Carmody, George. Columbia University. Two unusual strains of the *D. willistoni* sibling species group.

Two new strains of the *D. willistoni* sibling species group have been found that provide a potential bridge between the gene pools of *D. equinoxialis* and *D. paulistorum*. The first strain was collected near Girardot, Colombia. It produces fertile offspring with the following three strains of *D. paulistorum*: Angra (Andean-South Brazilian Race), Maranguape (Andean South-Brazilian Race), and Salvador (Centro-American Race). This last cross produces fertile offspring only when Girardot females are mated with Salvador males; the reciprocal cross produces no offspring at all. No offspring are produced in crosses of Girardot with 13 geographical strains of *D. equinoxialis*. However, crosses with three other *D. equinoxialis* strains (Belém O, Içana, and Puerto Rico) produce offspring which are sterile - both males and females.

The second strain, called Belém K, was collected in Belém, Northeastern Brazil. It is completely interfertile with the Girardot strain. Belém K produces fertile offspring with at least six geographical strains of *D. equinoxialis*: Belém O, Içana, Puerto Rico, Simla I, Skeldon, and Tefé. Crosses of Belém K with ten other strains of *D. equinoxialis* give no offspring. Belém K is interfertile with only one strain of *D. paulistorum*: Maranguape. No other cross between Belém K and *D. paulistorum* produces even sterile offspring.

Preliminary sexual isolation data that was gathered using the "male choice" method shows both strains about as isolated from *D. paulistorum* as from *D. equinoxialis*, with the Girardot strain slightly more highly isolated from *D. equinoxialis* than from *D. paulistorum* and the Belém K strain slightly more isolated from *D. paulistorum* than from *D. equinoxialis*. This high sexual isolation together with the fact that these two strains are geographically separated suggests that those crosses which can be obtained in the laboratory almost certainly do not occur in nature.

The salivary chromosomes of these two strains show polymorphism for inversions in chromosomes II and III. The banding pattern of chromosome III is unique in each of these two strains and both are different from that of either *D. paulistorum* or *D. equinoxialis*. In addition the salivary chromosomes of the hybrids have many inversions in all three chromosomes. Chromosome pairing in these hybrids is good, with only short regions apparently unpaired.

Mapping of the inversions and unpaired sections is currently in progress.

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Mukai, T. National Institute of Genetics, Japan. Position effect of spontaneous mutant polygenes controlling viability in *D. melanogaster*.

Spontaneous polygenic mutations affecting viability were accumulated under the minimum pressure of natural selection in 104 second chromosomes which were derived from a single second chromosome. In Generations 25, 32, 52, and 60, homozygous viabilities of these chromosome lines were estimated. In addition the viabilities of flies carrying random combinations of these chromosomes were estimated and the correlation coefficient between the sum of homozygote viabilities and the corresponding heterozygote viability was calculated for each generation. The estimated values were positive and highly significant.

On the other hand, in Generations 32 and 60, the viabilities of heterozygotes between these experimental chromosomes and a chromosome supposed to be identical to the original chromosome were estimated and the correlation coefficient between homozygote and heterozygote viabilities was calculated for each generation. The results showed significantly negative values. From these results it can be said that newly arising mutant polygenes clearly show overdominance in homozygous genetic background when the chromosomes carrying them are combined with the original normal chromosome, but are heterozygously deleterious in trans-phase heterozygotes. These phenomena are significant in clarifying the mechanism by which natural populations carry genetic variation.

The results are highly reliable because those conclusions were drawn on the basis of counting approximately 3 million flies. (This work has been supported by PHS grants GM-7836 and RH-34).