big space without food vials, the jumping rate of the species hybrids is greater than that of the parental species (ANOVA). Figure 4 shows the rate of grooming of the $p \times p$, $g \times g$, $p \times g$ and $g \times p$ genotypes. Statistically significant differences between the four genotypes were only found in big space vials without food, that is D. gaucha males substantially increase grooming in big space vials without food. On the other hand, in contrast with the males, females of the four types of genotypes show a similar behavior in the three environments where the male's behavior was studied (ANOVA) (data not shown).

Locomotion and turning are behavioral elements that configure patterns of movement in Drosophila adults and larvae (Godoy-Herrera et al., 1997). Our results indicate that in the same environment, males of the four groups of genotypes may modify those behaviors in different ways. Thus, in big-space vials with food, p x p males decrease locomotion and turning rate while g x p males increase these behaviors, indicating there exists a genotype-environment interaction for their expression. These results seem to suggest that the g x p hybrid males could adjust in different ways to stressful environments. It is also interesting to note that the jumping rate decreases when the males are confined in reduced space. Jumping seems merely to represent aborted flight of the males in the vials. Given that in a relatively reduced space male jumping behavior equally decrease in the four groups of genotypes, we conclude that there is no genotype-environment interaction for the expression of such behavior. Grooming seems to increase in stressful circumstances (Hoffman and Parsons, 1994), and it is believed that it counteracts the effect of stress (Equibar and Moyaho, 1997). Our results show statistically significant differences for grooming rate between the four groups of genotypes when the males are confined in big vials without food and water. This kind of environment is probably very stressful for the flies. The results indicate that $g \times g$ males exhibit the greater rate of grooming, suggesting that this genotype could be more sensitive to the absence of food and water. In contrast with the males of the four groups of genotypes, the females did not show significant differences among them for the behaviors observed. We are planning further experiments to better understand these findings.

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References: Brncic, D., and S. Koref-Santibañez 1957, Evolution 11: 300-310; Equibar, J.R., and A. Moyaho 1997, Pharmacol. Biochem. Behav. 58: 317-322; Godoy-Herrera, R., M. Bustamante, P. Campos, and J.L. Cancino 1997, Behavior. 134: 105-125; Hoffmann, A.A., and P.A. Parsons 1994, In: *Evolutionary Genetics and Environmental Stress*. Oxford University Press Inc., New York, U.S.A.; Val, F.C., C.R. Videla, and M.S. Barques 1981, In: *The Genetics and Biology of* Drosophila. (M. Ashburner, H.L. Carson, and J.N. Thompson, jr., eds.), Vol. 3a, Academic Press, London.

Perturbation of sex determination in the strain *In(1)BM2(reinverted)*.

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The strain In(1)BM2(reinverted) of Drosophila melanogaster, shows a mutation in the structure of the polytene male X chromosome (Mazumdar et al., 1978). In third instar male larvae reared at 18°C, about 25% of polytene nuclei reveal X chromosomes that appear twice as wide as the X chromosome of wild type larvae (Figure 1a). However, unlike polytene chromosome puffs, such puffy Xs do not manifest enhanced transcriptional activity (Kar and Pal, 1995). This characteristic thus classifies the puffy Xs as pompons (reviewed in Zhimulev, 1995). The absence of correlation between puffing and transcription suggests that the chromosomal rearrangement perturbs a pathway that controls the structure, but not the transcription, of the male X chromosome. The sex and chromosome specificity further suggests the possibility that the rearrangement affects the function of a regulator of the dosage compensation pathway.

The expression of the puffy Xs is controlled by the rearranged breakpoint at the 16A region of the polytene chromosome (Kar and Pal, 1995). In order to map the rearranged breakpoint, mutagenesis of segment 16A of In(1)BM2 (reinverted) X chromosome has been initiated. Freshly eclosed In(1)BM2 (reinverted) males were irradiated with 4000 rads of g-irradiation and mated to virgin Df(1)B females (Df(1)15F9-16A1; 16A6-7, Lindsley and Zimm, 1992). Flies emerging from such matings were scored for lethal or visible mutations, alteration in sex ratio and reversal of the puffy X phenotype.

In one of the matings, a single intersexual female was recovered. A stock was made from the females that were heterozygous for a balancer chromosome and the irradiated chromosome, and the line was designated as $B^{M2\neq l.36}$. Less than 5% of heterozygous females manifest transformation in sexual characteristics (Figure 1b). $B^{M2\neq l.36}$ males were viable. Sexually dimorphic characters of such males were unaffected, with the exception of one male where the orientation of the sex comb was altered. Cytological examination did not reveal the presence of any visible deletions at the 16A region of the X chromosome. Third instar male larvae of $B^{M2\neq l.36}$ however did not show any puffy X chromosomes when reared at 18°C. This indicated that reversal of the puffy X phenotype had been obtained. Mapping of the mutation in $B^{M2\neq l.36}$ is currently underway. Although there are three ealier reports of perturbation of the sexual phenotype in In(1)BM2 (reinverted) (Kar and Pal, 1995; Chakraborti et al., 1996; Mukherjee and Basu, 1997), it is not known whether the structural alteration of the X chromosome and the sexual transformation are brought about due to the perturbation in the function of the same gene or not.



Figure 1. (a), Puffy male X chromosome (\rightarrow) of the strain $In(1)B^{M2}$ (reinverted); (b), Phenotype of intersexual $B^{M2 \neq l.36}$ / FM7 female. \leftarrow indicates transformed genitalia and \rightarrow indicates sex combs on prothoracic leg.

References: Chakraborti, D., et al., 1995, Genome 38: 105-109; Kar, A., and J.K. Pal 1995, J. Genet. 74: 47-59; Lindsley, D.L., and G.G. Zimm 1992, *The Genome of* Drosophila melanogaster; Academic Press Inc., New York; Majumdar, D., et al., 1978, Cell Chromosome News Lett. 1: 8-12; Mukherjee, A. S., and S. Basu 1997, Indian J. Exp. Biol. 35: 203-211; Zhimulev, I.F., 1995, Adv. Genet. 34: 1-497.

Effects of insulin, wortmannin, LY294002, and rapamycin on protein phosphorylation in the *Drosophila* ovary.

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Abstract: Although *Drosophila* insulin-like peptide and insulin receptor have been isolated and characterized, the downstream signal of insulin has not been described well in *Drosophila*. To examine the regulatory mechanism of insulin in the ovary, we investigated the protein phosphorylation induced by insulin. Two proteins (appropriate Mr-20,000 protein and a Mr-30,000 protein) were identified as insulin-induced phosphoproteins at low molecular weight range (70,000 – 14,000 Dalton). As in vertebrates, these insulin-