

5 January 1945

Dear Taylor,

Thanks for your message on  $\eta$  data. The odds for significant association with H are already well beyond the 1% point ( $P = .002374$ ). I enclose sheet with the actual calculation.

Actually the evidence is stronger than this, seeing that the  $\eta$ -negative cases are more often of type  $R_2$  than  $R_1R_2$ , as classified by the other sera. Perhaps, however, the evidence from this latter source will appear more clearly when more H-positive cases have been tested and especially if it were possible to exclude false negatives so that whenever one of the rarer types such as  $R''$  or  $R_1R_2$  happens to be

-negative, it will be safely claimed as a homozygote  $R^+R^+$  or  $R_2R_2$ , respectively. While false ~~negatives~~ still are fairly frequent, however, it will scarcely be safe to draw such inferences, but I fancy the disproportion between apparent  $R_2$  and  $R_1R_2$  among  $\eta$ -negatives may soon be significant.

Yours sincerely,