This, in general, will not be the case, for on most soils there is a block difference. In this particular test the ground used had been previously filled in with well mixed soil.   The efficiency for the analysis given in [1] relative to the randomized complete blocks was less than 1.00.

This paper and the previous one show what a long tedious procedure is necessary to analyze the data, when the design does not follow the rules for the construction of the lattice, triple lattice, etc.   The complexity of these methods stresses the importance, to those designing experiments, of not deviating from the established design if the most information is to be secured from the data with simple calculations.

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FURTHER REMARKS ON LINKAGE THEORY IN MENDELIAN HEREDITY

By Hilda Geiringer

Wheaton College

In the following an explicit formula for the distribution of genotypes in case of three Mendelian characters will be given [formula (5)].   The complete discussion of the case $m = 3$ suggests a supplement (as stated in the last paragraph of this paper) to the general limit theorem dealing with m characters.

In an earlier paper[1] recurrence formulae have been derived which furnish the distribution of genotypes in the nth generation if the distribution in the $(n - 1)$th generation and the "linkage distribution" (l.d.) are known.   It was also shown how to "integrate" this system of difference equations so as to determine the distribution in the nth generation directly from that in the 0th generation. This last method, though straightforward, requires however in each particular case quite a few operations.

In case m, the number of Mendelian characters, equals two, an explicit formula for the problem in question had been known.   Denote by $p(x_1, x_2)$,

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[1] Hilda Geiringer, *Annals of Math. Stat.* Vol. 15 (1944), pp.25–57.   The notation in the present Note will be the same as in this paper.