Table 3. Estimation of P_∞ between Crete-Parnes populations.

	O_{ST} / O_{3+4+8} x O_{ST} / O_{3+4+8}	O_{3+4} x O_{ST} / O_{3+4+8}	O_{3+4} x O_{3+4}	Total
total no. of crosses	174	913	417	1553
no. allelic crosses	1	2	0	3
allelism frequency	0.00575 ±0.00573			0.0019 ±0.0011

Table 4. Estimation of Q, P, P_∞, p, p_∞, n and N_em in Crete-Parnes population.

		Q	P	P_∞	p	p_∞	n	N_em
Crete	uncorrected Q, P, P_∞	0.187	0.00540	0.00190	0.00505	0.00155	645	344
	corrected Q, P, P_∞	0.242	0.00704	0.00575	0.00568	0.00439	228	573
	corrected Q, P	0.242	0.00704	0.00190	0.00659	0.00145	689	175
Parnes	uncorrected Q, P, P_∞	0.248	0.00950	0.00190	0.00904	0.00144	694	115
	corrected Q, P	0.284	0.01449	0.00190	0.01396	0.00137	730	59

Diamantopoulou-Panopoulou, E. and H. Bacoulas. Agricultural College of Athens, Votanicos, Greece. "Sex ratio" in D. obscura.

One isofemale line of D. obscura from a Greek natural population (Mt. Parnes) produced offspring of only female sex; this continued for many generations (the male parent was taken from an obscura stock). A treatment was undertaken to clarify if this condition was similar to that of "sex ratio" in D. bifasciata. After penicillin G was given "per os" for one or two generations, the culture produced both sexes (males and females vs. females only) progressively to fifty-fifty percent. After enough time the culture began to produce again only female flies.

An attempt to find the causal factor, spirochaete in the haemolymph of the female fly, gave no results.

Doane, W.W. Arizona State University, Tempe, Arizona. Midgut amylase activity patterns in Drosophila: nomenclature.

A control gene for tissue specific expression of α-amylase in the adult posterior midgut (PMG) in D. melanogaster was located at 2-80± by Abraham and Doane (1976, 1978). This gene, called map for midgut activity pattern, lies approximately two crossover units to the right of the structural gene(s) for the enzyme (Amy). Strain specific differences in the regional expression of amylase in the PMG were attributed to allelic differences at the map locus. Three spatially different PMG patterns were found in an initial survey of isogenic laboratory strains. These patterns, which reflect the cellular dis-

tribution of amylase, were designated A, B and C (top three patterns in Fig. 1); they apparently correlate with alleles map^A, map^B and map^C, respectively. While clear-cut recombination data exist for map^A and map^C, an exact definition of the postulated map^B allele has not yet been achieved. Recombination data suggesting the existence of a map^B allele (Abraham and Doane, unpublished) are somewhat ambiguous because of overlapping phenotypes between heterozygotes bearing the so-called map^B allele and homozygous classes for it and other map alleles. An attempt is being made to resolve this situation.

Subsequent to the initial survey which revealed the above three PMG patterns, a search was made (Doane 1977a, b) for variability in the expression of amylase activity in the anterior midgut (AMG). (The highly acidic middle midgut region does not display activity.) Included in the search were 7 laboratory "wild" strains received from Dr. Bruce Wallace; these had been maintained at Cornell University for varying lengths of time up to 20 years. The strains derived from flies collected around the world, including the following localities: Capetown (CA 1), Chile (SC 1), Kentucky (4 B), New York (1 A, 1 B), South Africa (KSA 2), and Spain-France (PYR 3). An additional 49 newly established strains from single females collected in Puerto Rico in February, 1976, were provided by Dr. Donald F. Poulson of Yale University. The array of midgut activity patterns displayed by adults from these "wild" strains is diagrammed in Fig. 1.

A total of 15 different patterns is shown in Fig. 1, including five different AMG patterns. The three PMG patterns originally described were again found, but in various combinations with the AMG patterns. As pointed out by Abraham and Doane (1978), the AMG may be subdivided into three activity regions and the PMG into two such regions. The different patterns reflect these subdivisions, the precise boundaries of which remain to be clarified. Polymorphism for midgut activity patterns was common among the various strains surveyed, especially those from Cornell. All strains displayed Amy^1 phenotypes for the structural gene region, except the SC 1 strain (= $Amy^{2,3}$).

Because of the regional variability in expression of amylase activity in adult flies, a system of nomenclature for midgut patterns was developed, based on known phenotypes (Doane 1978). That system is presented in Fig. 1. Phenotypic classes are listed on the left. The three subdivisions in the AMG are numbered 1, 2 and 3 in an anterior-posterior direction. A strain with activity in all three subdivisions is classified as AMG-123, while another with activity in the first two subdivisions but little or none in the third subdivision is typed as AMG-120. "0" thus indicates no activity or almost no activity on the basis of the whole-mount starch-iodine technique used to prepare the patterns (Abraham and Doane 1978). The numerals 1, 2 and 3 indicate not only well defined amylase activity but the regional location of that activity as well. Five different AMG classes are so defined: AMG-123, AMG-120, AMG-103, AMG-100 and AMG-000. The PMG displays only two potentially active subdivisions according to this system of nomenclature. Three patterns were found: PMG-12, PMG-10 and PMG-00. These classes correspond to the A-, B- and C-patterns, respectively, of Abraham and Doane. The three PMG patterns were found in all possible combinations with the five AMG patterns, accounting for the total array of 15 adult patterns in the above survey. It seems likely that additional AMG patterns may still be found in D. melanogaster, such as AMG-023 or AMG-003, unless some unknown developmental restriction limits their appearance.

In most isogenic strains examined, the larval midgut pattern differs from that of the adult for a given strain. Nevertheless a nomenclature similar to that in Fig. 1 may be used for larval patterns as well, although the relative proportions for larval patterns differ somewhat from those of adults. In D. melanogaster, the most common larval pattern is AMG-003, PMG-12 among strains surveyed (e.g., see Doane 1969). The nomenclature in Fig. 1 may also be used for other species of Drosophila, c.f. D. hydei (Doane 1969) and D. pseudoobscura (Powell and Lichtenfels 1979).

Care must be taken in classifying strains according to their adult patterns because of an age-dependent "switch" which may occur in regions designated as having little or no activity in young flies. These "0" regions typically become fully active in older flies (Doane, unpublished). Thus, in D. melanogaster, the AMG-123, PMG-00 pattern (= "C-pattern") changes to the AMG-123, PMG-12 pattern ("A-pattern") at approximately 14 days of age in adult females. This change-over at about two weeks of age is typical for most of the isogenic strains of D. melanogaster examined, but not all. The time of the "switch" in amylase expression is strain-specific, some strains showing it earlier in adult life than others (e.g., 3-4 days or 7-8 days). In an isogenic line derived from the Cornell CA 1 strain, the "switch" does not seem to occur. Here, flies as old as 21 days retain the AMG-000, PMG-00 pattern; midgut preparations beyond that age are technically not feasible to make. The strain-specific "switch"

lends further credence to the hypothesis (Abraham and Doane 1978) that the midgut amylase activity patterns may be controlled by "temporal genes". A similar age-dependent transition in midgut patterns was independently described for D. pseudoobscura by Powell and Lichtenfels (1979) who noted that the exact time of the change-over is temperature dependent. No strain-specific differences in the age of onset of the transition were reported thus far in that species.

At least two control loci appear to control the midgut activity patterns in adults of D. melanogaster. The original map locus for the PMG has now been distinguished by recombination analysis from another locus which controls the AMG (Doane, unpublished; Table 1). Accordingly, the genetic symbols indicated on the right side of Fig. 1 are proposed. The first map gene described may now be called map-PMG with superscript numbers for alleles complementing the phenotypic classes, i.e., map-PMG^{12} (= map^{A}), map-PMG^{10} (= map^{B}), and map-PMG^{00} (= map^{C}). The second locus, map-AMG, is tentatively placed to the right of map-PMG on chromosome 2R, based on the preliminary data shown in Table 1. Recombination data exist for those genotypes indicated by an asterisk in Fig. 1. All other proposed genotypes have been deduced from these data and the 15 adult midgut phenotypes diagrammed and, accordingly, must be considered speculative until additional data are available.

Figure 1. Diagram of adult midgut amylase activity patterns found among isogenic and "wild" strains of D. melanogaster. Each horizontal line represents a midgut extending from its anterior or cardia end (left) to its posterior end (right) where Malpighian tubules attach. Thickened, black regions within the anterior midgut (AMG) and posterior midgut (PMG) are subdivisions expressing amylase activity. Other regions display little or no activity in young flies (including the MMG). Phenotypic classes are listed on the left, with corresponding homozygous genotypes on the right. Asterisks indicate which of the proposed genotypic symbols are supported by genetic data. The linear order of the two loci is not implied.

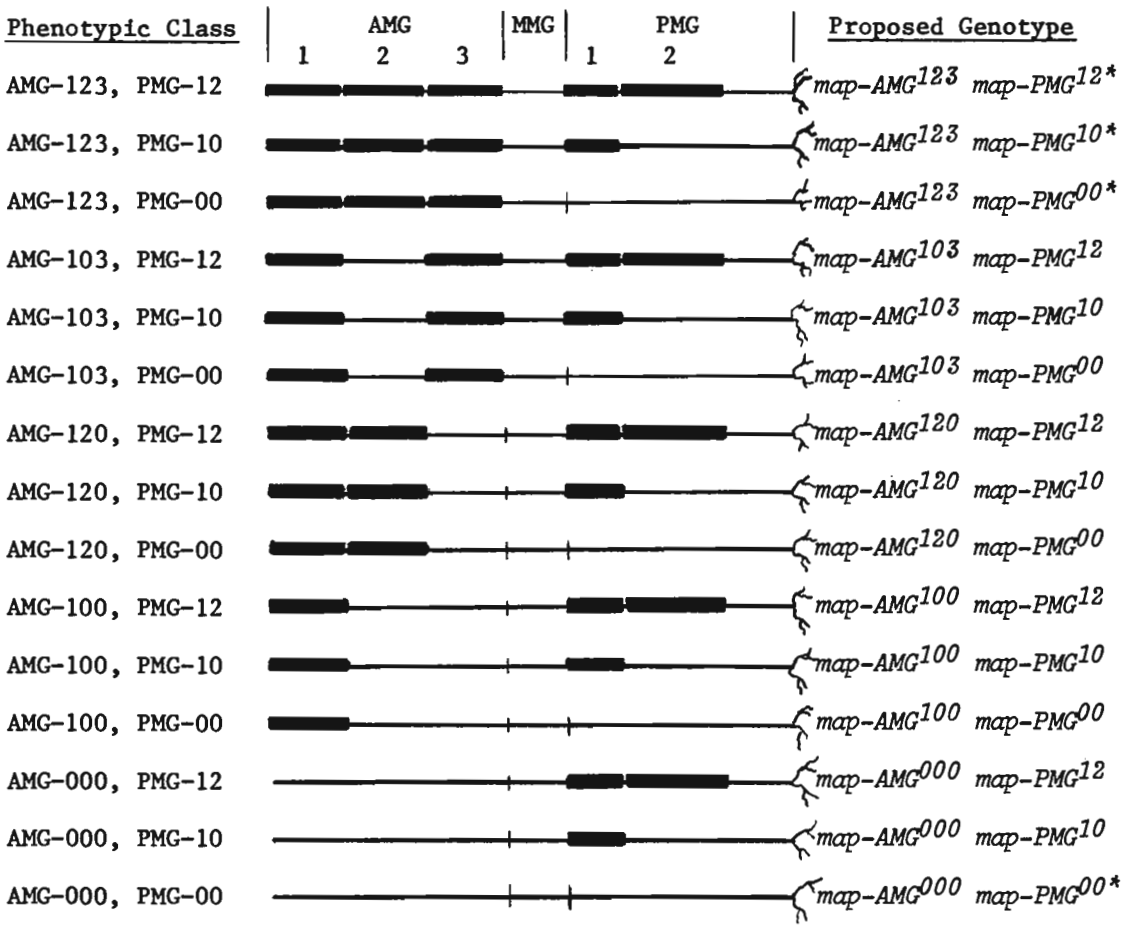


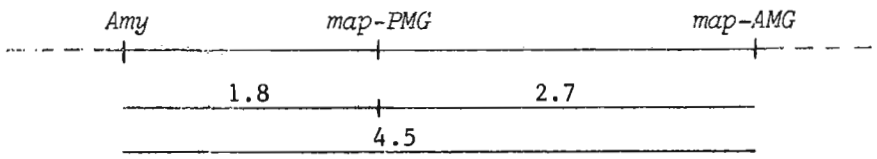
Table 1. Recombination analysis revealing two separable loci, *map-AMG* and *map-PMG*, which control the tissue-specific expression of amylase in the adult AMG and PMG, respectively, in D. melanogaster.

Amy^{1} $map\text{-}AMG^{000}$ $map\text{-}PMG^{00}$ ♀ x $Amy^{1,6}$ $map\text{-}AMG^{123}$ $map\text{-}PMG^{12}$ ♂
(= *iso-CA 1*) (= $Amy^{1,6}$ map^{A})

F_1 ♀ x Amy^{1} $map\text{-}AMG^{000}$ $map\text{-}PMG^{00}$ ♂

Female Progeny

	Amylase	Midgut Pattern	Number (N = 215)
Parental:	1,6	AMG-123, PMG-12	106
	1	AMG-000, PMG-00	102
Recombinant:	1,6	AMG-000, PMG-00	1
	1	AMG-123, PMG-12	2
	1,6	AMG-000, PMG-12	1
	1	AMG-123, PMG-00	3



This work was supported by NIH grants GM-18729 and GM-25255; it was mostly carried out at Yale University. I wish to thank Drs. Wallace and Poulson for the strains surveyed and Dr. J. R. Powell for providing a preprint of the paper on D. pseudoobscura.

References: Abraham, I. and W.W. Doane 1976, Genetics 83:s1; Abraham, I. and W.W. Doane 1978, Proc. Natl. Acad. Sci. USA 75:4446; Doane, W.W. 1969, in RNA in Development, E.W. Hanley, ed., p. 73, Univ. Utah Press, Salt Lake City; Doane, W.W. 1977a, Genetics 86:s15; Doane, W.W. 1977b, J. Cell Biol. 75(2, pt. 2):147a; Doane, W.W. 1978, Int. Conf. Mol. & Devel. Biol. Insects, Crete, Abstracts, p. 45; Powell, J.R. and J.M. Lichtenfels 1979, Genetics, in press.

Espinet, S. and M.L. Tracey. Florida International University, Miami. Detection of differences in the element patterning of D. melanogaster mating behavior.

The difficulties inherent in quantitatively measuring differences in the behavior of Drosophila are well known (Bastock and Manning 1955; Bastock 1956). However, careful description of behaviors, including an account of their patterning in time permits quantification of within and between strain variation. We report a technique in which all possible triplets of behavioral elements which occur at frequencies greater than 1% are graphically overlain to produce a standard sequence. Comparisons of graphical representations indicate both interpopulation and intrapopulation variation.

$X{\cdot}Y^{L}/Y^{S}y+$ males outcompete $X{\cdot}Y^{L}/Y^{S}$yellow males in female choice experiments where all females are $X{\cdot}Y^{L}/X{\cdot}Y^{L}$ ($P<0.001$); and $X{\cdot}Y^{L}y+/Y^{S}$ males outcompete X·/Y males (Tracey and Espinet 1976). To test the hypothesis that the observed differences reflect alterations in the sequence and frequency of courtship elements, pairs of flies were observed and courtship elements were recorded. Recordings were made with a Bell telephone push-button key board coupled