transfer factor, so that this strain, too, acquires an advantage in an environment in which the new character is needed for survival.

The transfer factor may be lost at some stage during the spread of an *R*-factor⁴. The resulting organism retains the *R*-determinant which it can transmit to its lineal descendants only and which appears to be stable. Superficially, these organisms resemble drug-resistant mutants.

The transfer factors have a very wide host range. For example, they may be transmitted, together with the resistance determinants they carry, and presumably with other genetic determinants, to the following 'genera' of Gram-negative bacilli: *Escherichia*, *Salmonella*, *Shigella*, *Proteus*, *Serratia*, *Pasteurella*, *Vibrio*, and others. The full range of characters for which the transfer factors can act as vectors is not yet known, but it may prove to be extensive. The same transfer factor will transfer different characters and the same character may be carried by different transfer factors.

The observations presented here suggest that the transfer factors may have more evolutionary importance in the bacterial systems in which they operate than has been hitherto imagined. Although devoid of the property of extra-cellular invasion, they have an immense ecological advantage because of their high communicability and wide host range. They can carry genetic determinants which may ultimately prove to be numerous. By this mechanism these determinants may be widely distributed among different species or genera of Gram-negative bacilli, so that determinants in a given strain may have originated in a bacterial species normally regarded as belonging to a different genus. Whether such genetic determinants can become integrated into the chromosomes of their new carrier cells is not yet known. If they can, it may be supposed that, once integrated, they are indistinguishable in origin from other chromosomal characters and are localizable on the bacterial linkage map. But even if they remain cytoplasmic in location they are stable cellular components. Whether they enter the chromosome or remain cytoplasmic, therefore, they become part of the genome of their host cells.

Extensive exchange of characters between the Gram-negative bacilli need not be expected to lead to genetic uniformity in the different host species, except in relation to the individual characters concerned. On the contrary, it may encourage diversification, because in each case the effect of a new character has to be assessed through its summation with the bacterial genome as it existed up to the time of acquisition of the new character, and the ultimate effect of the now modified genome on the ecology of the recipient organism.

I thought it worth while to voice these speculations because if the long-term activity of transfer factors has influenced bacterial evolution, the evolutionary time-scale may have been telescoped into a shorter span than that envisaged purely in terms of the selection of mutants with survival advantages. The obvious question that arises is whether efficient mechanisms of genetic distribution such as those I have discussed exist only in the Enterobacteriaceae, or indeed whether they are limited to the bacteria. If they operate in other forms of life, some re-thinking may be called for in relation to evolution in other fields of biology.

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Correlation of Temperature-dependent Water Properties and the Growth of Bacteria

In recent years there has been some evidence to suggest that biological activity may be affected by water structure^{1,2}. The premise of the above work was that water undergoes subtle structural changes at specific temperatures^{3,4} and, if biological growth is affected by water structure, growth should be affected at these temperatures. Since the effect of water structure on biological activity has not been substantiated, an investigation of the effect of temperature on bacterial growth was undertaken.

Fig. 1. Number of cells of *Streptococcus faecalis* at different temperatures

Using a polytemperature thermostat, similar to that described elsewhere², cultures of *Streptococcus faecalis* were simultaneously grown in broth culture at nineteen temperatures ranging from 20° to 40° C. The culture tubes were prepared and placed in the incubator at least 8 h prior to inoculation so that temperature equilibrium within the medium would be reached. Inoculum consisted of a loop of cells from a 24-h broth culture of the organism. Growth was stopped after a 20-h incubation period by placing the culture tubes in 50° C water. Bacterial multiplication was determined by direct cell counts in a haemocytometer.

Typical results are shown in Fig. 1. Near 30° C there is a marked reduction in number of cells. The temperature of reduced cell multiplication corresponds to a temperature at which a change in water structure takes place. These data support the postulate that biological activity is affected by water structure. This work is being extended to other bacteria and temperatures.

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Staphylococcus aureus Strains in the '52, 52A, 80, 81 Complex'

THE phage-typing pattern of a strain of *Staphylococcus aureus* is believed to be determined by two factors: the 'basic' sensitivity of the strain to lysis by the typing phages, modified by interference exerted by the prophage or prophages it carries. The specificity of this interference may be narrow, and prevent lysis only by the phage carried by the strain and by closely related phages, or it may be very broad. Sometimes a single prophage will block the sensitivity to a number of apparently unrelated phages and have a profound effect on the phage-typing pattern^{1,2}.

Under natural conditions the typing pattern of a strain may be changed by lysogenization, and this may lead to difficulties in the interpretation of long-term epidemiological investigations. It has proved possible, however,