

Nucleotide sequence of the streptothricin-acetyl-transferase gene sat-2

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The streptothricin resistance (St) gene of the transposon Tn1826 was cloned (1) and sequenced (Fig.) A 534 bp open reading frame could be translated starting with a GTG at position 506 (178 amino acids) or with an ATG at position 518 (174 amino acids). Translation as proposed (Fig.) would result in a polypeptide of predicted size 19670 daltons identical to the C-terminal part of the translation product of another St gene (sat-1) (2). Sequences with homology to the conserved regions of *E. coli* promoters (−35 at positions 323 and 475; −10 at positions 350 and 497) and possible Shine-Delgarno sequences (position 371 and 508) preceding the translated sequence are underlined. There is no optimal spacing between them. However, promoter functions are suggested by deletion derivatives lacking the region 5' to the *SphI* site at position 381 or deleted of the DNA between the *SphI* sites

at positions 381 and 487 but still mediating St in vivo (manuscript in preparation). Most of the sequence presented here can also be detected in the related transposon Tn7 (3, 4, 5) suggesting a sat gene in this transposon, too. In Tn7, an 'insert' comprising the trimethoprim resistance gene (4) might have replaced the G at position 508 of the sat-2 sequence (Fig.) thereby rendering the sat gene cryptic.

REFERENCES

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GGCTACATGCTGCTGTTTGGCTAAGCTGGATAAAAAACAGCCTGACCTCTTCACTGCCCATGGTCTGA 67
GGATGACGTTTTTTGTGAAACAGAATAAAACGGCTTAATCCAGTGCAGGTAAGTTTTTTCAGTTTTTCAGCGCATAA 142
CCTTTTTGTCGCATATCCGTGCGTATAGAATTTAAAAATGGACTGTTAGACATAAAACGGCTCCTTGTCTTGCAAC 217
TGCTGCGCTAAGCCTATTCTAGCTGGGATTTAAAAAGTGCCTGTTTTTTACGCCTAGAGATGCTTGTGTTAC 292
CGGTAGAGTTTTTAATTTAATGCTAAATAAAATTAATAATGTTATGAGTCTTTGGGTGAGATAATGTGCATCGTCA 367
AGCAGCATAGACGGCATGCACGATTTGTAATAACAGAGTGTCTTGTATTTTTAAAGAAAGCTATTTAATACAAAG 442
TGATTATATTAATTAACGGTAAGCATCAGCGGGTGCACAAAACGAGCATGCTTACTAATAAAATGTAGCGCTCAT 517
ATGAAGATTTCCGTGATCCCTGAGCAGGTGGCGGAAACATTGGATGCTGAGAACCATTTCATTGTTCCGTGAAGTG 592
M K I S V I P E Q V A E T L D A E N H F I V R E V 25
TTCGATGTCACCTATCCGACCAAGGCTTTGAACTATCTACCAGAAGTGTGAGCCCCTACCGGAAGGATTACATC 667
F D V H L S D Q G F E L S T R S V S P Y R K D Y I 50
TCGGATGATGACTCTGATGAAGACTCTGCTTGCTATGGCGCATTTCATCGACCAAGAGCTTGTCCGGGAAGATTGAA 742
S D D D S D E D S A C Y G A F I D Q E L V G K I E 75
CTCAACTCAACATGAACGATCTAGCCTCTATCGAACACATTGTTGTGTCGCACACGCGAGGCAAAGGAGTCT 817
L N S T W N D L A S I E H I V V S H T H R G K G V 100
CGGCACAGTCTCATCGAATTTGCGAAAAAGTGGGCACTAAGCAGACAGCTCCTTGGCATAACGATTAGAGACAA 892
A H S L I E F A K K W A L S R Q L L G I R L E T Q 125
ACGAACAATGTACCTGCGTCAATTTGTACGCAAAATGTGGCTTTACTCTCGGGCGGATTGACCTGTTACCGTAT 967
T N N V P A C N L Y A K C G F T L G G I D L F T Y 150
AAAAGTAGACCTCAAGTCTCGAACGAAACAGCGATGTACTGTTCTCTCGGGAGCACAGGATGACGCCATAA 1042
K T R P Q V S N E T A M Y W Y W F S G A Q D D A * 174
CAATTCATTCAAGCCGACACCGCTTCGCGGCGCGGCTTAATTCAGGAGTTAAACATCATGAGGGAAGCGGTGATC 1117
GCCGAAGTATCGACTCAACTATCAGAGGTAGTTGGCGTCATCGAGCGCCATCTCGAACCGACGTTGCTGGCCGTA 1192
CATTGTCACGGCTCCGCACTGGATGGCGGCTGAAGCCACACAGTATGATTTTCTGTTACGGTACCGGTA 1267
AGGCTTGATGAAACAACGCGCGC 1290

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