May 12, 1955

Dear Dave:

Thank you for your letter. Esther and I would like to visit you at Cold Spring Harbor, if we can work it out. However, our plans are still somewhat jumbled, and with various business and parental obligations, we won't know until after we're in NY.

The most probable opportunity would be on Sunday, May22. We have to go to Syracuse on an early flight (AA- 10:15) Monday morning; the Airline Guide is somewhat confused about this and I haven't found whether this should be 743 from Newark or 745 from LaG. If the latter, it would be especially convenient if we could come out Sunday afternoon * and spend the night there— but this may depend on whether we can have a place to stay, and the means of getting to the airport the next AM. We will get in touch with you or Norton or both in NY. We leave Madison Wednesday; you can leave any message for us with Norton or Ruth Sager at Rockefeller, or possibly at the Barbizon Plaza Hotel.

As to Hfr crosses, I have to say first that most of my single cell work has had to be with another system than W-1895 x W-1177; I've been using a multiple marked strain of another wg line, which is morphologically distinguishable from K-12, as the F- parent. I did do a good deal of work with W-1895 x W-1177, as you know, but not a single cell basis. Crosses here were diagnosed in three ways: selecting S^r Lac^+ recombinants on EMB Lac sm— I call this sr+ selection; detecting the phenotypically distinct Lac+Gal+ recombinants in a setup HfrGal-Lac+ x F-Gal+Lac- on EMB Lac (which has the advantage of leaving both parents alive); examining the characteristically sectored Lac+/- colonies on EMB Lac in W-1895 x W1177; a few various others, e.g., Xyl+SR or $Lac^+V_1^r$. My conclusions are not greatly different from yours: most (ab. 80%) of recombinants for any markers examined are Lac^+S^r, or rather are included in the same colonies which have sr+; there was a progressive decrease in the recovery of paratypic (from Hfr) markers as linkage distance increased away from Lac— taken together, these facts would indicate that there is a bias against the TL end of the Lac linkage group, again presumably a distal elimination since T and L themselves are so regularly heterozygous in diploids, and their segregation from such heterozygotes is so perturbed. I am fairly sure now that the eliminated segments including Gal-Lp, on the one hand, and Mal-S on the other are distinct from one another; I haven't definitely concluded whether this TL-linked one is a third, or a manifestation of one of these (if interstitial).

To summarize, for your purposes, the sr+'s (yours or mine) probably measures most of the zygotes that yield any recombinants at all; it is impossible to measure independently the zygotes that segregate to give only the parentals. In my mating pairs, the incidence of detectable recombinants has been about 25-30%, but I can't be sure whether the others were all proper zygotes or not. Hoping to see you in NY,