

16th January, 1957.

Dear Watkin Williams,

Thanks for your letter. The single gene totals I get from your expectations are:

<u>Expected</u>	<u>Observed</u>
38.3653	42
31.4454	32
25.8239	25
16.3031	15
10.0297	9
7.6620	7
<u>129.6294</u>	<u>130</u>

Common sense, I believe supported in this case by maximum likelihood, suggests that these single allele totals ought to check, and that the real fitting problem is to find expectations which do add up to the right single gene totals.

These will have to be based on single gene factors having higher ratios than the gene frequencies observed. This is understandable, for unequal allele frequencies are not in genetic equilibrium without balancing selections, such as you have

emphasized as favouring  $S_3$ . Consequently the factors to be used in the expectations are the observed gene ratios, inflated or deflated according as selection favours or disfavors them. I am sure that your reference to a hypothetical parent population is superfluous, and it might be useful to get Gilbert to try his hand at the direct problem of finding expectations based on factors at present unknown, but which have to satisfy the condition of fitting the margins.

Of course, I can let you know what I have done and go over it with you, but this would be rather too long for a letter and may be unnecessary.

There are really only three entries in the table that stick out:  $S_1 S_2$ , with 13 observed;  $S_3 S_6$ , with 7; and  $S_4 S_5$ , with 4. Balancing these there are too many zeros where a few plants are expected. You will notice that each of the six alleles in your panel occurs in one of the favoured genotypes. I forget whether I gave you the log likelihood test, or version, of  $\chi^2$ , but it makes the deviations quite strongly significant.

Sincerely yours,