A. faecalis and 110 Providence and *Proteus* cultures previously[5] used. A large number of *Escherichia coli* and *Pseudomonas aeruginosa* as well as *Shigella* and *Salmonella* spp. were also used in these experiments. Apart from their action on *A. faecalis* which enabled all 53 phages to be differentiated from one another, 5 of these phages productively lysed one or more of 4 *Proteus vulgaris* strains, 14 *P. mirabilis*, 2 *P. rettgeri* and 6 *Providence* strains. Two of these 5 phages were isolated from lysogenic strains of *A. faecalis* and lyse *P. rettgeri* N.C.T.C. 7480 and 7481 and *Providence* strain N.C.T.C. 9269. The remaining 3 phages (isolated from sewage) each lyse at least one strain each of *P. rettgeri*, *P. vulgaris*, *P. mirabilis* and *Providence*.

Organisms able to support the growth of a particular bacteriophage are considered[6] to be closely related and these results support previous findings[5] of relatedness between members of the *Proteus* group and between the latter and *Providence* organisms. With certain *Pasteurella pestis* phages[7] these 5 *A. faecalis* phages share the distinction of being able to attack members of two families.

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Interspecific Recombination in *Streptomyces*

Genetic recombination of Streptomycetes was first reported by Sermonti and Spada-Sermonti in 1955[1]. By crossing different nutritional mutants of *Streptomyces coelicolor* various auxotrophic and prototrophic types have been obtained.

Several authors have obtained true recombination by crossing different mutant strains of *S. coelicolor*[2]. Moreover, recombination of different nutritional mutants of the same species have been reported for *S. rimosus*[3], *S. fradiae*[4], and *S. griseoflavus*[5].

In this work recombination experiments have been carried out with mutants of the following species of *Streptomyces*: *S. rimosus* A.T.C.C. 10910, *S. aurofaciens* A.T.C.C. 10762 and *S. coelicolor* I.S.S.

Nutritional mutants of *S. rimosus* and *S. aurofaciens* were obtained by ultra-violet radiation using the replica plating technique. Mutants of *S. coelicolor* were kindly supplied by Prof. G. Sermonti, Istituto Superiore di Sanità, Rome. Nutritional mutants were used because of their stability and suitability for recombination.

Two parental strains have been inoculated together on slants of complete medium, and incubated four days at 30° C. Collected conidia were suspended in sterile water, filtered through a cotton filter in order to remove hyphal fragments and clusters of conidia, and seeded on selective media.

The number of recombinant colonies recovered in various experiments is reported in Table 1.

Recombination has been obtained in all the interspecific crosses examined, namely, *S. rimosus* × *S. coelicolor*, *S. rimosus* × *S. aureofaciens* and *S. aureofaciens* × *S. coelicolor*. Recombination rates ranged from about 10^{-6} to 10^{-4} according to the various strains used and the selective plating media.

Considerable changes in pigmentations of recombinants were observed in the progeny of crosses *S. rimosus* × *S. coelicolor*, ranging from cream-white colour (*S. rimosus*) through grey, pink and red, to strong blue pigment (*S. coelicolor*), more intense than the normal colour of this species.

Table 1. Interspecific Recombination in *Streptomyces*

Crosses	No. of spores plated per dish	Supplements to minimal medium	No. of recombinants recovered*
S. rimosus × *S. coelicolor*			
*M*1 arg × *M*10 his	12×10^6	—	(12)
		HIS, STR	(17)
*M*1 arg × *M*15 arg	4×10^6	—	9 (45)
*M*1 arg × *M*16 arg	5×10^6	—	7 (80)
*M*3 nic × *M*13 met phe str	2×10^6	—	(5)
		MET	(6)
*M*8 arg his × *M*13 met phe str	5×10^6	—	20
		HIS	21
		HIS, PHE	24
		ARG	528
		ARG, MET	532
*M*8 arg × *M*17 met arg ade	$4{\cdot}5 \times 10^6$	—	1 (114)
		MET, ARG	1 (128)
		HIS, ADE	2 (140)
S. rimosus × *S. aureofaciens*			
*M*4 his × *M*6 met	5×10^6	—	0
*M*9 his × *M*6 met	$2{\cdot}5 \times 10^6$	—	6
S. aureofaciens × *S. coelicolor*			
*M*5 his × *M*10 his	$4{\cdot}5 \times 10^6$	—	0
*M*5 his × *M*13 met phe str	1×10^6	—	20
		PHE	24
		MET	28

ARG, arginine; HIS, histidine; ADE, adenine; PHE, phenylalanine; MET, methionine; NIC, nicotinic acid; STR, streptomycin. The same symbols in small letters indicate mutant alleles for requirement of the growth factor, or for resistance to the drug (str).

* Mean values from 10 consecutive assays, each on 10 plates. The numbers in parentheses are small colonies.

Argineless recombinants were isolated from the combination *S. rimosus M*8 arg his × *S. coelicolor M*13 met phe str. Prototrophic recombinants were obtained from one of three isolated strains crossed with parent *M*13.

The relevance of the interspecific crosses in *Streptomyces* from the taxonomic, as well as from the biochemical point of view, needs no emphasis.

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A Medium for the Isolation of *Streptococcus faecalis, sensu strictu*

During the course of an ecological survey of the fæcal streptococci, the need has arisen for a medium which is more highly selective for *Streptococcus faecalis* than media devised for the enumeration of enterococci in general. A number of workers[1-4] have indicated that *Strep. faecalis* is the predominant streptococcus (Lancefield group *D*) of the gut of man, and that this species is relatively rare in the gut of animals. Hence a specific means of demonstrating this organism would be of some value to sanitarians as a means of assessing human fæcal pollution, at least in certain climatic regions[5].

Slanetz and Bartley have recommended an agar medium which is capable of recovering larger numbers of types of enterococci than media formerly used, and the efficiency of this medium is under investigation. It is claimed[6] that strains of *Strep. faecalis* may be distinguished from other enterococci, when grown on Slanetz and Bartley's medium, by the reduction of 2,3,5-triphenyl tetrazolium chloride (TTC) to the formazan, thus producing dark maroon