

## Supplementary Material

# Plant Growth, Antibiotic Uptake, and Prevalence of Antibiotic Resistance in an Endophytic System of Pakchoi under Antibiotic Exposure

Hao Zhang, Xunan Li, Qingxiang Yang, Linlin Sun, Xinxin Yang, Mingming Zhou, Rongzhen Deng, and Linqian Bi

### Table S1–S3

**Table S1.** PCR primers, annealing temperatures, and resistance mechanisms

**Table S2.** qPCR primers and annealing temperatures used in the present study

**Table S3.** qPCR standard curves for 16S rRNA gene and antibiotic resistance genes

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**Table S1.** PCR primers, annealing temperatures, and resistance mechanisms.

<b>Gene name</b>	<b>Primer</b>	<b>5'-3' sequence</b>	<b>Resistance Mechanism</b>	<b>Anneal temp. (°C)</b>	<b>Reference</b>
<i>tetA</i>	FW	GCTACATCCTGCTGCCTTC	efflux pump	55	[1]
	RV	CATAGATCGCCGTGAAGAGG			
<i>tetC</i>	FW	CTTGAGAGCCTTCAACCCAG	efflux pump	55	[1]
	RV	ATGGTCGTCATCTACCTGCC			
<i>tetG</i>	FW	GCTCGGTGGTATCTCTGCTC	efflux pump	55	[1]
	RV	AGCAACAGAATCGGGAACAC			
<i>tetK</i>	FW	CGAAAACAGACTCGCCAATC	efflux pump	55	[1]
	RV	TCCATAATGAGGTGGGGC			
<i>tetL</i>	FW	TCGTTAGCGTGCTGTCATTC	efflux pump	55	[1]
	RV	GTATCCCACCAATGTAGCCG			
<i>tetM</i>	FW	ACAGAAAGCTTATTATATAAC	ribosomal protection protein	45	[2]
	RV	TGGCGTGTCTATGATGTTAC			
<i>tetO</i>	FW	ACGGARAGTTTATTGTATACC	ribosomal protection protein	45	[2]
	RV	TGGCGTATCTATAATGTTGAC			
<i>tetQ</i>	FW	AGAATCTGCTGTTTGCCAGTG	ribosomal protection protein	55	[2]
	RV	CGGAGTGTCAATGATATTGCA			
<i>tetT</i>	FW	AAGGTTTATTATATAAAAGTG	ribosomal protection protein	45	[2]
	RV	AGGTGTATCTATGATATTTAC			
<i>tetW</i>	FW	GAGAGCCTGCTATATGCCAG	ribosomal protection protein	55	[2]
	RV	GGCGTATCCACAATGTTAAC			
<i>tetX</i>	FW	CAATAATTGGTGGTGACCC	enzymatic modification	55	[1]
	RV	TICTTACCTGGACATCCCG			
<i>tetB/P</i>	FW	AAAACCTTATTATATTATAGTG	ribosomal protection protein	45	[3]

	RV	TGGAGTATCAATAATATTCAC			
<i>sul1</i>	FW	CGGCGTGGGCTACCTGAACG	ribosomal protection protein	60	[2]
	RV	GCCGATCGCGTGAAGTTCCG			
<i>sul2</i>	FW	GCGCTCAAGGCAGATGGCATT	ribosomal protection protein	60	[4]
	RV	GCGTTTGATACCGGCACCCGT			
<i>sul3</i>	FW	TCAAAGCAAAATGATATGAGC	ribosomal protection protein	50	[5]
	RV	TTTCAAGGCATCTGATAAAGAC			
<i>dfrA1</i>	FW	AGCATTACCCAACCGAAAAGT	enzymatic modification	50	[6]
	RV	TGTCAGCAAGATAGCCAGAT			
<i>dfrA7</i>	FW	AAATGGCGTAATCGGTAATG	enzymatic modification	50	[6]
	RV	GTGAACAGTAGACAAATGAAT			
<i>bla<sub>ampC</sub></i>	FW	TGGCGTATCGGGTCAATGT	enzymatic modification	55	[5]
	RV	CTCCACGGGCCAGTTGAG			
<i>bla<sub>VIM</sub></i>	FW	GCACTTCTCGCGGAGATTG	enzymatic modification	55	[5]
	RV	CGACGGTGATGCGTACGTT			
<i>bla<sub>CTX-M</sub></i>	FW	ATGTGCAGYACCAGTAARGTKATGGC	enzymatic modification	55	[7]
	RV	ATCACKCGGRTCGCCNGGRAT			
<i>bla<sub>TEM</sub></i>	FW	TCGGGAAATGTGCG	enzymatic modification	50	[7]
	RV	GGAATAAGGGCGACA			
<i>bla<sub>SHV</sub></i>	FW	CTTTCCCATGATGAGCACCTTT	enzymatic modification	55	[5]
	RV	TCCTGCTGGCGATAGTGGAT			
<i>bla<sub>Z</sub></i>	FW	GGAGATAAAGTAACAAATCCAGTTAGATATGA	enzymatic modification	55	[5]
	RV	TGCTTAATTTCCATTTGCGATAAG			

**Table S2.** qPCR primers and annealing temperatures used in the present study.

Gene name	Primer	5'-3' sequence	Product size (bp)	Anneal temp. (°C)	Reference
16S rRNA	338F	CCTACGGGAGGCAGCAG	202	60	[8]
	518R	ATTACCGCGGCTGCTGG			
<i>tetX</i>	FW	AGCCITACCAATGGGTGTAAG	278	60	[9]
	RV	TTCCTACCTTGGACATCCCG			
<i>sul1</i>	FW	CCGTTGGCCTTCCTGTAAAG	67	60	[10]
	RV	TTGCCGATCGCGTGAAGT			
<i>sul2</i>	FW	CTCCGATGGAGGCCGGTAT	190	60	[10]
	RV	GGGAATGCCATCTGCCTTGA			
<i>bla<sub>CTX-M</sub></i>	FW	GGAGGCGTGACGGCTTTT	101	51	[5]
	RV	TTCAGTCCGATCCAGACGAA			

**Table S3.** qPCR standard curves for 16S rRNA gene and antibiotic resistance genes.

Gene name	Standard curves	R <sup>2</sup>
16S rRNA	$Y = -3.407 \times \text{Log}(X) + 36.004$	0.99497
<i>tetX</i>	$Y = -3.0462 \times \text{Log}(X) + 34.639$	0.99532
<i>sul1</i>	$Y = -2.9326 \times \text{Log}(X) + 34.148$	0.99082
<i>sul2</i>	$Y = -3.425 \times \text{Log}(X) + 36.19$	0.99686
<i>bla<sub>CTX-M</sub></i>	$Y = -2.7213 \times \text{Log}(X) + 33.879$	0.99391

**Table S4.** Root length, plant height, and fresh biomass values of hydroponic pakchoi under different dosages of antibiotic treatment.

Antibiotic concentration (mg L <sup>-1</sup> )	Root length		Plant height		Fresh biomass	
	average value (cm)	inhibition rate (%)	average value (cm)	inhibition rate (%)	average value (g)	inhibition rate (%)
<b>TC treatment</b>						
0	19.8 ± 3.12 b*		12.45 ± 1.14 b		10.72 ± 2.46 b	
50%MIC	22.8 ± 2.44 a	-15.15	13.85 ± 1.06 a	-11.24	20.75 ± 3.09 a	-93.53
MIC	15.6 ± 1.51 c	21.21	10.8 ± 1.23 c	13.25	8.01 ± 1.99 c	25.31
<b>CPL treatments</b>						
0	19.8 ± 3.12 b		12.45 ± 1.14 bc		10.72 ± 2.46 b	
50%MIC	25.6 ± 2.79 a	-29.29	14.5 ± 2.07 a	-16.47	15.06 ± 2.90 a	-40.44
MIC	24.5 ± 3.24 a	-23.73	13.1 ± 1.29 b	-5.22	12.97 ± 1.87 a	-20.99
<b>SMX treatments</b>						
0	19.8 ± 3.12 a		12.45 ± 1.14 b		10.72 ± 2.46 b	
50%MIC	20.3 ± 0.95 a	-2.53	13.95 ± 1.17 a	-12.05	12.73 ± 1.47 a	-18.72
MIC	12.05 ± 2.52 b	39.14	11.15 ± 1.20 c	10.44	6.51 ± 1.53 c	39.28

The values are mean ± SD (*n* = 10). \* Different letters indicate the differences in the value among the treatments based on the LSD (Least Significant Difference) test (*P* < 0.05)

Commented [Edit1]: Consider defining.

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