

March 8, 1960

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Dear Joshua and Esther:

I hope all has been well with you and that you have a pleasant journey to England next month. Alec Bernstein has been urging me to try and come as the Symposium looks good, but I cannot for lack of funds and time. It should be an interesting session.

I have a problem. We have been making more mutants for mapping purposes, etc., and at the moment have for these mutants some unwieldy numbers. Could it be possible to get a batch of Gal numbers assigned to us, to avoid the above problem and also to avoid confusing the literature? Stock cultures are becoming a problem with us, as our reference by page numbers are now intruding into the lower W- numbers.

The second problem has to do with information on W3142 and W2312. I believe these are deletion mutants. I have no record of obtaining reversions and recent experiments to obtain them, even employing UV have been unsuccessful. Reconstruction experiments on minimal Gal show that one is able to recover added Gal<sup>+</sup> to 100% recovery so that it is not likely to be a case of suppression of the reversions by the Gal<sup>-</sup> background. These mutants you will recall are not transformed to Gal<sup>+</sup> by any HFT lysate. I think that what this means is that although Gal<sup>+</sup> is dominant to Gal<sup>-</sup>, Gal<sup>+</sup> is not dominant to a deficiency. I have some experiments (Gal<sup>+</sup>/Gal<sup>def</sup> → HFT Gal<sup>+</sup>) in progress and will advise you of the results shortly.

We have had no success at obtaining HFT 3 or HFT 9 even employing W4654 as an indicator. I am suspicious of these mutants and perhaps the double mutant hypothesis (one mutation a lethal?) is really correct. We have several other HFT'S for our other mutants.

I expect within a couple of weeks to be able to classify, at least partially, our mutants for the biochemical steps involved. Kinase-less mutants should not be hard to identify in the group.

The mapping goes not too badly and a late estimate I enclose below. We have no cases of transductions of 4  $\rightarrow$  3 yielding position effect heterogenotes, with approximately 300 transductions streaked out. This may be another exceptional case. Incidentally, I talked with Benzer last week at Purdue and he now has mutants that resemble the 4, 7 interaction. Said he found them as soon as he looked for them.

Weather was very bad the last two weeks here, but I was away and didn't mind it. Helvise and Margaret had to put up with the below zero weather. Today is back to normal, a beautiful, bright, clear, warm day.

Best wishes,

MLM:lbn