McCune, Thomas. University of Hawaii, Honolulu, Hawaii. Amylase isozymes in natural populations of Drosophila melanogaster.

The terminology of the amylase isozymes has previously been described by Doane (DIS 41:93) and by Kikkawa (Jap. J. of Genetics 39:401-411). These isozymes are determined by a series of multiple alleles found on the second chromosome. The fastest migrating band towards the anode of the gel is called $Amy^{one}$ with slower migrating bands having the superscripts 2, 3, 4, and 6. The eight alleles which have been reported in natural populations are $Amy^{1}$, $Amy^{1,2}$, $Amy^{1,3}$, $Amy^{1,4}$, $Amy^{1,6}$, $Amy^{2,6}$, $Amy^{3,6}$ and $Amy^{4,6}$. Recently, Bahn (Hereditas 58:1-12) isolated another allele ($Amy^{2,3}$) from a Bennett population cage which was also found in the natural populations of this study.

The technique is described in a technical note in this issue. After electrophoresis the 7% cyanogum gel is soaked in a 1% soluble starch solution and then stained with a KI-$I_2$ solution. This permits large numbers of single flies to be tested in a relatively short period of time.

The natural populations examined in this investigation were from Texas and Wisconsin. The flies from Texas were collected and sent to Hawaii by Judd and Denell and those from Wisconsin were collected by Hiraizumi. These flies were typed for amylase and several different chromosome lines having different amylase alleles were isolated. The populations were polymorphic with a total of 5 alleles being found in both populations. The $Amy^{1}$ gene was most common. An estimate of the gene frequencies of the alleles is given in Table 1.

Table 1. Frequency Estimate of Amy Alleles

| Allele | Texas population | Wisconsin population |
|---|---|---|
| $Amy^{1}$ | 0.84 | 0.74 |
| $Amy^{1,3}$ | 0.12 | 0.12 |
| $Amy^{2,3}$ | 0.01 | 0.09 |
| $Amy^{1,2}$ | 0.02 | 0.04 |
| $Amy^{1,6}$ | 0.01 | 0.01 |
| Total number of flies typed in each population | 176 | 60 |

As can be seen from the table, the frequencies of the different alleles are quite similar in the two populations with the exception of the $Amy^{2,3}$ allele being considerably more frequent in the Wisconsin population than in the Texas population.

Before any viability tests, the background of the chromosome lines was made homogenous by backcrossing males to cn bw females (fixed for $Amy^{1}$) for several generations. The chromosomes to be tested were put over the SM5 balancer chromosome (fixed for $Amy^{1}$). In regard to the populations, matings were made within the Texas population (T x T), within the Wisconsin population (W x W), and between populations (T x W). In all matings the chromosomes being tested were from different chromosome lines. The preliminary analysis of the viability data does not seem to indicate any clear-cut difference between the viabilities of the various amylase types. However, differences are apparent when the total number of offspring are compared with the amylase genotype of the female. This is especially obvious for $Amy^{1}$ and $Amy^{1,3}$ which is summarized in Table 2.

From this table it can clearly be seen that females bearing the $Amy^{1,3}$ containing chromosome have a markedly higher average than those bearing the $Amy^{1}$ chromosome regardless of whether it was derived from the Texas, Wisconsin, or interpopulational origin. At present fertility tests which do not use the SM5 chromosome are being conducted. These will permit a direct comparison of $Amy^{1,3}$ homozygotes, $Amy^{1}$ homozygotes, and $Amy^{1,3}/Amy^{1}$ heterozygotes. The fertility of the $Amy^{1,3}$ homozygote will be especially interesting to compare with the other two. In addition to this, fertility tests using some of the rarer alleles will also be done. This work was supported by Grant GM 15421 from the U.S. National Institute of Health.

Table 2. Number of offspring produced. Mating: $\frac{3\ ♀\ +}{Cy\ Amy^1}$ x $\frac{3\ ♂\ +}{Cy\ Amy^1}$

| Mating type ♀ | ♂ | No. of crosses | No. of flies | Av. | Mating type ♀ | ♂ | No. of crosses | No. of flies | Av. |
|---|---|---|---|---|---|---|---|---|---|
| Origin of populations (T x T) | | | | | | | | | |
| 1,3/1 | 1/1 | 62 | 5442 | 87.77 | 1/1 | 1/1 | 129 | 9293 | 72.03 |
| 1,3/1 | 1,3/1 | 145 | 12031 | 82.97 | 1/1 | 1,3/1 | 54 | 4230 | 78.33 |
| Total | | 207 | 17473 | 84.41 | Total | | 183 | 13523 | 73.89 |
| Origin of populations (W x W) | | | | | | | | | |
| 1,3/1 | 1/1 | 93 | 7411 | 79.68 | 1/1 | 1/1 | 115 | 7356 | 63.97 |
| 1,3/1 | 1,3/1 | 143 | 11545 | 80.73 | 1/1 | 1,3/1 | 104 | 7232 | 69.53 |
| Total | | 236 | 18956 | 80.32 | Total | | 219 | 14588 | 66.61 |
| Origin of populations (T x W) | | | | | | | | | |
| 1,3/1 | 1/1 | 135 | 11108 | 82.28 | 1/1 | 1/1 | 110 | 8145 | 74.04 |
| 1,3/1 | 1,3/1 | 133 | 11995 | 90.18 | 1/1 | 1,3/1 | 106 | 7905 | 74.58 |
| Total | | 268 | 23103 | 86.20 | Total | | 216 | 16050 | 74.30 |

Alexandrov, I. D. Mira st. 9, ap. 37 Obninsk-I, Kaluga Region, USSR. Comparative mutability of wild-type alleles at the specific loci in D. melanogaster.

$\gamma$ -irradiation-induced mutability of the loci $y^+$, $w^+$, $b^+$, $cn^+$ and $vg^+$ in post-meiotic germ cells of the males from a mass-bred wild-type stock, "D-18", was studied. The methodical details of the detection, classification and analysis of the mutants have been described previously (DIS 44). Altogether, 1161 males were irradiated and 66,614 $F_1$ females and males were examined among which 121 mutants were found.

The results are shown in table 1. The overall mutation frequencies include cases of mutant $F_1$ females and males which were inviable, sterile or lethal. Point mutation frequencies include cases of mutants which were kept in stocks. The first and the second broods represent all sperm and spermatids, respectively.

Table 1

| Brood | Mutations | Mutation frequencies in loci (x $10^{-7}$/r) y | w | b | cn | vg |
|---|---|---|---|---|---|---|
| First | Overall | .59 | 1.49 | .34 | .88 | 1.52 |
| | Point | .29 | .59 | .04 | .14 | .34 |
| Second | Overall | - | 4.09 | .63 | 1.59 | 2.71 |
| | Point | - | 1.88 | .15 | .15 | .15 |

In the table 2, the average point and overall mutation frequencies of those loci for all post-meiotic stages germ cells of the males from two studied wild-type stocks "D-32" and "D-18" are compared.

Table 2

| Stocks | Mutations | Mutation frequencies in loci (x $10^{-7}$/r) y | w | b | cn | vg |
|---|---|---|---|---|---|---|
| D-32 | Overall | .34 | 1.81 | .19 | 1.00 | 2.52 |
| | Point | .14 | .21 | .07 | .37 | .37 |
| D-18 | Overall | .45 | 2.12 | .41 | 1.05 | 1.80 |
| | Point | .25 | .91 | .07 | .15 | .30 |