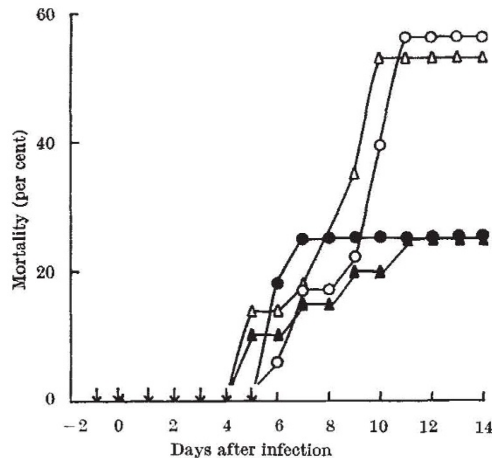

Fig. 2. Effect of kinetin riboside on endotoxin-induced resistance to intravenous infection with *S. enteritidis*. Open circles, saline; open triangles, kinetin riboside (2 mg per mouse); closed circles, endotoxin (40 µg/mouse); closed triangles, kinetin riboside plus endotoxin. Twenty animals in each group were infected 24 h after the first treatment, and treatment was continued as indicated by arrows. All materials were given intraperitoneally in total volumes of 0·2 ml.

The data presented here show that kinetin riboside, in amounts known to inhibit the effects of oligodeoxyribonucleotides in other biological systems[1,2], can reverse the effects of endotoxin on host resistance to infection with *Ps. aeruginosa*. This suggests that in this infection at least part of the endotoxin-elicited resistance may be associated with a release of DNA breakdown products. Similar effects of kinetin riboside were not, however, observed in the tests with *S. typhosa* or *S. enteritidis*, which suggests that endotoxin can modify host resistance by different mechanisms in different infections.

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Dissimilarity between Human and Bacterial Deoxyribonucleic Acids

THE evolutionary origins of human DNA are expressed in the fact that some 20 per cent of it is identical with the DNA of other mammals, 8 per cent with that of birds and 5 per cent with that of fish[1,3]. A search for possible remnants of the bacterial genome in human chromosomal DNA by DNA-hybridization is complicated by the greatly unequal size of their genome: the human genome contains about $3·5 \times 10^9$ nucleotide pairs, whereas the bacterial genome, for example, that of *Escherichia coli*, has only some 5×10^6 nucleotide pairs. If any similarity exists it will therefore involve less than 0·2 per cent of the human genome. If labelled human DNA is used with ordinary bacterial DNA in agar, such low values are below the sensitivity of the DNA agar column method[4]. In these conditions no similarity has been found between labelled DNA from HeLa cells and *E. coli*-DNA[3].

This approach can be refined by (1) reversing the situation and labelling the DNA of the smaller genome (the bacterial DNA); (2) saturating any homologous sites which may exist on the human DNA by using a ten-fold or twenty-fold excess of labelled fragments of bacterial DNA; (3) using as much human DNA as possible on the agar, if possible in the milligram range; (4) measuring complete homology with normal bacterial DNA of the same strain in amounts equimolar with those of the human DNA (and thus 600 times lighter than the human DNA); (5) determining the absorption of the labelled DNA on agar alone.

We used pure sheared denatured carbon-14-labelled DNA from *Xanthomonas pelargonii* (specific activity 640 c.p.m./µg) prepared as previously described[2] (genome: 4×10^6 nucleotide pairs). One gram of moist agar-gel contained about 600 µg HeLa DNA. In a series of experiments 10–114 µg of bacterial carbon-14-labelled DNA was incubated with an eighteen- to thirty-fold excess (by weight) of HeLa DNA embedded in agar (corresponding to a molar ratio bacterial DNA to HeLa DNA of 12–20 : 1). Hybridization and DNA-column elution was carried out according to the method of McCarthy and Bolton[4]. A variety of concomitant controls with HeLa-free agar in the same conditions were carried out. In both sets of experiments the amount of ^{14}C-DNA absorbed ranged between 150–340 c.p.m. out of the 6,400–73,000 c.p.m. added; no significant differences existed between the ^{14}C-DNA bound to HeLa DNA agar and the amount absorbed to the agar alone. Control experiments in which normal denatured bacterial DNA from the same strain was substituted in equimolar amounts for the HeLa DNA (5–10 per cent of the ^{14}C-DNA), the hybridization ranged from 750 to 1,280 c.p.m. The sensitivity of the method used enabled us to detect 5 per cent of this value, corresponding to 2×10^5 nucleotide pairs.

No homology between human and bacterial DNA was detected. If homology exists at all it can be estimated from the sensitivity of the method and assuming some 1,000 nucleotide pairs per cistron, that not more than 2×10^5 base pairs or 200 bacterial cistrons would be preserved in human DNA, corresponding to less than 0·01 per cent of the total human genome.

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Microbiological Transformation of Oxytetracycline

THE uptake and alteration of oxytetracycline (OTC) has been demonstrated with the ascomycete *Xylaria digitata*[1]. So far as we can trace, no reports have been published concerning the fate of this drug in bacteria. Izaki and Arima[2,3] have investigated the uptake and accumulation of OTC by *Escherichia coli K*12. They have reported that large amounts of the antibiotic are retained by the cells, but the chemical nature of the intracellular OTC was not investigated.

We have investigated alterations of OTC by analysis of cold trichloroacetic acid (TCA) soluble compounds extracted from washed cell suspensions of *E. coli* incubated in the presence of this antibiotic. The quantity of OTC used is about 250 times the 50 per cent inhibitory dose for the strain. The results of such an experiment are illustrated in Table 1.

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