Females were dissected at intervals ranging from 10 minutes to 50 hours after mounting of the female by the male, which included interrupted copulations. Details of these results will be reported elsewhere. There is a high degree of individual variation in the sperm storage process; the results reported here are in terms of least squares regression estimates of the population values and individual values. Uteral sperm numbers, when greater than 300, were estimated by measuring the area covered by the uteral sperm mass with an ocular micrometer and counting sperm density at random points in the mass. Receptacle and spermathecal sperm were counted directly. The entire counting time for a specimen ranged from 15 to 45 minutes. Only specimens for which two complete replicate counts could be obtained (N = 47) were analyzed. Counting error (mean coefficient of variation ± SEM) for the combined classes of receptacle, spermathecal and uteral sperm was 2.7 ± 0.91% per individual, after logarithmic transformation of counts. Table 1 lists the maximums and times of maximum sperm numbers for these sperm classes.

Table 1. Initial sperm storage parameters for Oregon-R matings, in terms of regression estimates of population values and individual observed values.

	Maximum number		Hour* of maximum	
Sperm class	Estimated	Observed	Estimated	Observed
Transferred sperm:				
Uteral sperm	5800	4690	0.28	0.25
Stored sperm:				
All organs	1120	1032	5.1	5.3
Receptacle	670	767	4.0	0.9
Spermathecae	390	449	7.0	5.3

*Hour post mounting of female by male.

An important aspect of these results is that the maximum storage of sperm greatly exceeds the commonly referred to value of 750 for maximum storage capacity (Kaplan et al. 1962, based on examination of 8 females). This high amount of storage appears to be balanced by a high degree of sperm waste (loss from the reproductive tract without fertilization) during the first 3 days after mating (Gilbert et al. 1981), causing progeny to stored sperm ratios of approximately 50%. Such an inefficient use of stored sperm, as well as transferred sperm (approximately 10% of transferred may ultimately fertilize eggs), suggests that sperm selection may be an important component of natural selection in D. melanogaster, particularly if sperm genotypes within or between ejaculates differ in their functional abilities.

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References: Fowler 1973, Adv. in Genetics 17:293-360; Gilbert et al. 1981, Evolution, in press; Kaplan et al. 1962, DIS 36:82; Richmond et al. 1980, Science 207:1483-1485; Strickberger 1962, Experiments in Genetics with Drosophila, p. 103, Wiley.

Goncharenko, G.G. and I.K. Zakharov. Institute of Cytology and Genetics, Novosibirsk, USSR. A phosphoglucomutase locus in D. virilis.

Polymorphism at the locus phosphoglucomutase (Pgm) has been extensively studied in may Drosophila species. The genetic localization of this structural locus was determined for some species (Hjorth 1970, Trippa et al. 1970, Lakovaara and Saura 1972, Charlesworth et al. 1977).

The total of 20 lines from seven members of the virilis group of Drosophila (D. virilis, D. americana texana, D. littoralis, D. ezoana, D. novomexicana, D. lummei) was included in this study. The genetic variability of phosphoglucomutase has been studied using starch gel electrophoresis. Each fly was homogenized in 0.025 ml double distilled water on the rough surface of a slide. The starch gel electrophoresis was performed vertically using 12-13% starch and 10% sucrose in medium containing 0.045M TRIS, 0.025M boric acid and 0.001M EDTA. The electrode buffer had 0.18M TRIS, 0.1M boric acid, 0.004 EDTA (anodal) and 0.13M TRIS, 0.07M boric acid, 0.003M EDTA, 10^{-5} NADP (catodal) (Porter et al. 1964). The electrophoresis took 4-5 hours at 5-10°C with a voltage of 320-360v and current intensity of 60-80 ma. Staining mixture as in Ayala et al. (1972).

The electrophoresis of Pgm revealed the presence of three variants, called $Pgm^{0.80}$, $Pgm^{1.00}$ and $Pgm^{1.20}$ on the basis of their mobilities (see Fig. 1). The data from different crosses indicate that these three variants are coded by three codominant alleles at one locus.

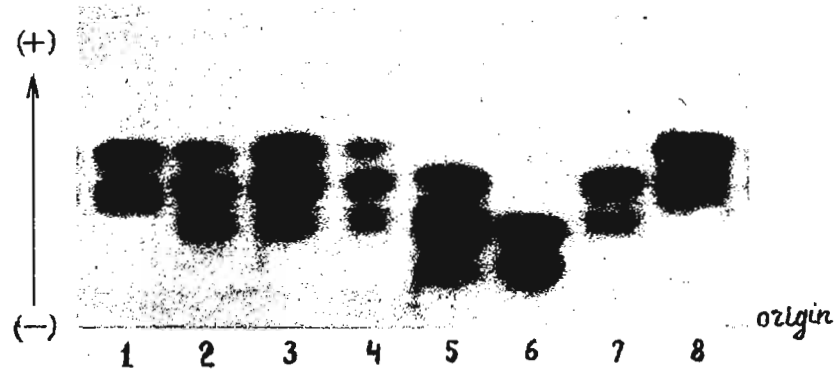

Fig. 1. Starch gel electrophoretic pattern of one fly homogenates of D. virilis. The following genotypes are shown:

1,8 - $\frac{Pgm^{1.20}}{Pgm^{1.20}}$; 2,3,4 - $\frac{Pgm^{1.20}}{Pgm^{1.00}}$; 5 - $\frac{Pgm^{1.00}}{Pgm^{0.80}}$; 6 - $\frac{Pgm^{0.80}}{Pgm^{0.80}}$;

7 - $\frac{Pgm^{1.00}}{Pgm^{1.00}}$

It is necessary to note that under the electrophoresis method used the homozygous variants were always revealed by two bends. The discussion of the causes of this phenomenon is beyond the scope of this report; further details will be published elsewhere.

The examination of the offspring from the backcross

♀♀ $(\frac{Pgm^{1.00}}{Pgm^{1.00}})$ $\frac{b\ gp\ cd\ pe\ gl}{b'gp'cd'pe'gl}$ X

♂♂ $(\frac{Pgm^{1.00}}{Pgm^{1.20}})$ $\frac{b\ gp\ cd\ pe\ gl}{+'+\ '+\ '+\ '+}$

demonstrated that the Pgm gene is linked to the gp (gapped,3-118.5) locus and therefore located in the third chromosome. For a more definite localization of the locus Pgm the following crosses were carried out:

♀♀ $(\frac{Pgm^{1.00}}{Pgm^{1.20}})$ $\frac{sv\ t\ tb\ gp}{+\ +\ +\ +}$ X ♂♂ $(\frac{Pgm^{1.00}}{Pgm^{1.00}})$ $\frac{sv\ t\ tb\ gp}{+\ +\ +\ +}$

According to the result of such crosses the recombination frequency between sv and t genes was 27.8%; between t and tb, 33.0%; and between tb and gp, 13.6%. This is in agreement with the position of the loci on the standard genetic map of D. virilis (Alexander 1976). In the D. virilis map four visible markers have the following localization: sv (shot veins, 3-24.5); t (telescoped, 3-57.5), tb (tiny bristles, 3-104.0), and gp (gapped, 3-118.5) m.u.

Table 1. Localization of Pgm locus.

Parent	Offspring maternal chromosome	$\frac{Pgm^{1.20}}{Pgm^{1.00}}$	$\frac{Pgm^{1.00}}{Pgm^{1.00}}$
♀ $(\frac{Pgm^{1.20}}{Pgm^{1.00}})$ $\frac{+\ +\ +\ +}{sv\ t\ tb\ gp}$	+ + + +	14	0
	sv t tb gp	0	13
	+ t tb gp	2	0
	sv + + +	0	4
	+ + tb gp	4	0
♂ $(\frac{Pgm^{1.00}}{Pgm^{1.00}})$ $\frac{sv\ t\ tb\ gp}{sv\ t\ tb\ gp}$	sv t + +	0	4
	+ + + gp	3	0
	sv t tb +	0	3
	+ t	41	2
	sv +	4	65

From Table 1 it is evident that 6/112 of crossovers occurred in the course of recombination between sv and Pgm genes and 106/112 between Pgm and t genes. Therefore, Pgm is placed at 26.3± on the genetic map of the third chromosome of D. virilis.

References: Alexander, M.L. 1976, in: The Genet. and Biol. of Drosophila, Vol. 1c:1365-1427, Academic Press; Ayala, F.J., J.R. Powell, M.L. Tracey, C.A. Mourao and S. Perez-Salas 1972, Genetics 70:113-119; Charlesworth, B., D. Charlesworth and M. Loukas 1977, DIS 52:133; Hjorth, J.P. 1970, Hereditas 64:146-148; Lakovaara, S. and Saura 1972, DIS 48:93; Porter, J.H., S.H. Boyer, E.J. Watson-Williams, A. Adam, A. Szienberg and M. Siniscalo 1964, Lancet 1:895; Trippa, G., C. Santolamazza and R. Scozzari 1970, Biochem. Genet. 4:665-667.