Supplementary data

Table S1. Amino acid identities (%) between *Klebsiella pneumoniae* carbapenemase (KPC-2), the Ambler class A β-lactamases produced by *Chromobacterium piscinae* strain ND17 (CRP-1)*, C. haemolyticum* DSM19808 (CRH-1), *Chromobacterium* sp. strain C-61 (CRS-1) and other previously described class A carbapenemases.

Enzymes	KPC-1	CRP-1	CRH-1	CRS-1	SFC-1	BIC-1	SME-1	IMI-1	NMC-A	FRI-1	KBC-1	GES-1	FTU-1	FPH-1
KPC-2	-													
CRP-1	76	-												
CRH-1	69	68	-											
CRS-1	68	68	96	-										
SFC-1	61	54	61	61	-									
BIC-1	61	58	59	59	65	-								
SME-1	53	52	53	53	55	55	-							
IMI-1	53	52	52	52	55	54	70	-						
NMC-A	53	52	52	52	55	54	70	97	-					
FRI-1	52	51	48	50	51	50	53	54	55	-				
BKC-1	36	35	36	36	34	33	33	31	31	36	-			
GES-1	34	34	36	36	33	33	34	31	31	32	36	-		
FTU-1	31	30	31	31	30	29	30	31	31	31	25	23	-	
FPH-1	30	29	30	30	31	28	30	30	30	30	24	24	74	-

Figure S1. Amino acid alignment of the three *Chromobacterium* ß-lactamases described in this study (CRP-1, CRH-1 and CRS-1) with the most closely related Ambler class A carbapenemases, i.e. *Klebsiella pneumoniae* Carbapenemase (KPC-2) and *Serratia fonticola* Carbapenemase (SFC-1). Residues important for carbapenemase activity are indicated by Greek letters.

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CRP-1   MRLSRRLVLLSCLLLPQAGFS.....AAMPANLADQKIARLERVFGGQIGVY
KPC-2   MSLYRRLVLLSCLSWPLAGFS.....ATALTNLVAEPFAKLEQDFGGSIGVY
CRH-1   M..FKHLILLASLTAPLTQAV.....AADPLSVAADKLAKLERDFGGSIGVY
CRS-1   M..FKHLILFASLAAPLTQAV.....AADPLAVAADKLAKLERDFGGSIGVY
SFC-1   MSRTGRLSVFFSAIFPLLTLTNMAEAASQPPQVTVDKLKRLENDFGGRIGVY

                                   70
CRP-1   ALDTGSGAAVSYRADERFPLCSSFKGFLAASALAHSQSKPGFLDQILHYGKE
KPC-2   AMDTGSGATVSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKN
CRH-1   AIDTGSGATVANRPNERFPLCSSFKGFLAAGVLAQSQDKPGLLDKRIRYSKA
CRS-1   AIDTGSGATVANRPNERFPLCSSFKGFLAAGVLAQSQEKPGLLDKRIRYSKT
SFC-1   AIDTGSNKTFGYRANERFPLCSSFKGFLAAAVLSKSQQQEGLLNQRIRYDNR
                             θ ß Ω
                                                130
CRP-1   ELIAWSPISEKHQSSGMTVAGLCAATVQYSDNAAANVLM.KQLDGPAGLTAF
KPC-2   ALVPWSPISEKYLTTGMTVAELSAAAVQYSDNAAANLLL.KELGGPAGLTAF
CRH-1   ALPNWSPITTKHQASGMTVAELNAASVQYSDNGAANLLL.KEINGPAALTTF
CRS-1   ALPNWSPITTKHQASGMTVAELNAASVQYSDNGAANLLL.KEINGPAALTAF
SFC-1   VMEPHSPVTEKQITTGMTVAELSAATLQYSDNGAANLLLEKLIGGPEGMTSF
            λ                                   π
                                  170
CRP-1   MRAIGDSTFRLDRWEPELNTAIPGDARDTSTPRAVAESLQKLTLGTALAAHQ
KPC-2   MRSIGDTTFRLDRWELELNSAIPGDARDTSSPRAVTESLQKLTLGSALAAPQ
CRH-1   MRSIGDASFRLDRLEPELNSAIPRDPRDTSTPKAVAESAQKLALGKALPEPQ
CRS-1   MRSIGDASFRLDRREPELNSAIPGDPRDTSTPKAVAESAQKLALGKALPEPQ
SFC-1   MRSIGDNVFRLDRWELELNSAIPGDDRDTSTPKAVAESMQKLAFGNVLGLTE
                        μ  ε    δ          η
                                220
CRP-1   RQQLVDWLKGNTTGNQRIRAAVPAGWLVGDKTGTCGVYGTANDYAVIWPTGR
KPC-2   RQQFVDWLKGNTTGNHRIRAAVPADWAVGDKTGTCGVYGTANDYAVVWPTGR
CRH-1   RQQLADWLKGNTTGNARIRAAVPAGWEVGDKTGTCGVYGTANDFAVIWPPKR
CRS-1   RQQLADWLKGNTTGNARIRAAVPAGWEVGDKTGTCGVYGTANDFAVIWPPKR
SFC-1   RHQLMDWFKGNTTGGARIRASVPANWVVGDKTGTCGVYGTANDYAVIWPVGH
                            φ                σ   Γ Λ
                                273
CRP-1   APIVMAVYTRASKKDIKHSDAVIADAAKAALEALGVM.......  ..TR
KPC-2   APIVLAVYTRAPNKDDKHSEAVIAAAARLALEGLGVN..........GQ
CRH-1   APIVLAVYTKHAKKEAKHSDEVIAAAARAALEAFNVK...........K
CRS-1   APIVLAVYTKHAKKEAKHSDEVIAAAARAALGAF...............
SFC-1   APIVLAVYTSKPDKNSKHSDAVIADASRIVLESFNIDALRMATGKSIGF
                          C
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Figure S2. Nucleotide sequence alignment of the five Tn*4401* isoforms (Tn*4401a to* Tn*4401e*) in the region upstream of bla_{KPC} with the 148-bp non-coding region upstream of bla_{CRP-1} (bla_{CRP-1} UPS). The 27-bp (A) and 11-bp (B) regions preceding the start codon of bla_{CRP-1} displayed high identity with the corresponding regions in the Tn*4401* isoforms.

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Tn4401b      ......TCCAGGTGGGTCAGTATTACTTTGGTGATTCAGGGGTAAAGTG...GGTCAGTT
Tn4401a      ......TCCAGGTGGGTCAGTATTACTTTGGTGATTCAGGGGTAAAGTG...GGTCAGTT
Tn4401d      ......TCCAGGTGGGTCAGTATTACTTTGGTGATTCAGGGGTAAAGTG...GGTCAGTT
Tn4401c      ......TCCAGGTGGGTCAGTATTACTTTGGTGATTCAGGGGTAAAGTG...GGTCAGTT
Tn4401e      ......TCCAGGTGGGTCAGTATTACTTTGGTGATTCAGGGGTAAAGTG...GGTCAGTT
blaCRP-1 ups GAGGACTCCAGCGCCGACAGCAGCGGCTAGTCCGGACAGGGGGGAGAGGCAAGAACAAGC

Tn4401b      TTCAGTTGGTGTTGACACCGGCGTACCCTCGGTGCTATCT.TCGCGCCCCAATAGTCGGG
Tn4401a      TTCAGTTGGTGTTGACACCGGCGTACCCTCGGTGCTATCT.TCGCGCCCCAATAGTCGGG
Tn4401d      TTCAGTTGGTGTTGACACCGGCGTACCCTCGGTGCTATCT.TCGCGCCCCAATAGTCGGG
Tn4401c      TTCAGTTGGTGTTGACACCGGCGTACCCTCGGTGCTATCT.TCGCGCCCCAATAGTCGGG
Tn4401e      TTCAGTTGGTGTTGACACCGGCGTACCCTCGGTGCTATCT.TCGCGCCCCAATA.....
blaCRP-1 ups CTGTTACGGCAGTTACACTTTTATGGGGTGAAAGCGGTTTGTTGCGGGGCGAGAATCACG

Tn4401b      GCTTGGCCAGGACTTCCTGAGGCCGTCCGTAACGTGGATGCCGAGGTCAGGCGAGGTGGC
Tn4401a      GCTTGGCCAGGACTTCCTGAGGCCGTCCGTAACGTGGATGCCGAGGTCAGGCGAGGTGGC
Tn4401d      GCTTGGCCAGGACTTCCTGAGGCCGTCCGTAACGTGGATGCCGAGGTCAGGCGAGGTGGC
Tn4401c      GCTTGGCCAGGACTTCCTGAGGCCGTCCGTAAC...........................
Tn4401e      ............................................................
blaCRP-1 ups ............................................................

Tn4401b      CGACCCATGAACGCCGACCTGATTCGTTTTTCAATAGCGCTGGACGTTGTGGTGCCAGGG
Tn4401a      CGACCCATGAACGCCGACCTGATTCGTTTTTCAA..........................
Tn4401d      CGACCCATGAACGCCGACCTGA......................................
Tn4401c      ............................................................
Tn4401e      ............................................................
blaCRP-1 ups ............................................................

Tn4401b      ACTTACCAACCCGATGTGTGCCCATCCGGGGCAGTTACAGCCGTTACAGCCTCTGGAGAG
Tn4401a      ............................................................
Tn4401d      ...............................GCAGTTACAGCCGTTACAGCCTCTGGAGAG
Tn4401c      ............................................................
Tn4401e      ............................................................
blaCRP-1 ups ............................................................

Tn4401b      GGAGCGGCTTGCCGCTCGGTGATAATCCCAGCTGTAGCGGCCTGATTACATCCGGCCGCT
Tn4401a      .............GCTCGGTGATAATCCCAGCTGTAGCGGCCTGATTACATCCGGCCGCT
Tn4401d      GGAGCGGCTTGCCGCTCGGTGATAATCCCAGCTGTAGCGGCCTGATTACATCCGGCCGCT
Tn4401c      ............................................................
Tn4401e      ............................................................
blaCRP-1 ups ............................................................
                                   A
Tn4401b      ACACCTAGCTCCACCTTCAAACAAGGAATATCGTTG
Tn4401a      ACACCTAGCTCCACCTTCAAACAAGGAATATCGTTG
Tn4401d      ACACCTAGCTCCACCTTCAAACAAGGAATATCGTTG
Tn4401c      .........TCCACCTTCAAACAAGGAATATCGTTG
Tn4401e      .........TCCACCTTCAAACAAGGAATATCGTTG
blaCRP-1 ups .......CTTCCACCTTCAAG.AAGGAGTGTTCCTG
                     B
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