Osborn Botanical Laboratory, Yale University, May 16, 1947.

Dear Mather-

Under separate cover, I shall shortly send you a manuscript entitled "Problems in the Genetics of Microorganisms". This is really only a preliminary draft, but it does indicate the scope and point of view of the review whose writing I had mentioned previously. I had planned a more extensive paper, but while I was writing, I was fortunate to see a manuscript of a review by Luria which has just been published in Bacteriological Reviews. Luria's paper is quite a competent job, which I should not like to duplicate, but I think there may be room for the more speculative, and more professionally genetic type of approach which my "Problems" represents. I am sending this draft in its present state for the benefit of any suggestions which you may care to make, and to learn, if you would be so kind as to transmit this letter and the script, to Dr. Darlington, whether it would be regarded as suitable in its general cast, for HEREDITY. If it is, I should like to learn what form of List of References would be preferred.

Thank you for placing me on the John Innes mailing list; the use of selectional techniques in genetics of higher plants, as represented by the report of mutations at self-sterility loci was particularly interesting; most of the mutational characters of microorganisms can be found by a similar type of genetic "sieve."

There is little further to be added concerning the genetic map of E. coli; a few drug-resistance characters have been tentatively located on the same single linkage group, and the comparison of the segregation of alleles in alternated crosses, as was done for the Y^r-Y^s alternatives has been extended to Lac+ Lac- and to Cla^r-Cla^s (chloroacteic acid resistance) with correspondingly satisfactory results; no crossover-suppressors have been detected still (with mustard or X-ray) so I am trying now to develop polyploids, using the suppression of new recessive mutations as a means of detecting them after various treatments. The results so far are highly encouraging, but not conclusive; but this is talked about in the review.

Have you given any further thought to the problem of estimating the absolute distances from the multiple crossover frequency in a four strand system? Or rather, have I made the problem clear? I can't think of anyone else whom I can bother to worry about that kind of case. There is still (after another experimental attempt) no evidence that there is more than one viable product of a zygote, but the set-up is still not optimal for the detection of others.

Luria is now talking about a fantastic story in phages: two phage particles each of which bears UV-induced 'lethal mutations' can interchange in a bacterial cell and give rise to non-lethal products; by using phages carrying many lethals and claculating the frequency of coincidence of lethal mutations in the two phages, the total number of genes is estimated, and turns out to range from 35-65 in various coli phages. There is no linkage, however. Thought you might be interested to hear this; the analysis is almost purely statistical.