19th January, 1957.

Dear Watkin Williams,

I have received a letter from Neil Gilbert which I do not at all understand, but in which he says that "it appears that your gene frequency analysis cannot be improved on". I take this to mean that he accepts the fact that values should be fitted so that the marginal frequencies are equalized as between observation and expectation. Such a fitting, of course, gives, by comparison of the factors used with those derived from observed gene frequencies, a measure of the selective advantage or disadvantage needed by each gene to maintain ~~their~~ its observed frequencies, i.e. that gene S_3 must have a selective advantage of nearly 20%, while gene S_6 and its neighbours have correspondingly large selective disadvantages.

I have pressed this different mode of analysis on your attention only because I think such data as you present are really much more informative than might at first appear, and that in this case they demonstrate not only largish and measurable selections between the different alleles, but also highly significant

interactions between these in determining those qualities for which the existing varieties of sweet cherry have been selected.

I rather gather that the problem I suggested of "finding expectations based on factors at present unknown, but which have to satisfy the condition of fitting the margins" has not attracted Gilbert's interest. It may be that he will think it up later, but alternatively, as it has not been published, I hope you will get me to put it down for you some time.

Sincerely yours,