A search for pleiotropic effects of a mutant gene: An exercise in ecological genetics.

**Huber, I.** Fairleigh Dickinson University, Madison, New Jersey. [reprinted from Dros. Inf. Serv. 58: 181-182, 1982].

In studying a population, ecologists often make the simplifying assumption that all members of a population are genetically identical. A large body of recent studies in population genetics, especially with electrophoretic techniques, indicates that this assumption is unrealistic. Ecological genetics is a field that has developed at the boundary of ecology and population genetics and is concerned with the effects of genes (such as those for eye color or body color in *Drosophila*) on biologically important parameters, such as longevity and fertility, as well as aspects of physiology and behavior which may affect viability.

From the viewpoint of the organismic geneticist, there is a major phenotypic effect by which the presence of a gene is identified and a multiplicity of minor effects on many aspects of the anatomy, physiology and behavior of an animal. Collectively, these effects are referred to as pleiotropic. As an example, the sickle-cell gene in homozygotes, in addition to causing sickling of erythrocytes, has an effect on virtually all organ systems (Neel and Schull, 1954). Both phenomena, namely the existence of pleiotropic effects of a mutant gene and the fact that these effects may be important in population dynamics, can be demonstrated with *Drosophila melanogaster*.

**Materials and Methods:** Three groups of *D. melanogaster* will be tested: wild-type, a recessive mutant, and their F<sub>1</sub> hybrid. Students are asked to select a trait unrelated to the major phenotypic effect and test samples of all three groups. Examples of adult traits which have been studied with interesting results are: dry weight, wet weight, longevity (for faster results, deprive flies of food but not water), longevity at elevated temperatures, resistance to standard dose of insecticide, number of eggs laid/female/day, O<sub>2</sub> consumption/gram body weight/hour. Other traits which could be investigated include behavioral characteristics such as walking speed, frequencies of grooming movements and components of courtship and rates of maze-learning ability.

Means for each group will be determined and (depending on the amount of statistical knowledge of the class) statistical tests run. For weights of flies, it is best to group them. For example, weigh four groups of 25 flies of each genotype, expressing the results as mean weight/25 flies.

**Interpretation:** Several kinds of outcomes are possible for this exercise. All of the mutants studied are recessive.

1. All three genotypes have the same mean. In this case, the mutant has no pleiotropic effect on the trait measured. This is entirely possible, though not as interesting, as the other kinds of results.
2. The heterozygote has a mean not significantly different from the wild-type. Since the mutant is completely recessive, the pleiotropic trait parallels the expression of the major phenotypic effect. This is the extreme of the range of values mentioned in #3 (below).
3. The heterozygote mean is closer to wild-type than to the mutant.
4. The heterozygote has a mean intermediate between that of the wild-type and the mutant. Therefore, the trait shows incomplete dominance in contrast to the recessive inheritance pattern of the mutant.
5. The heterozygote is closer to the mutant than to the wild-type.
6. The heterozygote mean is identical with the mutant mean. This is the extreme of the range of values mentioned in #5 (above).
7. The heterozygote mean is more extreme than either homozygotes, a phenomenon called overdominance.

Whether a gene is regarded as dominant, overdominant, incompletely dominant or recessive depends entirely on the criterion by which an individual is classified and is thus relative. The criterion may be the major phenotypic effect, a pleiotropic effect (or amounts of protein products of the genes). For example, by appropriate choice of criteria, the sickle-cell gene can be shown to resemble most of the dominance relationships listed above (see Mange and Mange 1980: 189-193 for a useful discussion).