

Nucleotide sequence of a chloramphenicol acetyl transferase gene from *Clostridium difficile*

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We report the DNA and deduced amino acid sequences of a previously reported clone (pPPM9) which expresses chloramphenicol acetyl transferase activity from *Clostridium difficile* strain (WL) isolated from a patient with pseudomembranous colitis [1]. The ATG start codon was preceded at the correct distance by a SD sequence GAGAGG and characteristic promoter regions (-10, TATAAT; -35, TTGAAA) were identified. The codon usage for the chloramphenicol acetyl transferase (cat D) gene showed a strong preference for A or T at the third codon position (72%). The cat D gene is highly homologous to previously characterised cat genes from other bacterial genera (2-5), however, it is noteworthy that the cat D gene contains a 4 amino acid deletion between amino acids 38 (Q) and 39 (I).

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-35                               -10
TCGAAGTGGGCAAGTTTGAAAAATTCACAAAAATGTCGTATAATATCTTTGGCTTATTAGACGCATAAACTTGAATT
SD
TGAGAGGCAACTTAGATGGTATTGAAAAAATGATAAAAAATAGTTGGAACAGAAAAGAGTATTTTIGACCCTACTAC
M V F E K I D K N S W N R K E Y F D H Y
TTTIGCAAGTGTACCTTTGTACATACAGCATGACOGTTAAAGTGGATATCACACAAATAAAGGAAAAGGGAAATGAAA
F A S V P C T Y S M T V K V D I T Q I K E K G M K
CTATATCCTGCAATGCTTTATTATATTTGCAATGATTTGTAAACCGCCATTCAGAGTTTAGGACGGCAATCAATCAA
L Y P A M L Y Y I A M I V N R H S E F R T A I N Q
GATGGTGAATTTGGGATATATGATGAGATGATAACCAAGCTATACAATATTTTCACAATGACTGAAACATTTTTC
D G E L G I Y D E M I P S Y T I F H N D T E T F S
AGCCTTTGGACTGAGTGTAAAGTCTGACTTTTAAATCATTTTTAGCAGATTTGAAAGTGTATCGCAACCGTATCGA
S L W T E C K S D F K S F L A D Y E S D T Q R Y G
AACAAATCATAAGAAAGGAAAAGCCAAATGCTCCGGAAAACATTTTTTAAATGTATCTATGATACCGTGTCAACC
N N H R M E G K P N A P E N I F N V S M I P W S T
TTGATGGCTTTAATCTGAAATTTGCGAAAAGGATATGATTTATTTGATTCCTATTTTTACTATGGGGAAAATTATA
F D G F N L N L Q K G Y D Y L I P I F T M G K I I
AAGAAGATAACAAAATTATACCTTCCTTTGGCAATTCAGTTTCATCAGCAGTATGTGACGGATTTTCACATTTGC
K K D N K I I L P L A I Q V H H A V C D G F H I C
CGTTTTGTAAACGAATTTGAGGAATGATAATAGTTACTCAGGTTTGTCTGTAACTAAAACAAGTATTTAAGCAA
R F V N E L Q E L I I V T Q V C L *
AAACATGTAGAAATACGGTCTTTTTTGTTCCTAAAATCTACAATTTTATACATAACCACAGGTTAGTACAAG
ACCTTGTGTTCTTTTTGAAAGGCTTAAAA

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