

Oshima, C. and T. Watanabe. National Institute of Genetics, Misima, Japan. The effect of insecticide selection on experimental populations of *Drosophila pseudoobscura*.

About forty homozygous strains of four kinds of chromosomes, ST, AR, CH and PP, were used in the experiments. These strains, originated from the Mather population in California, had been established by Dobzhansky in 1963.

Heterozygous female flies for ST and AR were crossed with heterozygous male flies for CH and PP. Two initial populations were made with 250 female and 250 male offspring and after two generations (one generation period lasts about 20 days), the salivary gland chromosomes of 150 larvae hatched from sampled eggs were observed for detecting the frequency of each chromosome.

In the F_2 generation of both populations, the frequencies of the four kinds of chromosomes should be theoretically equal, i.e. 25 per cent of each. However, the observed frequencies were ST:33.3, AR:26.3, CH:22.7, PP:17.7 per cent in Population I and ST:26.3, AR:28.0, CH:26.3, PP:19.3 per cent in Population II. Further, each population was divided into two populations A and B. Flies in Population A were exposed to insecticide test paper (DDT 1%, 2% or Dieldrin 0.1%) for one hour and transferred into a new cage in each new generation. Flies in Population B were transferred into a new cage without exposure. The test papers and test kits were prepared by WHO in Geneva and sent to us. These populations are being maintained in a constant temperature room (25°C) and the varying frequencies of chromosomes from F_2 to F_{12} in each population were observed as shown in Table 1.

Table 1. Changing frequencies of four kinds of chromosomes in DDT or Dieldrin selected and non-selected populations

F ₂			F ₃	F ₄	F ₅	F ₇	F ₉	F ₁₂	
Pop. I	ST 33.3 AR 26.3 CH 22.7 PP 17.7	IA (DDT selected)	ST	40.3	55.0	55.3	73.3	77.0	92.7
			AR	18.3	23.0	24.3	15.7	18.7	6.3
			CH	22.0	11.7	8.3	4.0	0.7	0.0
			PP	19.3	10.3	12.0	7.0	3.7	1.0
		IB (non-selected)	ST	42.0	45.7	53.7	65.3	72.3	67.0
			AR	24.7	25.7	26.3	22.0	17.0	27.0
			CH	18.3	17.3	10.0	7.0	6.3	4.7
			PP	15.0	11.3	10.0	5.7	4.3	1.3
Pop. II	ST 26.3 AR 28.0 CH 26.3 PP 19.3	IIA (DL. selected)	ST	43.7	41.0	43.0	71.0	84.3	90.3
			AR	19.7	30.0	29.7	16.7	5.7	2.0
			CH	15.3	9.7	10.3	4.3	6.0	4.7
			PP	21.3	19.3	17.0	8.0	4.0	3.0
		IIB (non-selected)	ST	36.3	45.7	49.3	52.3	64.3	68.7
			AR	21.7	29.7	27.3	30.0	25.3	26.3
			CH	23.3	14.7	13.3	12.0	5.3	3.0
			PP	18.7	10.0	10.0	5.7	5.0	2.0

The frequency of ST chromosomes has increased in both selected and non-selected populations, but after F_7 generation the increase in the former (IA, IIA) was greater than in the latter (IB, IIB). On the other hand, AR chromosomes showed changes which were opposite to those of ST, especially in the selected populations. The frequencies of both CH and PP chromosomes have gradually decreased. However, their relative frequencies in selected populations were slightly different from those in non-selected populations: PP became more frequent than CH after several treatments, while the CH frequency was found always a little higher than those of PP in non-selected populations.

These results seem to suggest that the remarkable evolutionary changes in natural populations of *D. pseudoobscura* in California during about twenty years might be due to insecticide selection: ST chromosomes increased and AR chromosomes underwent changes which were the reverse of those in ST. CH chromosomes decreased and became rare and PP chromosomes emerged spectacularly.

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MacIntyre, R. J. and T. R. F. Wright. The Johns Hopkins University. Recombination in FM4/+; SM1/+; Ubx¹³⁰/+ Heterozygotes.

In investigations on the selective value of different Esterase 6 alleles in experimental populations, an attempt was made to construct two stocks which were coisogenic except at the Est 6 locus and an unknown num-

ber of genes between hairy (26.0) on the left and thread (43.2) on the right. The balancers employed in the construction of these stocks were: for the X chromosome, FM4 (Mislove and Lewis, DIS 28:77); for Chromosome 2, SM1 (Lewis and Mislove, DIS 27:58); and for Chromosome 3, Ubx¹³⁰ (Lewis, PNAS, U.S. 38:953-961, 1952). In order to detect recombination within the three major chromosomes when they were simultaneously balanced over crossover suppressors, three testcrosses were set up. In the first, FM4/ sc ec cv ct⁶ v g² f; SM1/+; Ubx¹³⁰/+ females were mated to sc ec cv ct⁶ v g² f males, and their progeny were examined for recombinations between the X Chromosome markers. Likewise, offspring from two other matings, FM4/+; SM1/ al dp b pr cn c px sp; Ubx¹³⁰/+ females x al dp b pr cn c px sp males and FM4/+; SM1/+; Ubx¹³⁰/ ru h th st cu sr e^s Pr ca females x ru h th st cu sr e^s + ca males were checked for crossing over on Chromosomes 2 and 3 respectively.

In the testcross involving the Chromosome 2 markers, recombinations between al and dp, and between px and sp could not be detected since the SM1 chromosome contains mutant alleles at the al and sp loci. Of 507 chromosomes examined, none showed any recombinations of the markers between dp and px. Apparently, crossover suppression of Chromosome 2 by the SM1 balancer is complete, even when the two other major chromosomes are each heterozygous for several inversions.

Examination of Tables 1 and 2 reveals that this is not true of the FM4 and Ubx¹³⁰ balanced chromosomes. Table 1 indicates that about one out of every four X Chromosomes from FM4/+; SM1/+; Ubx¹³⁰/+ females will be a recombinant. If one compares the percentage of crossing-over with the approximate size of each block (as estimated from reference maps of the salivary gland X Chromosomes and the genetic distances between the markers involved), it can be seen that the recombinational events producing viable chromosomes are distributed fairly randomly both between and within the blocks delineated by the breakpoints on the FM4 chromosome. This is not the case in Chromosome 3 (Table 2). Here, almost all the recombinants result from either single crossovers near the end of the right arm or from multiple crossovers, nearly always including a double crossover in block II.

It is easy to see that when the "coisogenic" lines are initiated with 10 to 20 wild-type segregants from the last cross in mating schemes involving the use of the multiply rearranged balancer chromosomes, FM4, SM1, and Ubx¹³⁰, there is a very good chance that cryptic heterozygosity is introduced into the derived stocks. Uncontrolled regions on the genetic map, initially thought to be restricted to Chromosome 3 between hairy and thread, actually included the whole X Chromosome and in Chromosome 3, from the tip of the left arm to the vicinity of the thread locus and the distal one-fifth of the right arm. Furthermore, analysis of the recombinant progeny of the testcross involving markers on Chromosome 3 revealed that of the double-crossovers within block II, slightly over half included the Est 6 locus. Thus, since an Est 6 allele from the Ubx¹³⁰ chromosome may have been introduced into one of the coisogenic stocks, still another possible variable was detected and subsequently had to be taken into consideration when the results of the experimental populations founded by the "coisogenic" stocks were analyzed (see MacIntyre and Wright, Amer. Nat., In press).

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