

Budnik, M. and S. Koref-Santibañez.
University of Chile, Santiago, Chile.
Temperature, rate of development and
inversion polymorphism in *D. pavani*.

D. pavani Brncic 1957, is a species endemic to Chile and the eastern slope of the Andes Mountains in Argentina; it exhibits chromosomal polymorphism due to the presence of inversions on its second chromosome and in the right and left arms of the fourth chromosome. The poly-

morphism is of a rigid nature, for the frequency of heterokaryotypes is maintained under most of the environmental and breeding conditions in which the species has been reared. This is most probably due to the adaptive superiority of the heterokaryotypes, that has been measured in some components of fitness, such as longevity (Brncic and del Solar, 1961 Amer. Nat. 95: 211), mating activity (Brncic and Koref-Santibañez, 1964 Genetics 49: 585; Koref-Santibañez and Brncic, 1965 Genetics 52: 453), and rate of development (Brncic, Koref-Santibañez, Budnik and Lambrot, 1968 Genetics 61: 471). The present communication summarizes the experiments performed in order to analyze the behavior of the heterokaryotypes in relation to one of the fitness components, i.e., rate of development, at two temperatures.

A heterogeneous stock, originated from flies collected in the locality of Bellavista near Santiago, with a frequency of heterokaryotypes of around 55% in the left arm and of 48% in the right arm of chromosome IV was used. (The arrangements in the second chromosome were not considered). Eggs were collected every 24 hours, and placed in numbers of 50 in vials containing food medium. One set of vials was incubated at 16°C and another set of vials was left at 25°C. Adults were later sexed every 24 hours until all had emerged. At every temperature two groups were established, according to the time they took to develop from egg to adult: those of fast development, 29 to 35 days at 16°C, and 14 to 16 days at 25°C; and those of slow development: 44 to 65 days at 16°C, and 21 to 29 days at 25°C. The flies from each of these groups were crossed individually to imagoes of the opposite sex from a stock of Standard gene arrangement (*D. gaucha*) and the salivary gland chromosomes of eight larvae were analyzed in order to determine whether the parent was a homozygote or heterozygote.

The results are summarized in the Table, which shows the number of heterozygotes found in each group.

Temperature	R.D.	No.	Chromosome 4R		Chromosome 4L	
			Heterokaryotypes	χ^2	Heterokaryotypes	χ^2
16°C	fast	395	277	48.55*	266	45.31*
16°C	slow	375	170		162	
25°C	fast	238	143	9.53*	142	4.01**
25°C	slow	154	68		76	

*P 1 df < 0.001

**P 1 df 0.02-0.05

The significant Chi-square values between the "fast" and "slow" groups at each temperature reflect the fact that the frequency of heterokaryotypes is much greater among those flies that develop more rapidly, although the difference is significantly higher at 16°C. Thus, the heterozygotes are advantageous in this parameter of fitness, regardless of the environment at which they breed. This provides more evidence for the very rigid nature of chromosomal polymorphism in *D. pavani*.

(Research financed by grants from the Faculty of Medicine, Grant No. 45 of CONICYT and the Multinational Genetics Program of the O.A.S.)

Benedík, J. J.E. Purkyně University, Brno, Czechoslovakia. Viability and lethality studies in the natural population of *D. melanogaster*.

The changes in the mean relative viability and in the frequency of lethals due to the second chromosome genes were studied in a large, isolated natural population. In the experimental period from October to December, average temperature dropped from 16 to 8°C, the conse-

quence of which was change from optimal conditions into stressed ones.

The modified Cy-method was used for studying both second chromosomes of each male. Ten chromosomes in each of twenty males in each of two samplings (Oct. 23 and Dec. 9) were tested by this method for relative homozygote viability and for the presence of lethal genes. The mean relative viability for each male is presented in Table 1. The considerable shift in sampling mean was caused by the decrease of chromosome frequency with high viability values