

Complete nucleotide sequence of a 16S ribosomal RNA gene from *Streptomyces griseus* subsp. *griseus*

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The complete nucleotide sequence of the 1525 bp 16S ribosomal RNA gene from the *rrnE* operon of *Streptomyces griseus* subsp. *griseus* KCTC9080 was determined (1). The 5' and 3' ends of the 16S rRNA were located with the combination of previous data (2, 3, 4) and have not been determined experimentally. The nucleotide sequence presented here was determined following the dideoxy method (5) and using M13 universal as well as 16S rRNA specific synthetic oligonucleotide primers.

The 16S RNA sequence determined here showed homology values of 96.2% with *S. coelicolor* (2), 96.4% with *S. lividans* (3) and 96.1% with *S. ambofaciens* (4). It is notable that the homology values among other three reference sequences are more than 98%. Figure 1 shows the alignment of highly variable regions (from 171 to 199 nt in our numbering). This region may be valuable for the rapid identification and grouping of *Streptomyces* species.

Figure 2 shows a phylogenetic tree constructed based on the sequence alignment and *Knuc* values (6). Although the limited number of complete 16S rRNA sequences determined in the genus *Streptomyces* makes it impossible to ascertain the position of this species, it is certain that *S. griseus* subsp. *griseus* comprises a unique branch. *S. lividans* (2) and *S. coelicolor* (3) is more closely related with each other than other organisms.

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(a) CTGATCCGCTTGGGCATCCAGGCGGTTTCG
 (b) -AC..T..GT.CC...GG.ACG..G.TA
 (c)
 (d)T..G.TTG.....CAG.C.....

Figure 1. Alignment of highly variable regions. (a) *S. lividans* (3); (b) *S. griseus* subsp. *griseus*; (c) *S. coelicolor* (2); (d) *S. ambofaciens* (4). The 5' nucleotides of the regions are analogous to position 182 of the *E. coli* sequence. Identical nucleotides are indicated by dots.

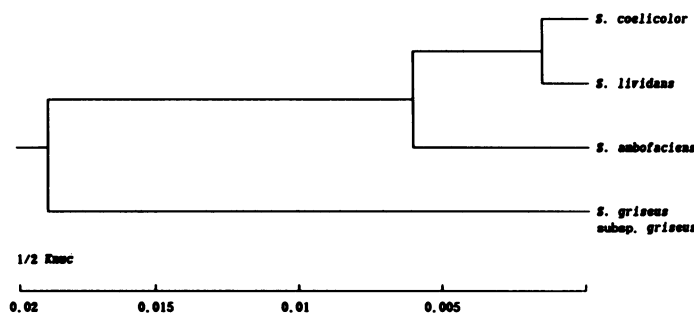


Figure 2. Dendrogram showing the relationships between the test and reference strains, based on the *Knuc* values calculated.