CARNEGIE INSTITUTION OF WASHINGTON
DEPARTMENT OF GENETICS
COLD SPRING HARBOR, LONG ISLAND, N. Y.

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Dr. Joshua Lederberg
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Dear Lederberg:

Thank you for your comments on my draft of nomenclature proposals. I feel that it is important for problems of nomenclature to be worked out by the whole group that will use the system, in order to insure general acceptance. Otherwise we may be in a worse position than we are now. I intend to put my proposals into the first issue of Bulletin, as suggestions to be used as a basis for discussion by the group.

I agree with you that for technical reasons subscript symbols should be avoided. I was not happy about suggesting subscripts to distinguish mimics from groups of similar characters. As you point out, there is no real fundamental difference between these two groups, and they can well be handled as one so that the necessity for subscripts will be eliminated.

I see no reason why a group of mutants like sugar deficiencies should not have three-letter symbols, as you propose. In this case it might be well not to use three-letter symbols for other mutants except when it is unavoidable.

I am not convinced that + and - signs should be used. They are not desirable because of typographical difficulties, because + has a very specific meaning in genetic nomenclature, and also because these signs can designate only two possibilities. It seems very probable that more than two alleles may be found; and indeed this is already the case with fermentation (slow fermenter), which would necessitate the use of letters in addition to + and - signs. For those who have become accustomed to using + and -, it may be hard to drop them; but I am certain that they would easily get adjusted to the other system, which is more flexible.

I like your suggestion of underlining the symbols of linked mutants in listing complex stocks. As long as there are no subscripts, underlining would be an effective way of showing linkage. I see no objection to having other symbols arranged in some order which need not be alphabetical.

I was glad to have the list of the symbols you are using in the laboratory. It might be well to change some of them to fit the proposed system of nomenclature--that is, to try to avoid the use of three letters except for the sugar-fermenting mutants. I would

also suggest the use of the chemical terms thiamin and riboflavin instead of vitamin B1 and vitamin B2. My suggestions for the whole list are as follows:

Ala	instead	of	Al	Ak	instead	of	Akg
As	"	"	Asp	Ni	"	"	Nic
Alb	"	"	Bal	Pg	"	"	Pga
Th	"	"	B1	Pr	"	"	Pyr
?	"	"	Vitamin B-12	Pt	"	"	Pnt
R	"	"	B2	Pl	"	"	Pnl
Py	"	"	B6	Arl	"	"	Ar
name?	"	"	Dpn	Cm	"	"	Cmy
Se	"	"	Ser	Am	"	"	Arm
Is	"	"	Ins	Pf	"	"	Pfl

I hope to see Tatum next week, and will discuss this problem with him. If you have any other comments, please let me know.

The results we are just getting now throw doubt on our previous interpretation that S22 is another S locus; but I hope that new experiments will give the answer to this question.

With best regards,

Sincerely yours,

M. Demerec

MD:af

DRAFT

Nomenclature

At present there are two systems of nomenclature in use by workers interested in the genetic aspects of research with bacteria. The older of these specifies the strain and denotes the mutant by some symbol. This system was adapted by Demerec and Fano (Genetics 30: 119-136, 1945) from the nomenclature ~~used~~ improved by Burnett, and is in use in studies dealing with bacterial resistance--specifically, resistance to viruses, radiations, and streptomycin. According to this system, if strain B of Escherichia coli is used in studies of resistance to bacterial viruses of the series T1 to T7, the symbol for a mutant resistant to T1 is B/1 (read "B bar one"), the bar standing for "resistant to," and the virus being designated by number only. Thus B/1,5 denotes a mutant resistant to both T1 and T5, obtained through one mutational step, whereas B/1/5 indicates a similar phenotype obtained in two mutational steps. The symbol B/r stands for a mutant resistant to radiation, B/r/1 for a two-step mutant resistant to both radiation and the virus T1. B/S stands for complete resistance to streptomycin, B/s for partial resistance (viz., resistance to low concentrations only), and B/Sd for dependence on streptomycin.

The second system of nomenclature evolved during studies of biochemically deficient mutants, and has been developed to the present stage by Lederberg (Genetics 32: 505-525, 1947) to take care of the requirements imposed by studies of linkages between various traits. This system is better suited to studies of conventional genetical relationships, for which it was primarily designed. It does not contain a symbol for the strain used in experiments; but it provides symbols for the alleles of all mutant loci considered in an experiment, and in general it follows the principles worked out by Drosophila geneticists.

I do not see any reason why both systems should not be used, for the present. In the case of E. coli it would be difficult, until the genetic analysis of resistance to the T series of viruses is worked out, and knowledge acquired about the number of loci involved, to express all the mutant types known in this series in terms of the second system. Nevertheless, it is to be expected that the second system will gradually replace the first as our information about bacterial genetics becomes more extensive.

Geneticists have put a great deal of thought and effort into developing a uniform system of nomenclature applicable to Drosophila, plants (particularly maize), and mammals; but, because of the different situations (?) existing ih the various organisms, these efforts have not been entirely successful. At present there is general acceptance of the main principles in regard to nomenclature, but minor differences exist among the systems of nomenclature and symbolism used in work with various organisms.

I propose here to outline a system of nomenclature for bacterial genetics which conforms to the general principles of genetical nomenclature and follows closely the system used by Drosophila workers, as elaborated by Bridges (Bridges-Brehme, The Mutants of Drosophila Melnogaster, Carnegie Inst. Wash. Pub. 552, 1944, pp. 1-7).

Mutant types. Mutant types are inherited departures from the standard phenotype. Each mutant is given a name suggestive of the main diagnostic feature. This name is preferably a simple descriptive adjective, such as "rough," or noun, such as "biotin," "leucine," "streptomycin," or "virus."

For convenience in listing and tabulation, a representative

symbol is assigned to each mutant type. This should be an abbreviation of the name of the mutant, and should start with its initial letter. When the first letter is already in use as the symbol for another mutant, other letters of the name are added, preferably those immediately following the initial letter. These additional letters are written on the same line with the initial (not as subscripts) and are in lower-case type (La--lactose; Th--thiamine).

Since the dominance relationship, even if it should be possible to determine it, does not play an important role in bacterial genetics, it is proposed to capitalize the first letter of the symbol of each mutant (B--biotin; M--methionine; S--streptomycin resistance).

Alleles. The name of a mutant and the symbol assigned to it stand for the locus name and locus symbol, respectively. Different alleles of the locus are differentiated by exponents. Since in bacteria the wild type is not always well-defined, it seems to me desirable to use a letter exponent to symbolize it, rather than the "+" used for Drosophila. The first letters of a word descriptive of the property of the particular allele should be used as exponents. It is suggested that exponents be written in lower-case letters, except when it is established that the allele is dominant, in which case the exponent should begin with a capital letter.

S^{s}--streptomycin-sensitive

S^{r}--streptomycin-resistant

S^{d}--streptomycin-dependent

S^{pr}--partially resistant to streptomycin

S^{d3}-- streptomycin-dependent, mutant number 3

R^s--radiation-sensitive

R^r--radiation-resistant

To attain uniformity in the system and to make it clearer, it is suggested that the use of "+" and "-" signs in exponents be avoided. As used at present, these signs have different meanings in different cases. For example, + may stand either for wild-type, for nutritional independence (B^+ = biotin-independent), or for ability to ferment (La^+).

B^i--biotin-independent (instead of B^+)

B^d--biotin-dependent (instead of B^-)

La^f--lactose-fermenting (instead of Lac^+)

La^n--lactose-nonfermenting (instead of Lac^-)

Mimics. Mutants of similar phenotype but different location are called mimics. It is proposed that the same symbol be used for each group and that the different loci be distinguished by subscript numerals.

S_1--streptomycin locus found first

S_2--streptomycin locus found second

(S_1^s; S_1^r; S_1^d.....S_2^s; S_2^r; S_2^d.....)

Groups of similar characters. When one is handling a group of mutants that affect a similar trait--for example, resistance to the T series of viruses in coli--it may be desirable to use the same letter symbol for all these mutants. In this case, the loci may be differentiated by numerals written on the same line with the letter symbol ($V1^s$--virus T1-sensitive; $V2^r$--virus T2-resistant).

Order of listing mutants. Whenever linkage relationships are known, the order of symbols in multiple stocks should correspond

to the linkage map, in serial order from left to right, It is suggested that, in listing multiple stocks that contain located as well as unlocated mutants, the symbols of the located mutants be given first in order, as they appear on the linkage map, and that they be followed by a semicolon and then the symbols of the other loci, arranged alphabetically (M^d $La^{\sim}$ T^d; R^r $S2^{d}$).