

that the activation of particular groups of genes in the polytene chromosomes of *Drosophila hydei* does not involve a change in the electrophoretic pattern of major histone fractions.

References: (1) MacGillivray, A.J., J. Paul and G. Threlfall, *Adv. Cancer Res.*, in press (2) Cohen, L.H. and B.V. Gotchel 1969 *Fed. Proc.* 28:600; (3) Asao, T. 1970 *Exptl. Cell Res.* 61:255; (4) Berendes, H.D., P.M.A. van Breugel and Th.K.H. Holt 1965 *Chromosoma* 16:35; (5) Panyim, S. and R. Chalkley 1969 *Arch. Biochem. Biophys.* 130:337; (6) Dick, G. and E.W. Johns 1969 *Comp. Biochem. Physiol.* 31:529.

Benner, D.B. East Tennessee State University, Johnson City, Tennessee. Some properties of Y-fourth chromosome translocations.

In addition to the Y-autosome translocations reported in DIS 47 Special Supplement, the Seattle-La Jolla *Drosophila* Laboratories recovered 24 presumed Y-4 translocations which were sent to Dean Parker's laboratory in Riverside for study. The following is a preliminary report on some of

the properties of these translocations.

Five of the original 24 translocations have been lost, and two have lost one of the elements. Three other translocations prove to lack 4R markers because on a  $ci\ ey^R\ spa^{pol}$  background  $y^+ B^S\ ci\ ey^R\ spa^{pol}$  progeny are recovered. Two additional cases (H162 and G51) may prove to be of special interest because they are  $y^+ ci^+ ey^R\ spa^{pol}$ .  $B^S$  individuals are  $ci$  and appear to be  $ey^R\ spa^{pol}$ . These 5 stocks are listed under the heading "Appear to Lack 4R" in Table 1 below.

Table 1. Summary of tests to determine position of nucleolus organizer, segregation properties, and fertility in Y-4 translocations. See text for explanation of tests.

Stock	Rescue C(1)DX, y f		Recovery of $y^+$ and $B^S$ males					Proportion recovered		X/ $y^+/B^S$ fertile
	$y^+$	$B^S$	$y^+$	$y^+B^S$	$y^2B^S$	$y^2$	N	$y^+$	$B^S$	
A 27		+	0	.478	.522	0	92	.47	.53	+
L 59	+		.292	.357	.399	.012	168	.50	.50	?
R 90	+		.143	.476	.333	.048	21	.50	.50	-
B 23		+	.034	.337	.600	.027	110	.38	.62	+
A 94 <sup>1</sup> .	+		.969	0	0	.031	128	-	-	
J113		+	.250	.448	.302	0	96	.43	.57	+
D 2	+		.482	.453	.036	.029	137	.55	.45	+
B126	+		.297	.398	.068	.237	118	.62	.38	-
R110	+		.091	.409	.487	.012	164	.47	.53	-
B 79	+		.223	.457	.255	.065	94	.50	.50	+
H112	+		.521	.438	.027	.014	146	.56	.44	-
B118 <sup>2</sup> .	+		-	-	-	-	-	-	-	+
Appear to Lack 4R										
R107	+		.022	.555	.423	0	137	.50	.50	-
P 54	+		.406	.311	0	.283	106	.67	.33	-
B244	+		.718	.266	.008	.008	124	.77	.23	+
H162		+	0	1.000	0	0	108	.50	.50	-
G 51		+	.218	.366	.416	0	101	.58	.42	+
One marker lost										
B147, $B^S$		-								
H119, $y^+$	-									

1. Only  $y^+$  males tested.

2. No accurate count of progeny obtained.

Attached-XY/ $B^S/y^+$  males were mated to C(1)DX, y f females in order to determine the relation of  $y^+$  and  $B^S$  to the nucleolus organizer region. C(1)DX females are NO deficient so should be rescued only by the fragment which has retained the NO region. As a first approximation this gives some indication of which marker may have retained the Y centromere. In 12 cases  $y^+$  rescues C(1)DX, and in 5 cases the recovered marker is  $B^S$ . In both of the cases where one marker has been lost the remaining element does not rescue the y f females. These

results are summarized in Table 1. In all but two cases 4R is associated with the element containing the NO region. In translocation D2  $y^+$  is recovered but the 4R markers are associated with  $B^S$ . In A27  $B^S$  rescues  $y$  f and has  $ey^+ spa^{pol+}$  associated with it, but  $ci^+$  appears to be associated with  $y^+$ . H119  $y^+$  also appears to have only  $ci^+$  associated with it. In this case the  $B^S$  marked element has been lost.

The segregational properties of the translocation elements have been examined in attached XY,  $y^2/B^S/y^+$  ♂♂ x  $y^2$  cv wy car ♀♀ crosses. Table 1 shows only the proportions of progeny recovered as males. H162 shows only  $y^+$   $B^S$  males recovered. The female class was all  $y^2$ . These factors have been observed to segregate so this represents preferential segregation, or recovery, not linkage. The total recovery of  $y^+$  and  $B^S$  is also given in Table 1. This was determined by using both male and female progeny. There are four cases (B23, B126, P54, and B244) in which there is preferential recovery of one marker. In other cases there are excesses which might not prove to be significant. In all cases where an excess is clearly shown, or indicated, the excess class is the class containing the NO region.

Finally,  $y^2$  cv wy car/ $B^S/y^+$  males were tested for fertility. Eight of the 16 X/T(Y;4) stocks tested were fertile. One stock is listed as questionable because two separate tests were done and only one offspring was produced.

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Studies on penetrance, expressivity,  
viability etc. of the mutant px in  
*Drosophila ananassae*.

The mutant plexus (px) causes network of venation in the distal region between the second and third longitudinal veins of the wing in *Drosophila ananassae*. It was obtained by X-irradiation in 1955 in the laboratory, was located in the third linkage group by Ray-Chaudhuri

et al. (1962), and was placed in the 3R by Hinton (1970). Previous workers (Mukherjee, 1957; Kale, 1969; Hinton, 1970) have attributed the abnormal behaviour of this mutant to lack of penetrance, pseudo-dominance, low viability etc. Since it was realized that this mutant was intimately associated with a system of segregation distortion (Mukherjee and Das, 1971), a detailed analysis was taken up to establish it as non-overlapping Mendelian gene and to rule out the trivial causes, viz., zygotic mortality, viability, penetrance and pseudo-dominance.

Morphological and genetic analysis of the mutant expression of px have shown that px shows a wide range of variation in expressivity, from a simple dot-like expression to extreme network. However, an individual with both wings "dotted" or one wing "dotted", the other without any dot or spot, has always proved to be px/+ in progeny tests. Thus all expressions of px except the "spot" character (one or both wings) are the result of homozygosity of px. Progeny tests for the transmission of px obtained either from px/px or pxpc/pxpc with any one kind of expressions have shown nearly 99.5% penetrance. Furthermore, segregation ratios of px to px or px to pxpc in appropriate crosses have also shown to be within expectations (tested by homogeneity as well as 2 x 2 contingency chi-square analysis).

Interestingly, among the progeny of px x + crosses as well as px/+ x px/+ the proportion of both wings spotted, or one wing spotted and the other normal, is within 13 to 20%. Considering these spotted winged flies as px/+ and not px/px, the proportions of px/px homozygotes among the progeny of px/+ x px/+ and px/+ x px/px crosses are within the range of expected values of around 25% and 50%, respectively.

The mean rating of wing expression (arbitrarily rated as 1 to 6, for extreme expression to wild type expression) of the px flies is about 5.6 in the px stock, and 10.5 in the progeny px/+ x px/+ cross. Heterozygous px/+ (with or without spot) when crossed to px/px yielded an average rating of about 9.0. These ratings are not affected markedly either by temperature, X-ray or by aging.

Analysis of the pre-adult development time, using E50 (i.e. days after first emergence of flies when 50% of all flies emerge) shows that the px as well as the wild type ( $a^{66+}$ ) of *D. ananassae* have the E50 value of 1.

These observations, therefore, clearly establish this mutant to be of fairly good category and may be placed in Rank 1 without any over-lapping with the wild type. Details of studies on its role in segregation distortion are in progress (see also Mukherjee and Das, 1971).

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