WILLIAM G. KERCKHOFF LABORATORIES
OF THE BIOLOGICAL SCIENCES

23 rd. March 1938

Dear Professor,

and to the General

Two days ago I dispatched to Mr. Douie, notice of my
intention to resign from the College at the end of this session, which I
suppose is September 30th. I have definitely taken the John Innes job now.
I expect that you will not be surprised that I have done this in view of our
various conversations on the possibility last year. I shall of course be sorry
to leave the Galton Laboratory, but the advantages of the other job, notably
the financial advantages are not to be overlooked. I hope and expect, however,
that I shall be a frequent visitor to the Galton Lab., and that we may
continue our collaboration on Lythrum. As far as I can see the Lythrum project
will be helped by the fact that I shall be in a position to get largish numbers
of plants grown at Merton.

I should very much like to have your advice on the question
of some work I have been doing. You will no doubt remember Smith's pet project
of working out a method for the exact use of F_3 segregations in families
carrying polymeric factors, and his various attempts to solve the problem.
I suggested that one way might be to postulate linkage between two of the factors
and thus get a continuously varying set of segregations in F_2 and F_3. By this
means one could find the deviation of the maximised log likelihood expression
from 0, and divide its square by the amount of information about the recombination
fraction to obtain a χ^2, when one of the two values, 0 or $\frac{1}{2}$, was used for p,
the recombination fraction. Thus one could get an exact test of significance for
deviations from either or both of two possible numbers of polymeric factors.
I have been working on this to some extent while here and have got the method
of calculation worked out. In as much as the likelihood expression for any F_3
family must take into account the possibility of the F_2 plant having been of
a number of different types, it is not possible, as far as I can see, to get *easily*
the log. likelihood expression. This is not a real difficulty, however, as the
deviation from the maximised log likelihood expression can be obtained in terms

of the likelihood and its first derivative. Similarly the amount of information
can be obtained from the likelihood and its deriavtives. The is, on the other,
hand considerable labour necessary to obtain the derivatives of the likelihood
expression and even more labour to compute them for a largeish number of F_3s
even when some chosen value, 0 or $\frac{2}{12}$, is substituted for p. The question at the
moment is this, I have shown to my own satisfaction that the problem is capable
of solution in terms of linkage, and I have also shown that the computational
labour is very large, but is the problem worth the labour? I find it difficult to
judge as having sunk some time into it I feel reluctant to throw it away but
hestitate to sink even more time into it unless the expenditure will be well
made. The calculation for 4 factors, two of them linked, i.e. the case for
distinguishing 3 from 4 polymeric genes, is, at least to me, quite heavy
going, though the cases of 1 or 2 factors, and 2 or 3 were not too awful. I have
decided not to do any more till I hear your opinion.

I have been raising an enormous number of flies in an effort to solve
the riddle of why certain left ends of the X chromosome appear in only half as
many flies as they should. I have got a lot of figures but not much sense out
of it yet. It definitely appears not to be due to interaction of the left end
with either an autosomal gene or a free fragment. I must have a concentrated
think about the figures once more but I really feel bogged at the moment. It is
very intriguing indeed.

I am just running some more experiments on crossing-over in homozygous
inversions. If they come out alright, without any bad abnormalities in segregation,
they should be very valuable from the point of view of position determination
such as I have written about in the past.

I have also fixed a lot of maize meiosis from trisomics and their
sister dipoids in the hope of finding out whether trisomy affects the negative
correlation , if maize has one, between the chiasma frequencies of the different
bivalents. I shall work this up at Harvard. Incidentally I have deferred my
advent in Harvard until the end of May.

I had a letter from Brandt and shall call on him in Washington on
my way to Harvard. Dobzhansky is now in Mexico collecting more Drosophila, but
otherwise there is no news from here. I had a rather hectic argument with

Dobzhansky about his book, which you may have seen. I did think that he missed much of the point of your writings on the subject and his interpretation of Harland's cotton was little short of scandalous. However, the book seems to be so much in advance of any other simple account of its kind that I feel that in spite of some flaws of this kind, it was well worh while. In comparison with, say, Watkins presentation it is positively classical. I should like to hear your opinion on it.

I must close now as we are going to see the lion farm at El Monte this afternoon. Sturtevant says they have a gene for albinsim in these lions as he has seen litters throwing albinos there. I hope I see some of them. There are no albino cats, are there?

Mrs Mather joins me in sending best wishes to you and Mrs. Fisher.

Yours,

K. Mather