19th. December 1949.

Dear Henningsen,

It is exceedingly kind of you to send me your
offprints, which I have been looking at with great interest.
Yours is, so far as I know, the first work on this interesting
factor sufficiently thorough to provide a basis for our further
understanding of the genetic situation.

Looking at your Table 5 of 183 families with 508 children,
I believe one could push the interpretation a step further by
estimating the proportion of individuals serologically classifiable
as Pstr., Pmed. and Pw. respectively who are genetically
heterozygous for the supposedly unique gene p.

Beyond what you publish this would only require listing the
number of children in the families (i.e. the number of children
actually tested and recorded in the Table) for 18 lists of
families made by subdividing the 9 classes in Table 5 into those
which do not and those which do contain at least one recessive
child.

If there are a children in a family, the chance that if
both parents are heterozygous there will be at least one
recessive child is

$$(1 - (\tfrac{3}{4})^{a}) \quad .$$

This quantity added for the values of a occuring in one of
your sub-lists, such as Pstr. x Pstr., gives the number of famili
with a recessive child to be expected in this group, and, dividing
the observed number by this expectation, we should obtain an
estimate of p^2, where p is the probability that an individual
classified as Pstr. shall be heterozygous.

Similarly the other 9 classes will provide estimates from
which an idea could be formed as to whether consistent estimates
for p, q and r, the proportions heterozygous in the three serological
classes, are likely to be possible, and, if so, what approximately
their values are.

Of course this is only a preliminary reconnaissance required
to obtain such approximate values and, for example, to see whether
the assumption that all Pw. persons were heterozygous would be
compatible with the data. With this guidance it might seem worth
while to do a more professional and efficient fitting, using the
principle of maximum likelihhod and the method of scoring in some
such way as I have illustrated in "The fitting of gene frequencies
to data on Rhesus reactions" and "Note on the calculation of the
frequencies of Rhesusallelomorphs", of which I am sending you
offprints.

Of course, if you would care to send me the lists of numbers of
children in each family, I could perhaps find time to get the job
done, or at least sufficiently advanced to report to you, during
next term, when I shall be at the University of Toronto.

Yours sincerely,