

19th December 1934

Dear Dr Hunt,

I have your letter of November 24th and will do my best to make clear the process of the evaluation of the sum of α mean, for all individuals of the population, of the product Xx between the genetic and the genotypic values of a metrical character.

X is defined as the sum, for all the genes in the organism, of a number of quantities, such as $q\alpha$ or $-p\alpha$. If a particular gene exists in a fraction, p , of the available loci, then the homozygotes for this gene will be assigned the quantity $q\alpha$. The heterozygotes will have $\frac{1}{2}(q-p)\alpha$ and the homozygotes of the allelomorphous gene will have $-p\alpha$. We now proceed to determine the coefficient of α as contributed by two moieties, into which the whole population is divided. One moiety contains all the homozygotes for a certain gene, together with half the heterozygotes. In the product, Xx , any homozygote will contribute $ax\alpha$ to the sum of the products, and each heterozygote will contribute $\frac{1}{2}qx\alpha$ so that the coefficient of $q\alpha$ in the sum of the values of Xx , will be the sum of the values of x for all the homozygotes plus a half the sum of the values of x for all the heterozygotes, or in all, p times the average metrical value in the one moiety. Similarly, the coefficient of $-p\alpha$

will be q times the average value of x in the second moiety. Consequently, all the terms involving α when added together will supply $p q \alpha$ multiplied by the difference between the averages of the two parts. Now this difference is already known to be \bar{a} . Consequently the sum of all the terms involving α is reduced to $p q \bar{a} \alpha$ and the sum for all the ingredients together to $\sum (p q \bar{a} \alpha)$, the summation being taken over all the factors which contribute to the variance.

The demonstration is given only for factors with ~~two~~ ^{two} alleles, but in lecturing on the subject I give it for the general case of multiple allelomorphism, which is not intrinsically more difficult, though naturally it needs a more complex notation.

Perhaps I may add that there is also one little point which often puzzles students, and that is I have arbitrarily and unnecessarily introduced the simplification of evaluating the genetic value as the average rather than the sum of the contributions of the genes at each locus. I think many might find it clearer if I had evaluated the sum, in which case we should have found $\sum (p q \bar{a} \alpha)$ for diploid species & $\sum (p q \bar{a} \alpha)$ for tetraploids, and so on. If we use this convention then for diploids we should evaluate the total increase in fitness, at the top of p 35, as $\sum (\alpha d p)$, and find this to be equal to $W d t$, where W is now evaluated as $\sum (p q \bar{a} \alpha)$.

I need scarcely add that students are greatly helped by concrete examples, e.g. a population mating at random with two or more factors having given effects and possibly interacting

with one another; when they can see for themselves that random mating, by ensuring the mutual independence of the different factors, causes σ^2 and σ^2 to be equal, and so demonstrates very simply the essentially positive character of σ^2 . Such examples are also useful in the conviction they provide that with factor interactions of the kinds with which geneticists are familiar the genetic variance is a rather large fraction of the whole of the variance determined by heredity.

Yours sincerely,

Dr R.H.Hunt,
Department of Zoology,
Michigan State College,
East Lansing