

## GENETIC DISSECTION OF THE *kl-3* Y-CHROMOSOME LOOP OF *DROSOPHILA MELANOGASTER*.

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Primary spermatocyte nuclei of *D. melanogaster* exhibit three giant lampbrush-like loops formed by the *kl-5*, *kl-3* and *ks-1* Y-chromosome fertility factors (1). These structures contain and abundantly transcribe highly repetitive, simple sequence DNAs (2) and accumulate large amounts of non-Y encoded proteins (3). The biological role of the Y-chromosome loops is still largely unknown. They may accumulate non-Y-encoded proteins involved in spermiogenesis, harbor genes encoding for axonemal components, or both (4, 5).

An approach to elucidate the biological role of the Y loops is the identification and of mutations affecting the formation and the morphology of these structures. To isolate mutants defective in loop formation we screened 210 male sterile mutants for the presence and normality of the Y loops. This analysis led to the identification of 5 mutants that specifically affect the formation of the *kl-3* loop. Two of these mutants [*ms(3)HB267* and *ms(3)HB223*] completely lack the *kl-3* loop, while the other three mutants [*ms(3)HB933*, *ms(2)HA30* and *ms(2)HB108*] exhibit extremely reduced *kl-3* loops; in all these mutants the *kl-5* and *ks-1* loops are normal. Complementation tests showed that *ms(3)HB267* and *ms(3)HB933* are allelic, indicating that the five mutants analyzed identify four loci necessary for proper development of the *kl-3* loop. All these mutations have been statistically mapped using a variety of marked chromosomes. In addition, two mutations, *ms(2)HA30* and *ms(3)HB267* have been mapped over deficiency. In both cases mutant/deficiency males were normally viable, completely sterile and devoid of the *kl-3* loop. This suggests that the genes specified by these mutants are specifically required for the formation of the *kl-3* loop in the male germ line.

Taken together our screens have led to the identification of four genes involved in the formation of the *kl-3* loop. We believe that these findings open the way to the molecular dissection of the *kl-3* loop that must be viewed as a complex organelle whose formation is controlled by a region of the Y chromosome and at least four different autosomal products.

REFERENCES: (1) Bonaccorsi S., Pisano C., Puoti F. and Gatti M. (1988) *Genetics* 120:1015-1034; (2) Bonaccorsi S., Gatti M., Pisano C. and Lohe A. (1990) *Chromosoma* 99:260-266; (3) Pisano C., Bonaccorsi S. and Gatti M. (1993) *Genetics* 133:569-579; (4) Gatti M. and Pimpinelli S. (1992) *Annu. Rev. Gen.* 26:239-276; (5) Hackstein J.H.P. and Hostenbach R. (1995) *Trends Genet.* 11:195-200.