When after 15 min incubation in the medium containing ecdysone and ethanol the induction of puffs in 87A and 87C begins, the small puff in 87B can be seen (Fig. 2a).

The new way, thus, is proposed for the induction of puffs in 87A, 87C and 93D, which are distinctive in their giant sizes and delay time of development. Inducing agents seem to be 20-OH-ecdysone (7.4×10^{-6}M) and 8% ethanol altogether since neither the former, nor the latter added separately do not induce these puffs. It is unclear whether the composition of the incubation medium is important for the induction of the giant heat-shock puffs. It is to be noted that when the multicomponent medium used in the experiments was changed by the simple salt Effrussi-Beadle's one (Ephrussi & Beadle 1936), the adding of 20-OH-ecdysone and ethanol also induced the heat-shock puffs though they had smaller sizes. It is unknown so far what the giant sizes of this puff are caused by: the increase of transcription or transport delay. The giant puffs incorporate ^{3}H-uridine actively, but quantitative analysis of labelling intensity and the rate of RNA transport has not been performed.

The mechanism underlying the induction of the giant puffs is unclear. Of interest is the fact that ecdysterone and ethanol significantly increase the activity of catalase, which is located in the mitochondria (Best-Belpomme & Ropp 1982). The giant puffs may arise as a result of drastic disturbance of mitochondrial function. This appears plausible because the heat-shock puffs can be induced by injection of the supernatant of heat-shock mitochondria (Ashburner & Bonner 1979).

The proposed technique can be useful at the investigation of control of heat-shock gene activity.

References: Ashburner,M. & J.J.Bonner 1979, Cell 17:241-254; Poluektova,E.V. V.G.Mitrofanov, & V.T.Kakpakov 1980, Ontogenez(USSR) 11:175-180; Ephrussi,B. & G.B.Beadle 1936, Amer. Naturalist 70:218; Best-Belpomme,M. & M.Ropp 1982, Eur.J.Biochem. 121:349-355.

Yardley, D.G. Clemson University, Clemson, South Carolina. Amylase midgut activity patterns in third instar larvae of Drosophila pseudoobscura.

Third instar larvae have been examined for amylase midgut activity patterns in two strains isochromosomal for the third chromosome and in 40 isofemale lines collected from a population at Bryce Canyon, Utah. Dissections and staining were carried out as described by Abraham & Doane). Amylase activity, seen as a cleared area against a dark blue background, was observed in the anterior midgut and posterior midgut regions. In most cases this activity is lower than that observed in adults. In the anterior midgut region, two subregions of activity were observed; in the posterior midgut region, three subregions of activity were observed (Fig. 1). Individuals showed considerable variability as to which subregions had activity, with greater variability observed in the posterior midgut region than in the anterior midgut region.

Table 1. Third instar midgut activity patterns resulting from genetic crosses between two isochromomal strains.

Cross	Midgut Activity Patterns		Observed No.
	AMG	PMG	
$Amy^{1.0/1.0}$ x $Amy^{1.0/1.0}$	00	100	14
	00	000	2
	00	023	1
	00	123	1
$Amy^{.84/.84}$ x $Amy^{.84.84}$	00	123	12
	00	100	13
	00	120	1
$Amy^{1.0/1.0}$ x $Amy^{.84/.84}$	00	100	14
	00	000	1
	00	123	1
	00	103	1

Figure 1 shows the approximate regions and subregions of activity as well as some of the variants observed. Letting "0" designate the lact of activity in a particular subregion, the numbers "1,2,3" designate activity in subregions 1, 2 and 3, respectively. Table 1 presents the results of genetic crosses using the two isochromomal strains. One strain was isogenic for the $Amy^{.84}$ allele and the other isogenic for the $Amy^{1.0}$ allele. Several points can be made about these data. First, the AMG patterns are the same in both strains and it appears to be a "true-breeding" phenotypic trait. Second, there is no simple Mendelian pattern evident in the PMG data. Third, the PMG data implies that whatever is the genetic basis for the PMG

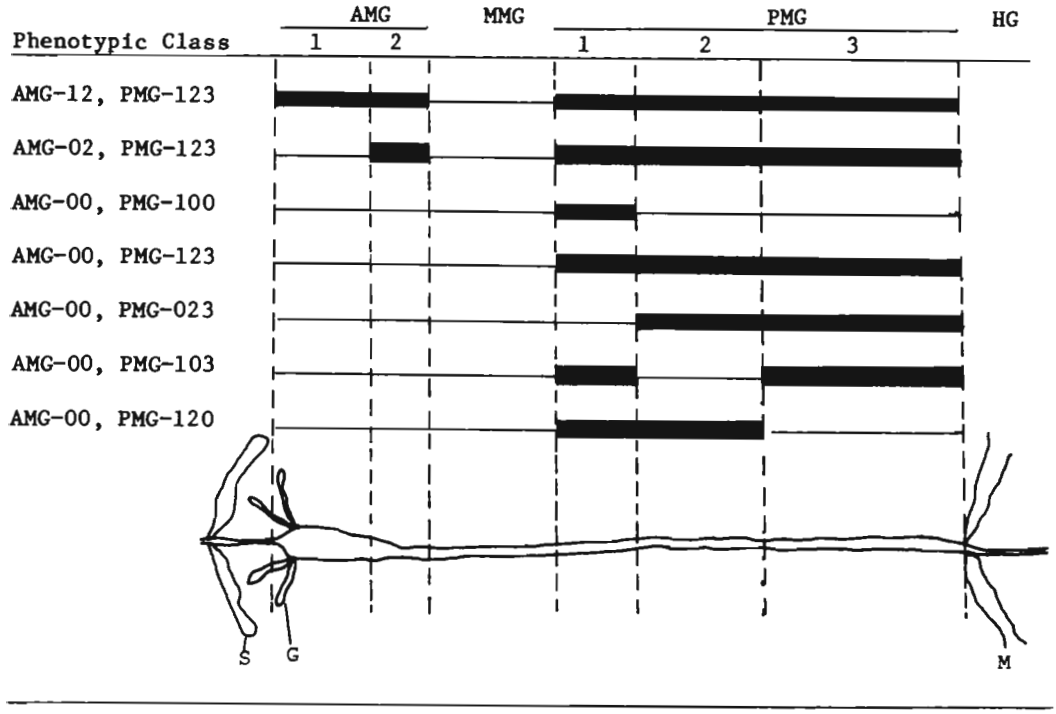

Fig. 1. Diagram of midgut amylase activity patterns and a representative midgut seen in 3rd instar larvae. These and additional patterns were observed among isogenic and wild strains of D.pseudoobscura. Solid vertical lines represent extent of the range of activity and demarcate anteriod midgut (AMG), middle midgut (MMG), posterior midgut (PMG) and hindgut (HG) regions. Each horizontal line represents a midgut extending from its anterior (left) to its posterior end (right). Darkened thick regions on the horizontal lines designate subdivisions showing amylase activity. Phenotypes are listed on the left. A representative late third instar larvae midgut is diagrammed below with appropriate regions aligned for the patterns above. S, salivary gland; G, gastric caeca; M, malpighian tubule.

activity patterns (assuming there is a genetic basis), non-third chromosomal factors are affecting the PMG phenotype. This is so because the strains used in these crosses were isochromosomal for chromosome three and isogenic for the Amy alleles. Amy is located on chromosome three.

Table 2. Number and frequency of third instar larvae midgut activity patterns (MAP) observed in isofemale strains from Bryce Canyon, Utah.

MAP		N	Frequency
AMG	PMG		%
00	100	17	14.2
00	100	66	55.0
00	120	8	6.7
00	103	1	0.8
00	123	11	9.2
00	020	1	0.8
10	123	4	3.3
02	123	1	0.8
12	100	2	1.7
12	120	2	1.7
12	103	1	0.8
12	123	6	5.0

Variability of midgut activity patterns were studied in 40 isogemale strains from Bryce Canyon, Utah (Table 2). For each strain three larvae were examined. As can be seen, the predominant midgut activity pattern was that of the AMG-00 PMG-100 in this population. For the anteriod midgut the predominant pattern was AMG 00 with a frequency of 87 percent. For the more variable posterior midgut region the predominant pattern was the PMG 100 pattern with a frequency of 57 percent. No associations were observed between the patterns seen in adults and those seen in larvae of the same strain (data not shown). This suggests that different factors (genetic?) determine midgut activity patterns in the two stages.

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Reference: Abraham & Doane, Proc. Natl. Acad. Sci. USA 75:4446-4450.