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Gene activity and histone patterns in salivary gland nuclei and chromatin of Drosophila hydei.

In many instances (1), it was reported that histones are involved in the specific response of the genome on various gene activating treatments. Incubation of Drosophila salivary glands in a medium containing the insect molting hormone ecdysone results in a specific quantitative decrease in one of the major histone fractions (2). It is well established that application of ecdysone to Dipteran salivary glands in vitro results in a characteristic pattern of local changes in genome activity. The aim of this study was to establish whether or not the change found in the histone pattern of Drosophila melanogaster is a specific effect of ecdysone or can be brought about by other treatments influencing genome activity as well. Histones were extracted with 0.2 N sulphuric acid (30 min at 4°C) or with 0.5 N sulphuric acid (15 min at 4°C) (3) from salivary gland nuclei of Drosophila hydei in which a specific change in genome activity was induced in the intact gland by either a temperature treatment (4) or by incubation of the glands with β-ecdysone (1mg/ml). Control glands were incubated in Ringer's solution for identical periods at room temperature. Electrophoresis of the sulphuric acid extracts from control glands on 15% polyacrylamide gels (5) reveals a pattern of histone fractions which is essentially the same as the pattern from Drosophila melanogaster fly histones obtained by extraction with 2 M NaCl (6).

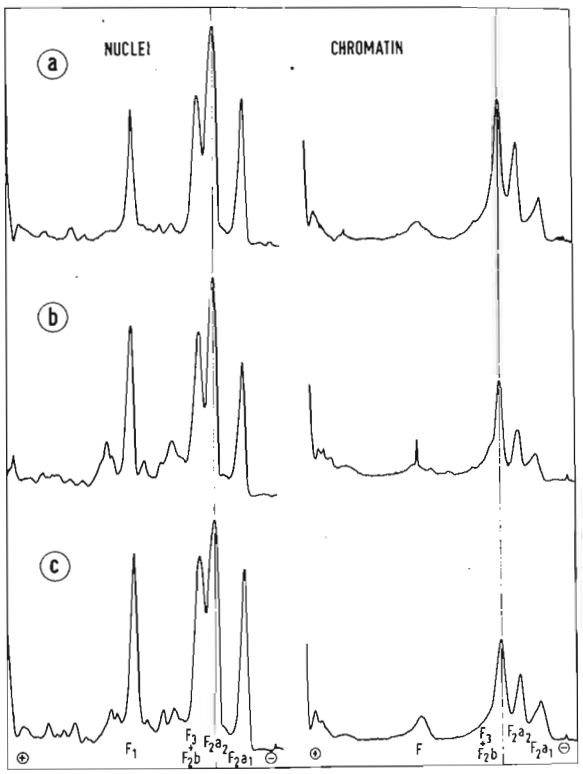

Fig. 1. Densitometric analysis of polyacrylamide gels containing histone fractions extracted from whole nuclei (left) and chromatin (right). (a) control, (b) after applying a temperature treatment to isolated salivary glands, which resulted in the formation of temperature puffs; (c) after incubation of isolated salivary glands with ecdysone. The measurements were performed at 550 nm.

For comparison of the histone fractions from nuclei in which specific changes in the puffing pattern were induced, a batch of 500-600 mg of isolated salivary glands was divided into three equal portions. One portion served as a control, another portion was submitted to a temperature treatment and the third portion was incubated with ecdysone. Following these different treatments some of the glands were squashed and stained to determine the presence of temperature- or ecdysone-specific puffs. From the rest of the glands nuclei were isolated. After repeated extractions of the isolated nuclei with sulphuric acid and electrophoresis it was found that all gels displayed 4 major components and 16-18 minor bands. Densitometric analysis showed that neither qualitative nor quantitative differences could be found in the major histone fractions of nuclei from temperature- or ecdysone-treated glands as compared with nuclei from control glands (Fig. 1, left side). Differences in the minor fractions do occur. However, these differences seem to be unrelated to the treatments applied.

Extraction and subsequent electrophoresis of histones from chromatin prepared from polytene nuclei resulted in a histone pattern with consistently different characteristics, if compared with extracts from whole nuclei. All major fractions present in extracts from whole nuclei are present in the extracts from chromatin (Fig. 1, right side), but the number of minor basic protein fractions was reduced to 5-6. Despite these general differences in the pattern of basic proteins between nuclei and chromatin extracts, no indication was obtained for specific differences in the patterns derived from treated and untreated samples. This indicates

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: y^+	Rescue C(1)DX, y f: B^S	Recovery of y^+ and B^S males: y^+	y^+B^S	y^2B^S	y^2	N	Proportion recovered: y^+	Proportion recovered: B^S	$X/y^+/B^S$ fertile
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[1].	+		.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[2].	+		-	-	-	-	-	-	-	+
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