



Horizontal gene transfer within streptomycetes

Currently, the wealth of data available for studying bacterial genotypes provided by genome sequencing has resulted in an increased interest in horizontal gene transfer (HGT). It appears that there has been considerably more gene flow horizontally than was first thought¹. The extent of HGT was reported in the case of *E. coli* and *Salmonella enterica*, where both lineages had each gained and lost more than 3Mb of novel DNA since their divergence some 100 million years ago².

Sequence analysis suggests that horizontal gene transfer followed by gene rearrangements has been involved in the evolution of pathways with catabolic and degradative functions. Biosynthetic pathways such as those involved in antibiotic production may equip organisms with a selectable trait, which is adaptive in certain environments such as soil.

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The gene cluster involved in streptomycin (Sm) production and resistance (Sm^R) has undergone recent horizontal gene transfer (HGT) and genes were recovered in complete functional clusters and also in partial clusters, which were not expressed³. Previous work has demonstrated that the resistance gene, *strA*, had undergone HGT and in some cases was expressed but not in others^{4, 5}. Some of the clusters recovered appeared to consist of gene

mosaics, with some genes having high similarity to homologues in *Streptomyces griseus*, while other were more diverse and did not group with any previously characterised genes.

A new gene cluster was detected in recently isolated strains of *S. griseus* (Sm^R) and this requires further characterisation to determine if it is responsible for production of a novel aminoglycoside with self resistance and resistance to streptomycin. Analysis of a soil recovered from a soft fruit orchard receiving plantomycin (contains streptomycin as major active component) to control fire blight showed that *S. griseus* was the dominant species isolated at all sites (Table 1).

In addition, all strains not identified still showed similarity to *S. griseus*, which was

Table 1. Identification of selected isolates from the four soil sites according to partial sequencing of 16S rDNA including the γ region (% of isolates having the same identification and resistance level).

Soil sites	% of identified isolates	Identification of isolates	Nucleotide similarity of 16S rDNA*	StrA [†]	StrB1 [†]
Apple	45	<i>S. griseus</i>	99-100	+	+
	22	<i>S. platensis</i>	99	+	+
	31	<i>Streptomyces. sp</i> ^Δ	96	+	-
Current	44	<i>S. griseus</i>	100	+	+
	28	<i>S. platensis</i>	99	+	+
	16	<i>S. setonii</i>	99	+	+
	11	<i>S. roseoflavus</i>	99	+	-
Cotswold	45	<i>S. griseus</i>	98-99	+	+
	43	<i>Streptomyces. sp</i> ^Δ	96	+	-
	14	<i>S. globisporus</i>	100	+	-
Coventry	67	<i>S. griseus</i>	100	+	+
	33	<i>Streptomyces. sp</i> ^Δ	96	+	-

* % blast nucleotide similarity of 16S rDNA.
[†] *strA* and *strB1* detected by PCR and hybridisation.
^Δ Isolates with <97% nucleotide similarity to *S. griseus* DSM (40236) were identified as *Streptomyces. Sp*.



recorded as the closest species. There was a correlation between the lower levels of phenotypic resistance and the absence of the biosynthesis gene *strB1*.

All isolates identified as *S. griseus* contained the *strB1* in addition to *strA*, and showed a high level of Sm^R. Isolates identified as *S. platensis* were found to be resistant to a high level of Sm and had *strA* genes homologous to *S. griseus* DSM 40236 (GenBank accession numbers are AF510495 and AY114134), thus providing clear evidence of horizontal gene transfer involving Sm^R.

This phenomenon was only observed in the orchard soils. However, we have now found *str* genes homologous to those of *S. griseus* in a number of other distinct species including *S. limosus*, *S. coelicolor* and *S. cinnamomeus*. The discovery of more highly diverse *str* genes in *S. griseus* was unexpected but it has yet to be shown if the *strA* detected in these strains is responsible for high level streptomycin resistance.

The streptomycin genes *strA* and *strB1* were widely distributed in isolates recovered from all sites; however, the percentage containing *strA* was higher in the streptomycin-treated soil isolates compared with the control. This suggested that selection for Sm^R had occurred and the resistance gene recovered from the *S. griseus* streptomycin biosynthesis cluster was predominant.

Previous studies provided evidence for horizontal gene transfer (HGT) of both an intact functioning streptomycin gene cluster and a partial gene cluster from *S. griseus* into a set of diverse streptomycetes. However, the recovery of a new more diverse *str* cluster distinct from all known previously reported clusters is intriguing especially as it was recovered in *S. griseus*. All the isolates identified as *S. griseus* by 16S rRNA sequence homology did show diversity when examined phenotypically and were recovered in separate clusters as shown in Figure 1. The type strains grouped together in cluster B and C, whilst the soil

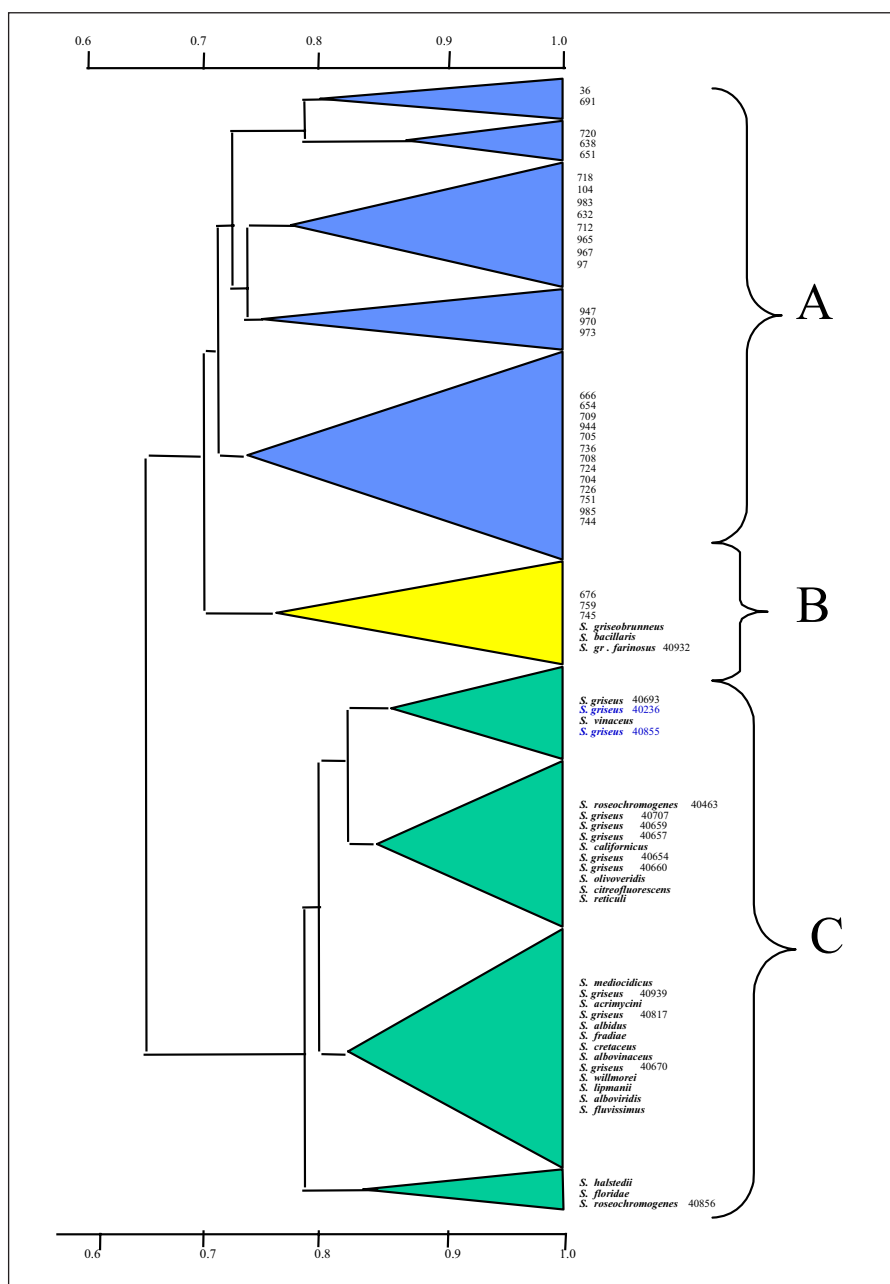


Figure 1. Phenogram of soil isolates and type strains based on UPGMA analysis of 41 phenotypic characteristics⁶. The type strains in cluster B and C were previously grouped as members of the *Streptomyces albidoflavus* cluster 1.

isolates formed a distinct cluster A. It is possible that strains, once isolated and cultured in the laboratory, can undergo quite significant genetic and phenotypic change.

References

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