sub>c</sub>	2OD <sub>c</sub>	4OD <sub>c</sub>
VPC16	0.36±0.08	0.136±0.02	0.272±0.02	0.544±0.02
VPC17	1.23±0.03	0.136±0.02	0.272±0.02	0.544±0.02
VPC18	0.70±0.13	0.136±0.02	0.272±0.02	0.544±0.02
VPC19	0.74±0.02	0.136±0.02	0.272±0.02	0.544±0.02
VPC20	1.14±0.02	0.136±0.02	0.272±0.02	0.544±0.02
VPC21	3.40±1.13	0.136±0.02	0.272±0.02	0.544±0.02
VPC22	0.75±0.11	0.136±0.02	0.272±0.02	0.544±0.02
VPC25	0.73±0.18	0.136±0.02	0.272±0.02	0.544±0.02
VPC26	0.95±0.44	0.136±0.02	0.272±0.02	0.544±0.02
VPC27	0.57±0.17	0.136±0.02	0.272±0.02	0.544±0.02
VPC28	1.25±0.28	0.136±0.02	0.272±0.02	0.544±0.02
VPC29	0.43±0.17	0.136±0.02	0.272±0.02	0.544±0.02
VPC32	1.04±0.17	0.136±0.02	0.272±0.02	0.544±0.02
VPC33	0.45±0.01	0.136±0.02	0.272±0.02	0.544±0.02
VPC34	0.71±0.03	0.136±0.02	0.272±0.02	0.544±0.02
VPC35	0.88±0.26	0.136±0.02	0.272±0.02	0.544±0.02
VPD8	0.35±0.08	0.193±0.01	0.386±0.01	0.772±0.01
VPD14	1.15±0.48	0.193±0.01	0.386±0.01	0.772±0.01
VPD18	0.85±0.14	0.193±0.01	0.386±0.01	0.772±0.01
VPD33	0.70±0.02	0.193±0.01	0.386±0.01	0.772±0.01
VPD34	0.51±0.01	0.193±0.01	0.386±0.01	0.772±0.01
VPD57	0.40±0.02	0.193±0.01	0.386±0.01	0.772±0.01
VPD58	0.39±0.04	0.193±0.01	0.386±0.01	0.772±0.01
VPD61	1.09±0.06	0.193±0.01	0.386±0.01	0.772±0.01
VPR101	0.96±0.03	0.193±0.01	0.386±0.01	0.772±0.01
VPR103	0.26±0.03	0.193±0.01	0.386±0.01	0.772±0.01
VPR104	0.43±0.22	0.193±0.01	0.386±0.01	0.772±0.01

VPR105	0.42±0.74	0.193±0.01	0.386±0.01	0.772±0.01
VPR106	0.37±0.29	0.193±0.01	0.386±0.01	0.772±0.01
VPR108	0.50±0.04	0.193±0.01	0.386±0.01	0.772±0.01
VPR110	0.49±0.07	0.193±0.01	0.386±0.01	0.772±0.01
VPR111	0.23±0.01	0.193±0.01	0.386±0.01	0.772±0.01

Notes: The values are mean value ± standard deviation.

**Table S2** Details of primer pairs

Target Genes	Primer Sequence	Expected Size (bp)
<i>pckA</i>	TCGGTAGGACGAATGAACATG	108
	TGACGGTTATTGTGGTGCTAA	
<i>gspC</i>	GCAGGATTATCAAGCAGACC	102
	TATCGCAATAAATAGGCAAGTAAG	
<i>gspD</i>	GTGACTCAGATACTGGTGCTAT	187
	ATACTTGGAGAAGATAGGATGTTTG	
<i>gspE</i>	TACGCTCTGTTCTGACTGTAAAG	270
	CTTAGACCATCACTGCGAATACTT	
<i>gspG</i>	GGTGGTTACATCAAGCGTCTT	165
	GAAGTCTTGCATGTTCCAGTTG	
<i>gspH</i>	AACCACCGCAAGTCTTCATT	169
	GCATTTCGCATCCTCTTCCA	
<i>gspL</i>	TGCGGGCGTTTTGTTAGTG	228
	GCAGCAAGCCAAGACAACAT	
<i>parE</i>	CGTTGAAGCGGGTCATATCTAT	280
	ACCTAGCAGCATGTCCATCA	
<i>parC</i>	GAGCGTGACCTAGTACCAAGT	204
	GTGCGACTCAAGCGAGTAAC	