The equipment used by us was the first successful transducer fabricated in our laboratory with the capability of injecting short ultrasonic pulses into teeth and recovering the pulse echoes. While improved transducers have been developed more recently, a diagnostic tool has not yet been produced. We have demonstrated that one must use solid-to-solid contact for detection of the internal structure of teeth, and that the loss of sonic energy is negligible for the required depth in hard dental tissues. However, the transducer must be improved so that it may be applied to the tooth surface without the need to grind a flat area to ensure a sonic path. We are continuing our efforts to shorten the sonic pulse, aiming at a pulse duration no longer than 30 nsec and a transducer tip no greater than 1 mm in diameter. We believe that the ultrasonic transducer will be employed differently from x-rays for diagnostic purposes, and that new techniques will be necessary for its successful utilization.

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Escherichia coli: High Resistance or Dependence on Streptomycin Produced by the Same Allele

Abstract. *Mutations to streptomycin resistance in* Escherichia coli *K12, when transferred to a C strain, can confer dependence on streptomycin. These alternatives in expression of the allele are probably a result of interaction between two ribosomal proteins.*

We have found in strains of *Escherichia coli* that one allele can confer either resistance to streptomycin or dependence on the drug. The alternative expressions of this allele depend, we believe, on another closely linked gene that, like the *str* gene, specifies a ribosomal protein.

The alternatives in expression of the allele were observed in a transduction experiment when STR-R (streptomycin-resistant) strains, derivatives of *E. coli* K12, were donors and a strain of *E. coli* C (N873) was the recipient. A large proportion of the streptomycin-resistant transductants were dependent on streptomycin (Table 1).

To be able to conclude that the expression of the allele (dependence or resistance) is a function of strain background in *E. coli* C, we carried out the following controls.

Donor strains K12 *str*-HR (streptomycin high resistance) do not harbor either a masked *str*-HD (streptomycin high dependence) allele that is occasionally separated from a *str*-HR allele during transduction, or a *str*-HD allele and a modifier that change the phenotype to streptomycin resistance. We repeated the transduction experiment, using two K12 strains as recipients, one (N4) directly related to the donor strain and the other (AB258) from a different strain collection. In both experiments not a single STR-D (streptomycin-dependent) recombinant was detected (Table 1). [In notations, symbols in capital letters refer to phenotype; italicized letters, to genotypes; for further detail, see (*1*).]

In another control, *E. coli* B strains were used as recipients. Again, only STR-R recombinants were isolated (Table 1), which again indicates that the donor strain did not harbor a *str*-HD allele, and that the observed change in phenotype was characteristic of the C strain.

The STR-R transductants were not due to an interaction between elements that do not involve the *str*-HR allele of the donor strain, since, in an experiment in which the streptomycin-sensitive parental strain JC12 was used as a donor and the C strain (N873) was the recipient, neither STR-R nor STR-D recombinants were isolated. (Here, as in the other transduction experiments, transfer of auxotrophic markers was measured to ensure that transduction took place.)

The recipient strain N873 can give rise to *str*-HR and *str*-HD derivatives by mutation, like any other *E. coli* strain. The STR-D transductants (Table 1) were compared and found to be equivalent to *str*-HD mutants of N873 in their pattern of resistance to different levels of streptomycin.

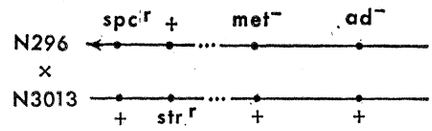

Fig. 1. Diagram of the cross of N296 and N3013.

The STR-D transductants had indeed received and maintained the *str*-HR allele, for the allele can once again be expressed as STR-R in recombinants of a cross with a K12 strain.

For example, N3013, one of the STR-D transductants of the C strain N873, was crossed to K12 strain N296, a spectinomycin-resistant (*spc^r*) (*2*) derivative of strain JC12 (further details about strains are given in the legend to Table 1). From the cross of N296 with N3013 (Fig. 1), 8500 STR-D SPC-R recombinants and 94 STR-R SPC-R recombinants were isolated, showing that the *str*-HR allele had been retained in N3013. The number of STR-R SPC-R recombinants is probably a low estimate, since this class is apparently selected against during the transition from dependence to resistance, when cells are relatively sensitive (*3*). Examination of the 94 STR-R

Table 1. Transduction experiments. In all experiments, the donors were the K12 strains N316, N321, and N707, derivatives of JC12, an Hfr strain auxotrophic for methionine and adenine, which transfer the chromosome clockwise starting somewhere before *arg* G (obtained from Dr. B. Low, New York University). Strain N316 is a *str*-HR derivative, N321 is a spectinomycin-resistant (*2*) *str*-HR derivative of JC12, the *str* mutation being independent from the one in N316; and N707 is a *nek* derivative (a strain resistant to neomycin and kanamycin) of N316. In all experiments at least 25 transductants obtained in the cross of the donor N316 and one of the recipient strains were analyzed. The C recipient was N873, a *gal*$^-$ derivative of strain C obtained through Dr. J. Eigner from this department, originally from Dr. R. L. Sinsheimer. The K12 recipients were N4 and AB258. Strain N4 is a methionine prototroph obtained from a transduction experiment in which strain JC12 was the recipient; AB258 is a threonine, leucine, thiamine auxotroph obtained from Dr. E. Adelberg, Yale University. The B recipients were J961, a *thy*$^-$ *gal*$^-$ strain obtained from Dr. N. Melechen, St. Louis University, and strain B148, a *ura*$^-$ strain from this laboratory. The transduction conditions with phage Plkc were similar to those of Hashimoto (*7*), with the modification described by Apirion and Schlessinger (*1*).

Donor	Recipient	Transductants (No.)	
		STR-R	STR-D
K12 *str^r*	C *str^s*	36	40
K12 *str^r*	K12 *str^s*	65	0
K12 *str^r*	B *str^s*	72	0

SPC-R isolates for adenine and methionine requirements showed that at least the bulk are genuine recombinants, for they include 68 *ad*$^+$ *met*$^+$, 19 *ad*$^-$ *met*$^-$, and 7 *ad*$^+$ *met*$^-$ colonies; the first and third groups differ from each parent by two characters that arise only rarely by mutation.

We conclude from these results that streptomycin resistance and dependence are allelic, and infer that the *E. coli* C strain (N873) differs from K12 donor strains in at least two mutational sites. One of these is the allele that specified streptomycin sensitivity or resistance; the other is a modifier which, in its form in N873, changes the phenotypic expression of the resistance allele from resistance to dependence. These genetic sites are closely linked, since they can be cotransduced to yield STR-R transductants of strain C (Table 1), but are probably in different genes, since they are frequently separable (Table 1). From the transductions and the cross diagramed above, the "modifier" locus would lie between the *str* and *met* loci, closely linked to the *str* locus.

Since resistance resides in the 30*S* ribosome (*4*), and there is evidence that the *str* gene specifies a ribosomal protein (*5*), we suggest that resistance to and dependence on streptomycin, as well as the modifier, result from specific changes in 30*S* ribosomal proteins. The effects of this modifier are in accord with the model of the ribosome as a complex of highly interacting components, a notion we have proposed also on the basis of some other data (*6*).

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Bivalves: Spatial and Size-Frequency Distributions of Two Intertidal Species

Abstract. *Individuals of* Mulinia lateralis *are randomly distributed over a homogeneous area (0.25 square meter) of a mudflat. Second-year individuals of* Gemma gemma *also are randomly distributed, but its total population is aggregated because of its ovoviviparous habit. As expected for two species having different life histories, their size-frequency distributions are very different, the indication being that the nature of a size-frequency curve may not be a reliable index of the degree of transport or integrity of a fossil assemblage.*

The horizontal spatial distributions of two species of intertidal bivalves, *Mulinia lateralis* Say, 1822, and *Gemma gemma* Totten, 1834, were studied in an inlet off Long Island Sound, west of Guilford, Connecticut; they were collected on a small mudflat at an arbitrarily determined spot 10 m shoreward of low water, an area of 0.25 m^2 being chosen to ensure homogeneity of environment throughout the sample. A metal grid with cells 5 by 5 by 3.5 cm deep was used to divide the sampling area; 100 such cells covered 0.25 m^2. The sample from each cell was washed through a 1-mm sieve, and the bivalves were counted, the lengths of their shells being measured in increments of 0.1 mm.

The frequency distributions of the individuals per cell were compared with the expected random frequency of the binomial distribution (*1*) by the chi-square goodness-of-fit test. Populations were taken as random when the observed distribution did not differ from the expected at the 95-percent level of confidence.

Fisher's variance-ratio statistic (*2*) was computed for each of the species distributions (live and dead), and the criterion of randomness was again set at the 95-percent level of confidence. This duplication of tests was necessary in order to avoid difficulties in interpolation of binomial values for "half individuals" in the dead-shell distributions.

The results of the analyses (Table 1) show that *M. lateralis* was always randomly distributed as was to be expected for a population in a homogeneous environment—one in which biological parameters are not important in determination of the distribution of individuals of the population. Thus each individual is independent of all others within the area observed, and the arrival of new individuals is independent of those either already present or entering the area at the same time; this condition is provided for *Mulinia* by its planktonic larval stage and consequent random settling within a limited area of uniform substrate. Moreover, *Mulinia* is somewhat unusual among the suspension-feeding bivalves, at least in the adult stage, in its apparent ability to withstand the high content of silt and clay in mudflat sediments; thus it can utilize the very high concentrations of organic matter characteristic of these

Table 1. Variance, means, and spatial distributions for living and dead populations of *Mulinia lateralis* and *Gemma gemma*. Aggr., aggregation.

Year class	Nos. (N, n)	Variance	Mean	Spatial distribution	
				Variance ratio	Binomial
		Live Mulinia lateralis			
	100, 27	0.26	0.27	Random	Random
	25, 27	.66	1.08	Random	Random
		Dead Mulinia lateralis			
	100, 54.5	0.38	0.55	Random	
	25, 54.5	2.46	2.18	Random	
		Live Gemma gemma			
All	100, 575	11.83	5.75	Aggr.	Aggr.
All	25, 575	53.67	23.00	Aggr.	Random
1st	100, 434	7.72	4.34	Aggr.	Aggr.
2nd	100, 141	1.66	1.41	Random	Random
		Dead Gemma gemma			
All	100, 729.5	282.83	29.18	Aggr.	
All	25, 729.5	51.02	7.29	Aggr.	
1st	100, 465	19.52	4.65	Aggr.	
2nd	100, 264	7.70	2.64	Aggr.	