

**Table S3. Resistance phenotype-genotype correlations among *Campylobacter* isolates**

Drug class	Antibiotic tested	Phenotypes (no. of isolates) <sup>a</sup>	Genotypes (no. of isolates)	Correlation % <sup>b</sup>	p-value <sup>d</sup>
Tetracyclines	Tetracycline	R, 235	<i>tetO</i> (n=194)	82.3 (194/235)	<0.001
		S, 20	None	100 (20/20)	
Macrolides	Erythromycin	R, 27	<i>ermB</i> (n=1)	3.7 (1/27) <sup>c</sup>	0.11
		S, 227	None	100 (227/227)	
Aminoglycosides	Streptomycin	R, 82	<i>ant-like B</i> (n=6), <i>ant-like A</i> (n=34), <i>sat-1</i> (n=3), <i>aad9</i> (n=18), <i>ant(6)-Ib</i> (n=23), <i>ant(6)-Ia</i> (n=14), <i>sat-4</i> (n=14), <i>aph(3)-IIIa</i> (n=5), <i>hpt</i> (n=9), <i>aph(2) IIIa</i> (n=7), <i>apmA</i> (n=2)	69.5 (57/82)	<0.001
		S, 172	<i>ant-like B</i> (n=5), <i>ant-like A</i> (n=5), <i>ant(6)-Ia</i> (n=2), <i>sat-4</i> (n=2), <i>aph(3)-IIIa</i> (n=2)	4.1 (7/172)	
	Gentamicin	R, 12	<i>ant-like B</i> (n=1), <i>ant-like A</i> (n=3), <i>aad9</i> (n=9), <i>ant(6)-Ib</i> (n=9), <i>ant(6)-Ia</i> (n=6), <i>sat-4</i> (n=7), <i>hpt</i> (n=6), <i>aph(2)-IIIa</i> (n=7), <i>apmA</i> (n=2)	91.7 (11/12)	<0.001
		S, 242	<i>ant-like B</i> (n=10), <i>ant-like A</i> (n=36), <i>sat-1</i> (n=3), <i>aad9</i> (n=9), <i>ant(6)-Ib</i> (n=14), <i>ant(6)-Ia</i> (n=10), <i>sat-4</i> (n=9), <i>aph(3)-IIIa</i> (n=7), <i>hpt</i> (n=3)	21.9 (53/242)	

<sup>a</sup> R, resistant; S, susceptible

<sup>b</sup> Number of isolates carrying an AMR gene conferring resistance to the associated antibiotic/number of isolates with the resistant phenotype

<sup>c</sup> A number of 27 isolates were resistant to erythromycin, but only one isolate contained the corresponding resistant gene

<sup>d</sup> Fisher's exact test with 95% confidence interval