

Supplementary Materials

Reference genes for expression analyses by qRT-PCR in *Enterobacter cancerogenus*

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Table S1. Specificity verification of 13 candidate house-keeping genes.

Gene name	Description	Per. Ident	Accession number
<i>gyrB</i>	<i>E. cancerogenus</i> EcHa1	100.00%	CP082280.1
<i>gyrA</i>	<i>E. cancerogenus</i> 3.2.17	100.00%	CP134403.1
	<i>E. cancerogenus</i> EcHa1		CP082280.1
<i>era</i>	<i>E. cancerogenus</i> 3.2.17	100.00%	CP134403.1
	<i>E. cancerogenus</i> EcHa1		CP082280.1
<i>secA</i>	<i>E. cancerogenus</i> 3.2.17	100.00%	CP134403.1
	<i>E. cancerogenus</i> EcHa1		CP082280.1
<i>dnaG</i>	<i>E. cancerogenus</i> EcHa1	100.00%	CP082280.1
	<i>E. cancerogenus</i> 3.2.17		CP134403.1
<i>ftsZ</i>	<i>E. cancerogenus</i> EcHa1	100.00%	CP082280.1
	<i>E. cancerogenus</i> 3.2.17		CP134403.1
<i>RPSD</i>	<i>E. cancerogenus</i> EcHa1	100.00%	CP082280.1
	<i>E. cancerogenus</i> 3.2.17		CP134403.1
<i>16S rRNA</i>	<i>E. cancerogenus</i> EcHa1	100.00%	CP082280.1
	<i>E. cancerogenus</i> 3.2.17		CP134403.1
<i>rpoB</i>	<i>E. cancerogenus</i> EcHa1	100.00%	CP082280.1
	<i>E. cancerogenus</i> 3.2.17		CP134403.1
<i>proC</i>	<i>E. cancerogenus</i> EcHa1	100.00%	CP082280.1
<i>pyk</i>	<i>E. cancerogenus</i> EcHa1	100.00%	CP082280.1
<i>rho</i>	<i>E. cancerogenus</i> EcHa1	100.00%	CP082280.1
	<i>E. cancerogenus</i> MiY-F		CP045769.1
	<i>E. cancerogenus</i> CR-Eb1		CP025225.1
	<i>E. cancerogenus</i> 3.2.17		CP134403.1
<i>rplD</i>	<i>E. cancerogenus</i> EcHa1	100.00%	CP082280.1
	<i>E. cancerogenus</i> JY65		CP081105.1
	<i>E. cancerogenus</i> FDAARGOS 1428		CP077290.1
	<i>E. cancerogenus</i> UPC1		LR881936.1

Table S2. Primers of 13 candidate house-keeping genes and pathogenic factor Hcp used in qRT-PCR.

Gene	Primer sequences (5' to 3')	Length of amplicon sequence (bp)	Slope	R ²	Efficiency (%)
<i>gyrB</i>	F- CTGAAAGCGCTGGTGTATCA R- GTGCTGTTTCGTTCTCGTTCA	114	-3.2358	0.992	103.72
<i>gyrA</i>	F- GGTAATATCACCCGCATGG R- CAGCATGTAACGCAAGGAGA	84	-3.1297	0.995	108.70
<i>era</i>	F- GGCAAATCCACCCTGTAAAA R- TTCAGTATGGATGCCCCACAA	102	-3.3982	0.996	96.91
<i>secA</i>	F- GCGTACCGGTGAAGGTAAAA R- TCACGCTGTGCCAGATAGTC	111	-2.6125	0.937	141.42
<i>dnaG</i>	F- TACCGGGCAGCTTTTAGAGA R- TCGTTCAGGCTGAGAGTTT	75	-2.9280	0.998	119.55
<i>ftsZ</i>	F- GCAAGAAGCGTATGGCTTTC R- AAGCGTCAAGCAGGGAGATA	129	-3.1010	0.999	110.12
<i>RPS</i>	F- AGGGCACCGACTTATTCCTT	136	-3.6251	0.994	88.74
<i>D</i>	R- TTTTGCTTTTCACGCAACTG				
<i>16S</i>	F- CGATCCCTAGCTGGTCTGAG	93	-3.1003	0.997	110.16
<i>rRNA</i>	R- GTGCAATATTCCCCACTGCT				
<i>rpoB</i>	F- GATCAACTCCCTGTCCGTGT R- GAGTTCGCCTGAGCGATAAC	150	-2.7870	0.992	128.46
<i>proC</i>	F- GCTGGTCAATGCTGGTATGA R- CACATCGGCAATGTCTTCAG	70	-2.8402	0.991	124.95
<i>pyk</i>	F- TCAGTTCGACAACGTGGAAG R- ATACGGGAGGTCATCAGTGC	126	-3.3120	0.991	100.42
<i>rho</i>	F- ACTGCGTACTGATGGTGCTG R- GATGCTGGTTCGTCAAAGGT	109	-3.2561	0.997	102.82
<i>rplD</i>	F- ATGGCTCTGGAAGATGTGCT R- CGTACGTCAACCTTGTGCAG	89	-2.7904	0.993	128.23
<i>Hcp</i>	F-TCTTCTGAACCGTCTCCTGC R-AACTGCCCCTTAAGCTCCTT	177	-3.1726	0.999	106.63