

22nd. June 1949.

My dear Rob,

I have at last finished your sums, after having made every possible mistake.

If one does a simple  $\chi^2$  versus  $\chi^2$  test of the five lots in your data, one gets  $\chi^2$  4.479 for four degrees of freedom, which does not suggest any heterogeneity between the several sera. Of course, if ~~it~~<sup>they</sup> had been heterogeneous one would have had to examine further whether perhaps there was heterogeneity in the ratio  $\underline{M}$  to  $\underline{N}$ .

The results of fitting your whole lot of 1419 are

	$\underline{M}$	$\underline{N}$
s	24.71722	8.02080
s	<u>28.31308</u>	<u>38.94890</u>
	53.03030	46.96970

I think last time I sent you also a covariance matrix giving the sampling variance of each of the four estimates and the six covariances of these taken two at a time. If you want it I could recalculate this for the new data. Alternatively, I expect the old table would be good enough if reduced in ~~the~~<sup>the</sup> ratio in which the sample observed has been increased.

For the six phenotypes observable one has with these estimates

	Exp.	Obs.	Diff. a-m	$\frac{(a-m)^2}{m}$
MM S	285.302	295	+ 9.698	.3297
MM ss	113.751	107	- 6.751	.4007
MN S	393.930	379	-14.930	.5658
MN ss	312.964	322	+ 9.036	.2609
NN S	97.788	102	+ 4.212	.1814
NN ss	<u>215.265</u>	<u>214</u>	- 1.265	<u>.0074</u>
	1419.000	1419		1.7459

Consequently for two degrees of freedom  $\chi^2$  at 1.7459 is below expectation. One could separate two components, one due to the deviation in the number of MN heterozygotes irrespective of S, and a second due to deviations from expectation of the ratio S to s in the three MN genotypes. Of these the first is quite small <sup>the</sup> deviations, which are necessarily balanced, being, in fact, +2.947, -5.894, +2.947. Consequently the other degree of freedom contains most of the total, and, of course, 1.7459 is far from significant even if it had to be ascribed to one degree of freedom only.

Yours sincerely,