CORRIGENDUM

The Nucleotide Sequence of a Streptomycin 6-Phosphotransferase Gene from a Streptomycin Producer

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Journal of General Microbiology (1987), **133**, 1289–1296.

Throughout the paper, streptomycin 6-phosphotransferase (streptomycin 6-kinase) should read streptomycin phosphotransferase (streptomycin kinase).

Corrected versions of Fig. 2, Table 1 and Fig. 3(a) are given overleaf.

GGTACCGGGGCCAGCAGGGGGATGA
 CCATGGCCCCCGTTCGTCCTTACT
KpnI

CGTTTCCGGCGGCGAGCACCAGGTCGAAGCCGGGTTCAGGCCGAGGTCGTCCAGCCGGGCCAGGTCGCCGAGGAGCCA
 CAGGAAGGCCGCCGCTCGTGGTCCAGCTTCGGCCCAAGGTCGGCTCCAGCAGGTCGGCCCGGTCCAGCGGCTCCTCGGT
 *27

GTCCTGTGCGGGCGCTTCGCGGCGGGCGACGGCGAGCATCGAGGAGTCGACGTCCACGCCGGTGCAGTGGTGGCCCCAG
 CAGGTGACGCCCGCGAAGCGCCCGCTGCCGCTCGTAGCTCCTCAGCTGCAGGTGCGGCCACGTACCCACCGGGGTC
 *106 *SalI*

CTCGGCGAGGCGGATCGCGATCCGGCCGGTGGCGACCCCCGCGTCGAGCACTCGGGAGGCCGGGTGAGCAACGCCGCGC
 GAGCCGCTCCGCTAGCGCTAGGCCGGCCACGGCGTGGGGCGCAGCTCGTGAGCCCTCCGGCCCCAGTCGTTGGCGCGC
 *185

AGAAGGAGGCCTCGCCGTGGACGTCGTGGCACCGACGCGCGGAGCCGTGCGAACCTCCGGGCGTATTCCTCCCCAGCCT
 TCTTCTCCGGAGCGGCACCTGCAGCACCGTGGCTGCGCCGCTCGGCACGCTTGGAGGCCCGCATAAGGAGGGGTTCGGA
 *264

GTCCACCGGTTCAGTTCCGCCCCAAGGTCGCGTTGCCAGTCATGTTTCAGCTCGCCTTCGGGTTCAGCCCCAGCGGGAGC
 CAGGTGGCCAGTCAAGCGGGTTGCCAGCGCAACGGGTTCAGTACAAGTCGAGCGGAAGGCCAGTCGCGGGGTCCGCTCG
 *343

ATAAACGAGCCCCGACACACCGGGTTCGGTTCGGGTGCTCCGGGACGGCCGAGGCGTCGGGTGTTAGAGTCTGCGCC
 TATTTGCTCGGGCTGTGTGGCCCAAGCCAAAGCCACGAGGCCCTGCCGGCTCCGCGACCCGACCAATCTCAGACGCGG
 *422

Met	Ser	Asp	His	Pro	Gly	Pro	Gly	Ala	Val	Thr	Pro	Glu	Leu	Phe	Gly	Val	Gly	Gly	Asp
ATG	AGT	GAT	CAC	CCC	GGG	CCG	GGG	GCC	GTC	ACG	CCG	GAG	CTG	TTC	GGC	GTG	GGC	GGC	GAC
TAC	TCA	CTA	GTG	GGG	CCC	GGC	CCC	CGG	CAG	TGC	GGC	CTC	GAC	AAG	CCG	CAC	CCG	CCG	CTG

*501 *BclI* *SmaI*

Trp	Leu	Ala	Val	Thr	Ala	Gly	Glu	Ser	Gly	Ala	Ser	Val	Phe	Arg	Ala	Ala	Asp	Ala	Thr
TGG	CTG	GCC	GTC	ACC	GCG	GGC	GAA	TCG	GGC	GCC	TCC	GTG	TTT	CGC	GCC	GCG	GAC	GCC	ACC
ACC	GAC	CGG	CAG	TGG	CGC	CCG	CTT	AGC	CCG	CGG	AGG	CAG	AAA	GCG	CGG	CGC	CTG	CGG	TGG

*561

Arg	Tyr	Ala	Lys	Cys	Val	Pro	Ala	Ala	Asp	Ala	Ala	Gly	Leu	Glu	Ala	Glu	Arg	Asp	Arg
CGG	TAC	GCC	AAG	TGC	GTG	CCC	GCC	GCG	GAC	GCG	GCC	GGT	CTT	GAG	GCG	GAA	CGC	GAC	CGG
GCC	ATG	CGG	TTC	ACG	CAC	GGG	CGG	CGC	CTG	CGC	CGG	CCA	GAA	CTC	CGC	CTT	GCG	CTG	GCC

*621

Ile	Ala	Trp	Leu	Ser	Gly	Gln	Gly	Val	Pro	Gly	Pro	Arg	Val	Leu	Asp	Trp	Tyr	Ala	Gly
ATC	GCC	TGG	CTG	AGC	GGG	CAG	GGC	GTA	CCG	GGC	CCC	CGC	GTC	CTC	GAC	TGG	TAC	GCC	GGT
TAG	CGG	ACC	GAC	TCG	CCC	GTC	CCG	CAT	GGC	CCG	GGG	GCG	CAG	GAG	CTG	ACC	ATG	CGG	CCA

*681

Asp	Ala	Gly	Ala	Cys	Leu	Val	Thr	Arg	Ala	Val	Pro	Gly	Val	Pro	Ala	Asp	Arg	Val	Gly
GAC	GCG	GGC	GCC	TGC	CTG	GTC	ACC	CGT	GCC	GTC	CCC	GGC	GTA	CCC	GCT	GAT	CGG	GTG	GGC
CTG	CGC	CCG	CGG	ACG	GAC	CAG	TGG	GCA	CGG	CAG	GGG	CCG	CAT	GGG	CGA	CTA	GCC	CAC	CCG

*741

Ala	Asp	Asp	Leu	Arg	Thr	Ala	Trp	Gly	Ala	Val	Ala	Asp	Ala	Val	Arg	Arg	Leu	His	Glu
GCC	GAT	GAC	CTT	CGC	ACT	GCC	TGG	GGG	GCC	GTC	GCG	GAC	GCG	GTC	CGT	CGG	CTG	CAC	GAG
CGG	CTA	CTG	GAA	GCG	TGA	CGG	ACC	CCC	CGG	CAG	CGC	CTG	CGC	CAG	GCA	GCC	GAC	GTG	CTC

*801

Val	Pro	Val	Ala	Ser	Cys	Pro	Phe	Arg	Arg	Gly	Leu	Asp	Ser	Val	Val	Asp	Ala	Ala	Arg
GTG	CCC	GTG	GCC	TCG	TGT	CCG	TTC	CGC	CGG	GGG	CTG	GAC	TCC	GTG	GTC	GTC	GCC	GCC	CGT
CAC	GGG	CAC	CGG	AGC	ACA	GGC	AAG	GCG	GCC	CCC	GAC	CTG	AGG	CAC	CAG	CTG	CGG	CGG	GCA

*861 *SalI*

Asp	Val	Val	Ala	Arg	Gly	Ala	Val	His	Pro	Glu	Phe	Leu	Pro	Val	Glu	Gln	Arg	Leu	Val
GAC	GTG	GTG	GCC	CGT	GGC	GCG	GTG	CAT	CCG	GAG	TTC	CTG	CCG	GTG	GAG	CAG	CGG	CTC	GTT
CTG	CAC	CAC	CGG	GCA	CCG	CGC	CAC	GTA	GGC	CTC	AAG	GAC	GGC	CAC	CTC	GTC	GCC	GAG	CAA

*921

Pro	Pro	Ala	Glu	Leu	Leu	Ala	Arg	Leu	Thr	Gly	Glu	Leu	Ala	Arg	Arg	Arg	Asp	Gln	Glu
CCC	CCG	GCG	GAG	CTG	CTG	GCC	CGG	CTC	ACC	GGG	GAG	CTC	GCC	CGT	CGG	CGC	GAT	CAG	GAG
GGG	GGC	CGC	CTC	GAC	GAC	CGG	GCC	GAG	TGG	CCC	CTC	GAG	CGG	GCA	GCC	GCG	CTA	GTC	CTC

*981 *SacI*

Fig. 2 (continued on facing page)

Ala Ala Asp Thr Val Val Cys His Gly Asp Leu Cys Leu Pro Asn Ile Val Leu His Pro
GCC GCC GAC ACG GTC GTC TGC CAC GGT GAT CTC TGC CTG CCC AAC ATC GTC CTC CAT CCG
CGG CGG CTG TGC CAG CAG ACG GTG CCA CTA GAG ACG GAC GGG TTG TAG CAG GAG GTA GGC
*1041

Glu Thr Leu Glu Val Ser Gly Phe Ile Asp Leu Gly Arg Leu Gly Ala Ala Asp Arg His
GAG ACC CTG GAG GTG TCG GGC TTC ATC GAC CTG GGA CGG CTC GGG GCG GCC GAC CGC CAC
CTC TGG GAC CTC CAC AGC CCG AAG TAG CTG GAC CCT GCC GAG CCC CGC CGG CTG GCG GTG
*1101

Ala Asp Leu Ala Leu Leu Leu Ala Asn Ala Arg Glu Thr Trp Val Asp Glu Glu Arg Ala
GCC GAC CTG GCG CTG CTG CTG GCC AAC GCG CGC GAG ACC TGG GTG GAC GAG GAG CGG GCG
CGG CTG GAC CGC GAC GAC GAC CGG TTG CGC GCG CTC TGG ACC CAC CTG CTC CTC GCC CGC
*1161

Arg Phe Ala Asp Ala Ala Phe Ala Glu Arg Tyr Gly Ile Ala Pro Asp Pro Glu Arg Leu
CGG TTC GCC GAC GCG GCG TTC GCC GAG CGT TAC GGC ATC GCC CCG GAC CCG GAA CGG CTG
GCC AAG CCG CTG CGC CGC AAG CGG CTC GCA ATG CCG TAG CGG GGC CTG GGC CTT GCC GAC
*1221

Arg Phe Tyr Leu His Leu Asp Pro Leu Thr Trp Gly ***
CGC TTC TAC CTC CAT CTC GAT CCG CTC ACC TGG GGC TAG GTCCTGTCGTGCAACTGCCGTCGTCGC
GCG AAG ATG GAG GTA GAG CTA GGC GAG TGG ACC CCG ATC CAGGACAGCAGCTTGACGGCAGCAGCC
*1281

CCGAAGGGCGGCCCTGCGGGGTGAAGCCCCGCCTGCGCGGGCGGCCTGGCAGGCACGCTCGCTTCGCAACACGCCCTA
GGCTTCCC GCCGGGACGCCCCACTTCGGGGCGGACGCGCCGCGGACCCGTCCTGCGAGCGAAGCGTTGTGCGGGAT'
*1347

ACGGGCTCCCCAGGGTGCGGAGTCCGCTGTGTCTGGACGCGTCCGGTCCGGCGGCGGGTGCGGGCGGGCCGTGGTGGTCC
TGCCCCAGGGCTCCCACGCCTCAGGCACACAGCCTGCGCAGGCCAGGCCGCCGCCACGCCCCGCCGGCACCACCAAG
*1426

GTCGCGATGACCACCACCTGGTCTCGGCGTACCAGACGCGCCGTTCGCCCTTCGGCGGGTTGAGCCTGATGCCCTGGT
CAGCGCTACTGGTGGTGACAGGAGCCGCATGGTCTGCGCGGCAAGCGGGAAGCCGCCCACTCGGACTACGGGACCA
*1505

CCCCGGTCCCGGTGCGGGTGATGTCGTGCCGGCGGTAGCCGATC
GGGGCCAGGGCCACGCCCACTACAGCACGGCCGCCATCGGCTAG
*1584

Fig. 2. Nucleotide sequence of the 1.6 kb of *S. griseus* DNA containing the streptomycin kinase gene. The amino acids predicted by the sequence are shown. Two inverted repeats which could potentially form hairpin-loop structures as putative transcription-termination signals are indicated by underlining.

Table 1. Codon usage in the streptomycin kinase structural gene

TTT-Phe	1	TCT-Ser	0	TAT-Tyr	0	TGT-Cys	1
TTC-Phe	7	TCC-Ser	2	TAC-Tyr	4	TGC-Cys	4
TTA-Leu	0	TCA-Ser	0	TAA-***	0	TGA-***	0
TTG-Leu	0	TCG-Ser	3	TAG-***	1	TGG-Trp	6
CTT-Leu	2	CCT-Pro	0	CAT-His	3	CGT-Arg	6
CTC-Leu	10	CCC-Pro	8	CAC-His	4	CGC-Arg	9
CTA-Leu	0	CCA-Pro	0	CAA-Gln	0	CGA-Arg	0
CTG-Leu	17	CCG-Pro	11	CAG-Gln	3	CGG-Arg	12
ATT-Ile	0	ACT-Thr	1	AAT-Asn	0	AGT-Ser	1
ATC-Ile	4	ACC-Thr	7	AAC-Asn	2	AGC-Ser	1
ATA-Ile	0	ACA-Thr	0	AAA-Lys	0	AGA-Arg	0
ATG-Met	1	ACG-Thr	2	AAG-Lys	1	AGG-Arg	0
GTT-Val	1	GCT-Ala	1	GAT-Asp	6	GGT-Gly	3
GTC-Val	12	GCC-Ala	29	GAC-Asp	18	GGC-Gly	14
GTA-Val	2	GCA-Ala	0	GAA-Glu	3	GGA-Gly	1
GTG-Val	12	GCG-Ala	16	GAG-Glu	14	GGG-Gly	7

Fig. 3 (a) Dot-matrix analysis of the amino acid sequence of the streptomycin kinase (SMK) from *S. griseus* (272 amino acid residues) and the aminoglycoside 3'-phosphotransferase (APH) from *S. fradiae* (268 amino acid residues).