

LOCUS **blaCMH-1** 1146 bp DNA linear BCT 15-FEB-2012

DEFINITION Enterobacter cloacae strain 6 class C beta-lactamase CMH-1 (blaCMH-1) gene, complete cds. **JQ673557**

ACCESSION blaCMH-1

SOURCE Enterobacter cloacae

ORGANISM Enterobacter cloacae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Enterobacter; Enterobacter cloacae complex.

REFERENCE 1 (bases 1 to 1146)

AUTHORS Yu, W.-L., Lee, M.-F. and Chuang, Y.-C.

TITLE A novel **plasmid-borne ampC gene** (blaCMH-1) in an Enterobacter cloacae isolate from southern Taiwan

JOURNAL Submitted (15-FEB-2012) Departments of Intensive Care Medicine, Chi-Mei Medical Center, No. 901 Zhonghua Rd., YongKang Dist., Tainan, Taiwan 710, Republic of China

FEATURES

source 1..1146
/organism="Enterobacter cloacae"
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/isolation_source="blood"
/db_xref="taxon:550"
/note="[cultured bacterial source]"

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CDS 1..1146
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YTAGGLPLQVPDDVTDNASLLRFYQSWQPKWAPGTTRLYANTSIGL
FGSLAVKPSGMCFEQAMAERVFKPLKLNHTWINVPHAEPPHYAWGY
REGKAVHVSFGMLDAEAYGVKSNVKDMASWVMANMAPETLPQST
LQGGIALAQSRVWRVGAMYQGLGWEMLNWPVDAKTVDGSDNK
VALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIVM
LANKSYNPNVRVETAYRILDALQ*"

BASE COUNT 252 a 316 c 334 g 244 t

ORIGIN

1 atgatgacaa aatccetaag ctgcgcgctg ctgcctcagg ttgcctgctc tgettttgc
61 gcgcgcgatg cagaaaaaca gctggctgac gtcgtggaac gtaccgttac gcctctgatg
121 aagggcgagg ccataccggg aatggcgctg gcgcctattt atcaggggcca gccacactat
181 tttaatttcg gtaaagcaga cgtgcggcgc aataagcccg tcacgcgcga aacctattt
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421 gtaccggatg atgtcacga taacgctct ctgctgcgtt tctaccagtc ctggcagcca
481 aagtgggccc cgggtaccac gcgtctgtac gccaacacca gcacgggttt gtttggtca
541 ctggcgggta aaccgtccgg catgtcttc gacgagccca tggcggagcg ggtctttaag
601 cccctgaaac tcaaccatac gtggataaac gtccacacg ctgaagaacc gactacgca
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1081 aataaaagct atccgaaccc ggtacgggtg gaaacggctt accgtatctc cgaacgcgcta
1141 cagtaa

Supplementary Figure1. Complete DNA sequence of *bla*_{CMH-1} gene (accession number JQ673557).

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>[ref|YP_003611068.1| G class C beta-lactamase [Enterobacter cloacae subsp. cloacae ATCC 13047]
gb|ADF60119.1| G class C beta-lactamase [Enterobacter cloacae subsp. cloacae ATCC 13047]
Length=381

GENE ID: 9123062 ampC | class C beta-lactamase
[Enterobacter cloacae subsp. cloacae ATCC 13047] (10 or fewer PubMed links)

Score = 777 bits (2007), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 379/381 (99%), Positives = 379/381 (99%), Gaps = 0/381 (0%)

Query 1 MMTKSLSCALLLSVACSAFAAPMSEKQLADVVERTVTPLMKAQAIPGMMAVAVIYQGQPHY 60 Ent. C 6 (CMH-1)
Sbjct 1 MMTKSLSCALLLSVACSAFAAPMSEKQLADVVERTVTPLMKAQAIPGMMAVAVIYQGQPHY 60

Query 61 FTFGKADVAANKPVTPTQLFELGVSVKTFVTGVLGGDAIARKEISLADPVTKYWPELTGKQ 120
Sbjct 61 FTFGKADVAANKPVTPTQLFELGVSVKTFVTGVLGGDAIARKEISLADPVTKYWPELTGKQ 120

Query 121 WQGIRLLDLATYTAGGLPLQVPDDVDNLSLLRFYQSWQPKWAPGTTIRLYANTSIGLFGS 180
Sbjct 121 WQGIRLLDLATYTAGGLPLQVPDDVDNLSLLRFYQSWQPKWAPGTTIRLYANTSIGLFGS 180

Query 181 LAVKPSGMCFEQAMAERVFVKPLKLNHTWINVPHAEAPHYAWGYREGKAVHVSFGMLDAEA 240
Sbjct 181 LAVKPSGMCFEQAMAERVFVKPLKLNHTWINVPHAEAPHYAWGYREGKAVHVSFGMLDAEA 240

Query 241 YGVKSNVKDMASWVMANMAPETLPQSTLQQGIALAQSRVWVGAMYQGLGWEMLNWPFVDA 300
Sbjct 241 YGVKSNVKDMASWVMANMAPETLPQSTLQQGIALAQSRVWVGAMYQGLGWEMLNWPFVDA 300

Query 301 KTVVDGSDNKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIVMLA 360
Sbjct 301 KTVVDGSDNKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIVMLA 360

Query 361 NKSYPNPFVRVETAYRILDALQ 381
Sbjct 361 NKSYPNPFVRVETAYRILDALQ 381

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Supplementary Figure 2. The *bla*CMH-1 gene has high identities of 99% to a chromosomally intrinsic ampC gene in *Enterobacter cloacae* ATCC 13047 strain (accession number YP_003611068).

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>[ref|YP_004712370.1| G class C beta-lactamase ACT-9 [Pantoea agglomerans]
gb|AEI70575.1| G class C beta-lactamase ACT-9 [Pantoea agglomerans]
Length=380

GENE ID: 10929439 ampC | class C beta-lactamase ACT-9 [Pantoea agglomerans]

Score = 699 bits (1804), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 333/380 (88%), Positives = 354/380 (93%), Gaps = 0/380 (0%)

Query 1 MMTKSLSCALLLSVACSAFAAPMSEKQLADVVERTVTPLMKAQAIPGMMAVAVIYQGQPHY 60 EntC-6 (CMH-1)
Sbjct 1 MTKSLCALLLS+CSAAPMSEKQL+DVVERTVTPLMKAQAIPGMMAVAVIYQGQPHY 60

Query 61 FTFGKADVAANKPVTPTQLFELGVSVKTFVTGVLGGDAIARKEISLADPVTKYWPELTGKQ 120
Sbjct 61 FTFGKADVANKPVTPTQLFELGS+SKTFVTGVLGGDAIAR EISLDPVTKYWPELTGKQ 120

Query 121 WQGIRLLDLATYTAGGLPLQVPDDVDNLSLLRFYQSWQPKWAPGTTIRLYANTSIGLFGS 180
Sbjct 121 WQGIR+LDLATYTAGGLPLQVPD+VDNLSLLRFYQWQ+WPGTTIRLYAN SIGLFG+ 180

Query 181 LAVKPSGMCFEQAMAERVFVKPLKLNHTWINVPHAEAPHYAWGYREGKAVHVSFGMLDAEA 240
Sbjct 181 LAVKPSGMNFEQAMTKRVFKPLKLDHTWINVPEEEAHYANGYRDGKAHVHVSFGMLDAEA 240

Query 241 YGVKSNVKDMASWVMANMAPETLPQSTLQQGIALAQSRVWVGAMYQGLGWEMLNWPFVDA 300
Sbjct 241 YGVK+N+DMASW+ANM P+LSTL+QGIALAQSRVWVGAMYQGLGWEMLNWPFV+A 300

Query 301 KTVVDGSDNKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIVMLA 360
Sbjct 301 KTVV+GSDNKVALAPLVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEK++GIVMLA 360

Query 361 NKSYPNPFVRVETAYRILDAL 380
Sbjct 361 NKSYPNPARVEAAYRILSAL 380

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Supplementary Figure 3. The *bla*CMH-1 gene has 88% identities to a chromosomal ACT-9 gene in *Pantoea agglomerans* (accession number YP_004712370).

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>  emb|CAJ28994.1 Class C beta-lactamase ACT-2 [Enterobacter asburiae]
Length=381

Score = 699 bits (1803), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 331/380 (87%), Positives = 355/380 (93%), Gaps = 0/380 (0%)

Query 1 MMTKSLSCALLLSVACSAFAAPMSEKQLADVVERTVTPLMKAQAIPGMAVAVIYQGQPHY 60 EntC-6 (CMH-1)
Sbjct 2 MMTKSLCALLLS +CS A PMSEKQLA+VVERTVTPLMKAQAIPGMAVAVIY+GQPHY 61

Query 61 FTFGKADVAANKPVTPTLTFELGSVSKTFTGVLGGDAIARKEISLADPVTKYWPGLTGKQ 120
Sbjct 62 FTFGKADVAANKPVTPTLTFELGS+SKTFTGVLGGDAIAR EISL DPVTKYWPGLTGKQ 121

Query 121 WQGIRLLDLATYTAGGLPLQVPDDVIDNASLLRFYQSWQPKWAPGTTIRLYANTSIGLFGS 180
Sbjct 122 WQGIRMLDLATYTAGGLPLQVPDEVIDNASLLRFYQNWQPKWAPGTTIRLYANASIGLFGA 181

Query 181 LAVKPSGMCFEQAMAERVFPLKLNHTWINVPAAEAPHYANGYREGKAVHVSFGMLDAEA 240
Sbjct 182 LAVKPSGMSYEQAITTRVFPLKLDHTWINVPKAAEAHYANGYRDGKAVHVSFGMLDAEA 241

Query 241 YGVKSNVKDMASWVMANMAPETLPQSTLQQGIALAQSRVWVGAMYQGLGWEMLNWPFVDA 300
Sbjct 242 YGVKTNVQDMASWVMNMKPDLSLQDNLRLKGLTLAQSRVWVGAMYQGLGWEMLNWPFVDA 301

Query 301 KTVVDGSDNKVALAPLPVAEVPAPPPVNASWVHKTGSTGGFGSYVAFIPEKQIGIVMLA 360
Sbjct 302 KTVVVGSDNKVALAPLPAREVNPPAPPPVNASWVHKTGSTGGFGSYVAFIPEKQLGIVMLA 361

Query 361 NKSYPNPVRVETAYRILDAL 380
Sbjct 362 NKSYPNPARVEAAYRILSAL 381

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Supplementary Figure 4. The *bla*CMH-1 gene has 87% identities to a chromosomal ACT-2 gene in *Enterobacter asburiae* (accession number CAJ28994).