Temporal and spatial trends in allozyme frequencies in house fly populations, *Musca domestica* L.*

W. C. Black IV and E. S. Krafsur

Department of Entomology, Iowa State University, Ames, IA 50011, USA

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Summary. Allelic and genotypic frequencies were sampled from a single age class of the common house fly, *Musca domestica* L., at five farms on six dates from July 6 to October 12, 1982. Allozymes at six loci were resolved with vertical polyacrylamide gel electrophoresis. No consistent departures from random mating were detected. No consistent linkage disequilibrium was observed. Allele frequencies at the farms changed in independent and unpredictable ways. Gene frequencies at the five farms were initially divergent, converged in midsummer, and then progressively diverged. The divergence occurred in mid-August when fly populations were large. Variation in gene frequencies at adjacent farms accounted for a large proportion of the variance in allele frequencies among all farms. These observations are consistent with the hypothesis that allele frequencies in young adult flies reflected the habitat in which they matured as larvae.

Key words: Breeding structure - Allozymes - Linkage disequilibrium - *Musca domestica*

Introduction

The house fly, *Musca domestica* L., enjoys a cosmopolitan distribution and is genetically one of the best known insects (Milani 1975). In temperate climates, populations seasonally become dense and the age structure and dynamics vary continuously (Krafsur et al. 1985; Krafsur 1985). Its broad distribution and capacity to colonize rapidly a wide variety of habitats suggest that house flies are greatly adaptive. In a study of genetic variability and ecological genetics of house flies, we electrophoretically surveyed 51 loci distributed among 26 enzyme systems and found that 40% of loci were polymorphic (Black and Krafsur 1985a). Observed and expected heterozygosities were 0.0981 and 0.1148, respectively. These approximated the heterozygosity estimates made electrophoretically in other Diptera (excluding *Drosophila* spp) (Graur 1985).

We report here the results of work on the spatial and temporal variation in gene frequencies in flies sampled at farms in central Iowa. Gene frequencies were surveyed in flies of the youngest adult age group. These were assumed to represent flies which had matured at each farm. Flies were sampled from a variety of farms that differed qualitatively in the breeding resources they offered reproducing fly populations, thus presenting the possibility of local adaptation. We sought to determine if gene frequencies at six loci were homogeneous among flies emerging at different farms and if frequencies remained constant through time.

Materials and methods

Field procedures

Adult house flies were captured with sweep nets at five farms near Ames, Iowa (Fig. 1), that included a beef cattle farm, a swine farrowing facility, a dairy farm, a sheep farm, and a pork confinement unit. House fly larvae utilized for resources the dung and spilled feed.

Flies were collected for electrophoresis and age grading on six sampling occasions, from early July until mid-October, 1982. In each collection, adults were captured with sweep nets, placed in cages, returned alive to the laboratory, frozen, and stored at −70°C. Later, female flies were brought individually to room temperature, dissected in 0.75% saline and age graded.
Age grading were calculated by dividing the number of previtellogenic flies by the number of nulliparous and parous flies. The proportions parous were calculated by dividing the numbers parous by the numbers of nulliparous and parous.

Electrophoretic procedures

For each sampling date and location, 50 previtellogenic and vitellogenic nullipars (i.e., flies 0–5 days old) were examined electrophoretically. After age grading, nullipars were put directly into grinding buffer and frozen. Electrophoretic methods were described in Black and Krafsur (1984, 1985a). Genotypes of flies were determined at six loci: Alcohol Dehydrogenase (Adh), Amylase + (fast) (Amy), Glutamate Oxaloacetate Transaminase (Got), Octanol Dehydrogenase (Odh), Phosphoglucomutase (Pgm), and Superoxide Dismutase (Sod). We found 26 alleles distributed among the 6 loci. Sod was the only diallelic locus. Electrophoretic assays were made on a total of 1,500 females representing 30 collections.

Analysis of data

“Linkdis” (Black and Krafsur 1985b) was used to calculate linkage disequilibrium coefficients and check for significance. “Genestats” (Black and Krafsur 1985c) was used to calculate allele frequencies and perform chi-square tests. Chi-square tests for significant departures from random mating and Wright’s F-statistics were estimated in “Genestats” according to the methods of Weir and Cockerham (1985). Contingency Chi-square tests on allele frequencies were computed following Workman and Niswander (1970).

Wright’s (1978) hierarchical analysis of breeding structure for a subdivided population was used to identify sources of spatial differentiation in gene frequencies. In the analysis, sampling units are grouped into subpopulations according to their relative distances from one another. Farms (F) were the sampling units. They were grouped into subpopulations (S), which formed the total population (T). Farms were grouped into subpopulations according to their relative proximities (Fig. 1). The swine farrowing facility and dairy farm constituted a subpopulation, the southern pork and sheep farms formed a second and the beef nutrition farm was treated as a third.

Three variance components were calculated. The variance in allele frequencies among farms (Fst) is a function of the variance in allele frequencies among subpopulations (Fst) and the variance in allele frequencies among farms in subpopulations (Ffs). The three statistics are related by the equation,

\[ F_{\text{ST}} = F_{\text{ST}} + F_{\text{FS}} - (F_{\text{ST} \times F_{\text{FS}}}) \]

Where flies are completely panmictic, all F-statistics are zero. When flies produced at farms are differentiated by selection or genetic drift then allele frequencies within the same subpopulation will be heterogeneous and \( F_{\text{ST}} > F_{\text{FS}} \). If flies produced within subpopulations are panmictic and subpopulations are differentiated because of distance, local selection pressures, barriers to mating, etc., then \( F_{\text{ST}} \geq F_{\text{FS}} \).

Correlation coefficients between allele frequencies and house fly densities were calculated by using SAS (1982). These coefficients were converted to a normalized scale with Fisher’s z-transformation. Chi-square tests for the homogeneity of z-values were computed following the procedure in Sokal and Rohlf (1969). A mean z-value of all possible correlations was calculated and back-transformed to estimate a common correlation.