Polygenic Analysis of Larval Locomotor Activity in
Drosophila melanogaster

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The genetic basis of larval locomotor activity in Drosophila melanogaster was studied by comparing four strains that differ significantly in activity levels. The inbred wild-type strain Canton-S had the lowest activity level, while the relatively heterogeneous wild-type OK1 genotype had the highest. Activities could not be explained simply in terms of a difference in catecholamine levels. The analysis of heterozygous whole-chromosome effects suggested that chromosome 2 carried modifiers that increased activity, but an interchromosomal interaction balanced its effect in OK1. A sex-limited interaction countering an X-chromosome effect in Canton-S was also consistent with the conclusion that stabilizing interactions are an important part of the genetic control of this behavioral phenotype.

KEY WORDS: polygenes; chromosome interaction; larval activity; dopamine; norepinephrine.

INTRODUCTION

Although major mutations have been used extensively to analyze behavior in Drosophila (Grossfield, 1975; Hall and Greenspan, 1979; Erhman and Parsons, 1981; Burnet and Connolly, 1981), polygenic variation also offers powerful ways to study the expression of behavioral phenotypes. It is quite clear that many traits, including various activity measures (Connolly, 1966; Hay, 1972; Burnet et al., 1977; van Dijken et al., 1979), mating...
speed (Fulker, 1966), duration of copulation (Manning, 1961; MacBean, 1970, in Parsons, 1973), phototaxis (Dobzhansky et al., 1975), geotaxis (Hirsch, 1967), and preening (Hay, 1972), have a major polygenic component. While detailed polygenic analysis has not been feasible in most instances, one interesting result to come from some studies is that nonallelic interactions are frequently important in determining behavioral expression.

In adult locomotor activity (Hay, 1972; van Dijken et al., 1979) and in larval feeding activity (Burnet et al., 1977), for example, nonallelic interactions were often found to be important, though dominance and sex-linked modifiers also played a major role in distinguishing high and low activity strains. Nonallelic interactions and dominance are stabilizing forces in such a genetic architecture. We were interested in determining the extent to which similar buffering systems also contribute to the polygenic basis of larval locomotor activity. These stabilizing forces are a strong indication that the trait has undergone selection for some optimized phenotypic expression.

Not very much is known about the genetic control of Drosophila larval locomotion. Sewell et al. (1975) showed that larval locomotion in selected lines is not correlated with other measures of behavior, such as adult locomotion or larval feeding. Yet it is still possible that in unselected genotypes some components of the genetic system are pleiotropic, having effects upon movement in general. One might ask, for example, whether neurotransmitter levels affect larval locomotor activity in the same way they appear to influence adult activity (Tunnicliff et al., 1969).

We have, therefore, measured heterozygous whole-chromosome effects in strains that differed significantly in larval locomotor activity. Some evidence of balancing interactions was found, supporting the idea that genetic stabilizing systems contribute to the amount of activity. On the other hand, dopamine and norepinephrine levels were not correlated with larval locomotor activity, suggesting that, if they play a part in determining general activity levels, some other variable such as turnover rates may be more important than catecholamine levels per se.

MATERIALS AND METHODS

Larval locomotor activity was measured in four unselected strains of Drosophila melanogaster. OK1 is a wild-type stock collected in Oklahoma City, Oklahoma, in 1973 as an isofemale line (Woodruff and Thompson, 1977) and is maintained by mass transfers; Canton-S is an inbred wild-type stock that has been in laboratories for many years (our culture