strain maintained under uniform conditions in the laboratory and the significant excess of heterozygotes observed during the present investigation extend evidence that the heterotic property of subterminal inversion is maintained even after the alteration of gene arrangements within the inverted segment caused by the new inversion. Thus the property of a chromosome depends on its gene content rather than on the gene arrangement itself.

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Genetic variability in mating activity of *Drosophila melanogaster* males

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Summary. Male mating activity was measured for 29 lines of *D. melanogaster*, made homozygous for the second chromosome. Genetic differences between lines were found to be highly significant. Mating activity of homozygous males was much lower than that of heterozygous ones.

Drosophila melanogaster females are generally refractory to mating for a certain period after they have mated once[1]. On the other hand, males generally mate with several females within a limited period[2-4]. Male multiple mating is a very important phenomenon from the population-biological standpoint, since it implies that a proportion of males may be eliminated from a reproductive population. This would make the effective size of a population much smaller than its logistic potential, and would constitute an important component of sexual selection.

To study the genetic variability in male mating activity in natural populations, 2nd chromosomes of *D. melanogaster* were extracted from a natural population in Katsunuma, Japan, and made homozygous by means of the complete marked inversion technique. 29 homozygous lines having no lethal or sterility genes were finally established. The genetic background of these 2nd chromosome homozygote lines is the same as that of the natural population, since the genetic background of the *Cy/Pm* balancer strain used was previously substituted with that of Katsunuma population. Chromosomes, except for the 2nd one, were not under control. The tendency was found that chromosomes with low viability in the homozygous condition often show low fertility or even sterility (Kosuda, unpublished observation). Male mating activity was measured by the number of females inseminated by single males within 24 h under conditions of permanent artificial light at 25 °C. 10 out of 12 females of a standard line (designated 2SG) were placed together with 1 male in a 3×8 cm culture vial and were examined as to whether or not they had sperms in their ventral receptacles or spermathecaes. The 2 remaining females were kept as a provision against technical failure. The age of the 2SG females was 3 or 4 days and 3-day-old males were always utilized. 12 replicates each were made for 29 homozygous lines for the measurement of male mating activity.

The frequency distribution of mating activity for all 348 males is given in figure 1. 25 out of 348 males (7.2%) did not mate and 8 males (2.3%) mated more than 10 times

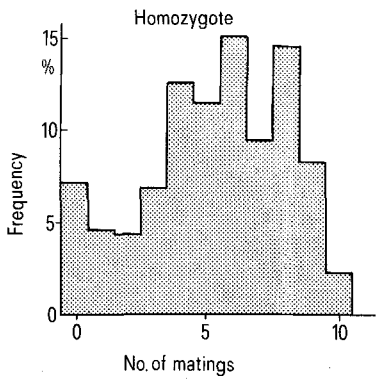

Fig. 1 Frequency distribution of mating activity in homozygous males.

Analysis of variance for mating activity among 29 homozygous second chromosome lines

Source	d.f.	S.S.	M.S.	F
Line	28	838.01	29.93	5.95**
Error	319	1604.92	5.03	
Total	347	2442.93		

** Significant at 1% level.

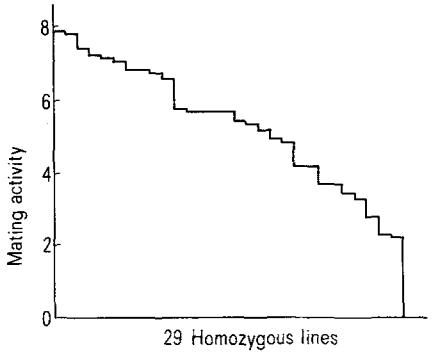

Fig. 2 Male mating activity of 29 homozygous lines.

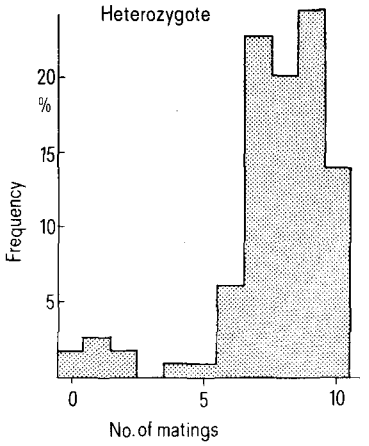

Fig. 3 Frequency distribution of mating activity in heterozygous males.

within 24 h. The mean mating activity expressed as the number of matings on an individual basis was calculated to be 5.348 ± 0.142. Figure 2 represents the male mating activity of 29 homozygous lines. The male mating activity over the array of 29 lines was 5.261 ± 0.311. The number of copulations in the highest line (7.83 ± 0.37) is more than 3 times as large as that in the lowest one (2.17 ± 0.73). Analysis of variance disclosed that the genetic difference among 29 lines is significant at the 1% level (table). If we include the sterile lines, then genetic variability becomes even more distinctive. Male mating activity in heterozygous individuals, that is, progenies from the natural population is given in figure 3. They are assumed to be random heterozygotes for the 2nd chromosome and to have the same genetic background as homozygotes. The distribution of mating activity in heterozygotes differs greatly from that in homozygotes (fig. 1), essentially in that mating activity is enhanced. The majority of heterozygote males mated at least 6 times within 24 h. The frequency of 'low' individuals who mated less than 6 times is very low in comparison with homozygous males. 16 out of 109 males (14.7%) mated at least 10 times. Mean mating frequency in heterozygous males was 7.670 ± 0.207, and this is significantly higher than that in homozygous ones. The coefficient of variation in homozygous males is much smaller, indicating perhaps a homeostatic nature of this behavioural character. The observed variation in mating activity suggests that mate selection may be unexpectedly intense in natural populations. It may also imply that fertility including mate selection, in a broad sense, is a more important fitness component than are fitness variants in preadult stages[5].

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Submandibular gland-conditioned medium enhancement of bone marrow colony-forming cells in tumor-bearing murine recipients[1,2]

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Summary. Soft-agar clonogenic assay techniques were used to examine 2 sources of colony-stimulating activity (CSA), submandibular gland-conditioned medium (SMG-CM) and pregnant mouse uterine extract (PMUE), for potentiation of granulocyte-macrophage (GM-CFUc) or monocyte-macrophage (M-CFUc) progenitor cell populations. The femoral populations being examined were aspirated from normal mice and from those bearing 1 of 2 types of tumor: Lewis lung carcinoma (3LL) or thymic lymphoma ascites tumor (EL-4). When PMUE was used as a CSA source, normal animals showed a greater clonogenic response per population than either of the tumor-bearing groups. When SMG-CM was used as a CSA source, the pattern of GM-CFUc response was much different: GM-CFUc magnitudes increased by fourfold to sixfold over normal levels in tumor-bearing animals. M-CFUc response patterns were also significant, being similar in response but smaller.

Generally speaking and regardless of etiology, cancer is a known disruptor of normal hemopoiesis even though the blood-forming tissues (as we know them) are not directly involved. It is generally accepted that lymphopoiesis is suppressed[3-5] and myelopoietic homeostasis is disturbed[6]. The degree and direction of disruption may depend on the time and type of tumor being investigated, since both myeloid increases[7,8] and decreases[6,9] have been reported. Divergences in the literature may be due to a number of factors, among which may be: a) regulatory factors are being produced by the tumors mass(es)[8,10] or b) an altered bone marrow response pattern could be due to specific cellular metabolic prerequisites[11] or a change in makeup of the femoral matrix pattern, i.e., microenvironment.