INTERSPECIFIC GENETIC HOMOLOGY IN THE
ACTINOMYCETES

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SUMMARY. It is proposed that similarity between genetic determinants is the most appropriate criterion for setting up a microbial classification. Genetic homology between organisms can be discovered by biological tests for hybridization, or by physicochemical tests for renaturation between single-stranded DNA's of diverse origin.

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In systematic studies, only a small portion of an organism's attributes is considered. The more completely a group of microbes has been characterized morphologically, physiologically, antigenically, chemically, by infrared spectrography, and for susceptibility to phages, the more reliable should be the judgments about relationships. Until recently, microbial taxonomists have relied on overt expressions as bases for classification, but as new instruments have been developed and analytical procedures have become standardized, more subtle attributes of an organism are being considered. It should be noted that intense, quantitative study of a limited number of characteristics, for example, enzymatic reactions, actinophage susceptibility, and cell-wall compositions, provides sufficient information for satisfactorily classifying actinomycetes. Although reasonably useful taxonomic systems have been devised on the bases of a limited number of cardinal features on the one hand, and of over-all similarity with respect to multitudes of unselected characteristics on the other hand, similarity between the genetic determinants themselves seems the most appropriate criterion for setting up a microbial classification. It must be emphasized that the problems and procedures for routinely identifying previously classified organisms are separable from, if not distinct from, those for establishing a taxonomic system.

Gross analyses of the composition of deoxyribonucleic acid (DNA) can be made by quantitative chromatography of hydrolyzed, purified DNA, by buoyant-density centrifugation in a cesium chloride gradient, and by determining the mid-point (melting point or T_m) of the hyperchromic shift resulting from thermal denaturation. Two organisms having dissimilar DNA compositions are unrelated; two organisms having the same DNA composition may be, but are not necessarily, closely related. For example, Myxococcus xanthus and Nocardia asteroides have similar DNA base compositions (68 mole per cent guanine + cytosine) but differ substantially morphologically, physiologically, biochemically and in almost all other tested features (Jones and Bradley, 1964).

Obviously, base composition of DNA provides helpful but limited systematic information. For definitive studies on biological relatedness, genetic homology *per se* must be determined. Two organisms possess extensive genetic homology if they are able to undergo syncytic recombination. It must be noted that failure to obtain recombination does not necessarily indicate a lack of genetic homology. The inability to demonstrate recombination may be due to inadequacy of the detection system, improper experimental conditions, or incompatibility of the particular cultures tested. Conversely, a limited number of genetic determinants can be transferred from one organism to another by autonomous episomes, whose DNA may be appreciably unlike that of the recipient (Falkow et al., 1964).

It has been possible to obtain interspecific hybrids from pairwise mixtures of Streptomyces griseus and S. viridochromogenes and of S. aureofaciens and S. violaceoruber (Bradley, 1964). Hybridization indicates that there is extensive genetic homology between these pairs of organisms. Because syncytic recombinational studies are technically tedious and are biologically restricted by factors such as compatibility systems, the extent of genetic homology can be better assessed by measuring renaturation between single-stranded DNA's of diverse origin. One of the DNA's must be labeled with N^{15} , C^{14} , or P^{32} . Methods for measuring genetic homology are practical (DeLey and Friedman, 1964); the results of these analyses provide a most reliable basis for setting up a classification. It should be noted that in order to examine genetic homology efficiently, a sound

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(cardinal or phenetic) partial identification is needed. For this purpose it would be most useful if future issues of Bergey's Manual of Determinative Bacteriology were printed on punched cards. In addition to facilitating recognition of related organisms, sections of a card-file edition of Bergey's Manual could be brought up to date as needed and whenever warranted. However, these innovations will not resolve problems of nomenclature. For example, what per cent DNA renaturability is to constitute a species? Obviously, the type-culture principle remains a necessary part of microbial taxonomy. It merits emphasis that discrete, well-defined groups of organisms merge into a biological continuum as more organisms of novel origin are examined. Because microbial taxonomists are working with selected cultures, rather than with valid samples of natural populations, the category currently designated as a species probably should be denoted as a cultivar or horticultural variety.

A classification should strive to reflect biological affinities, indeed, to discover ancestral identities. Contrary to recent assertions (Heslop-Harrison, 1962), evolutionary convergence is not an insoluble problem and a phylogenetic classification need not be based upon a fossil record. Anyhow, it should be noted that there is a microbial fossil record (Cloud, 1965)!

REFERENCES

- Bradley, S. G. 1965. Genetic analysis of an unstable mutant of Streptomyces violaceoruber. Develop. Indust. Microbiol. 6:296-301.
- Cloud, P. E., Jr., 1965. Significance of the gunflint (pre-Cambrian) microflora. Science 148:27-35.
- DeLey, J. and S. Friedman. 1964. Deoxyribonucleic acid hybrids of acetic acid bacteria. Jour. Bact. 88:937-945.
- Falkow, S., J. A. Wohlhieter, R. V. Citarella and L. S. Baron. 1964. Transfer of episomic elements to Proteus. II. Jour. Bact. 88:1598-1601.
- Heslop-Harrison, J. 1962. Purposes and procedures in the taxonomic treatment of higher organisms. Symp. Soc. Gen. Microbiol. (Microbial Classification) 12:14-36.
- Jones, L. A. and S. G. Bradley. 1964. Phenetic classification of actinomycetes. Develop. Indust. Microbiol. 5:267-272.