8.10†

Genetic analysis of the 67 region of Drosophila melanogaster. B. G. LEICHT and J. J. BONNER. Indiana University, Bloomington, IN.

We have been investigating the function of the small heat shock proteins (hsp28, 26, 23, and 22) of D. melanogaster. These proteins exhibit an interesting pattern of developmental regulation (Ireland et al. 1982. Dev. Biol. 93:498-507; Zimmerman et al. 1983. Cell 32:1161-1170) and have been implicated in the development of thermotolerance (Berger and Woodward, 1983. Exp. Cell Res. 147:437-442). These observations suggest that these proteins may have an essential function.

To address the function of the small hsps, we have initiated a genetic analysis of region 67B, the cytological location at which the genes for these proteins are clustered. We obtained a deletion extending from 67A-D (generated by Adelaide T. Carpenter) and have used it to screen for smaller deletions and point mutations within the 67 interval. Both DEB- and EMS-induced mutations have been isolated. We are currently in the process of mapping these and doing complementation analysis among the various mutants. This approach should lead not only to the identification of mutations affecting the small hsps, but should provide information about this region of the third chromosome in general.

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8.11

Fine structure analysis; unc-60 gene of Caenorhabditis elegans. K. S. McKIM, L. M. Turner and D. L. BAILLIE. Simon Fraser Univ., Burnaby, B.C., Canada.

As part of our labs intensive study of the left half of linkage group V in the nematode Caenorhabditis elegans (see Johnsen et al. abstract), we have begun a study of the unc-60 gene. unc-60 mutants are paralyzed to varying degrees. The five available alleles from strongest to weakest are e677, e890, e723, m35 and r398 (from P. Anderson). We have fine structure mapped the first four alleles but r398 moved too well for mapping. The procedure involved unc-34(e556)unc-60(x)+ / +unc-60(y)dpy-11(e224) heterozygotes self-crossing through the second generation and looking for rare non-Unc-60 worms. Both reciprocal and putative non-reciprocal exchange events were recovered. Only two mutant sites appear on the present map represented by e677 and m35. The recombinational size of unc-60 is large (0.01-0.017 map units). e723 and e890 map very close to m35; of these three, e890 has not been separated from m35 or e723. Based on one recombinant, e723 is on the order of 10^{-4} map units to the right of m35. All alleles mentioned above are hypomorphs as assayed by deficiency testing and of e677, e890, e723 and m35, none are sup-7 suppressed. Our work at present involves isolating new alleles both for mapping and in the hope of obtaining null alleles. Since both e677 and e890 are lethal when heterozygous to a deficiency, we predict that null unc-60 mutations will be recessive lethals and can only be recovered as heterozygotes. An F1 screening procedure was therefore devised using unc-60(s1310) induced on an eT1 lethal chromosome. The induction frequency with 0.012M EMS is 1/3000 (4/12000). The four new alleles are currently being mapped and tested to see if they are amorphs. This research has been supported by NSERC, National Cancer Institute (Canada) and Muscular Dystrophy Association (Canada) grants to D.L.B.

8.12

Mendelian segregation and assortment for 7 genetic characters in ringneck doves, Streptopelia risoria. W. J. MILLER. Iowa State University, Ames, Iowa.

Over 3,000 offspring from 603 matings in single pair cages were classified for some or all mutants at 7 genetic loci: silky plumage; sex-linked dilution; albino; ivory; pied; rosy color; and peanut -Maakia lectin reactivity of the erythrocytes. The sex-linked dark (wild type)-blond-white was verified as a triple allelic series in decreasing order of dominance as reported by Cole (1930). The autosomal partial dominant silky plumage also was confirmed. The albino mutant from Japan (Tange, 1949) was confirmed as an autosomal recessive. Ivory (Taibel, 1969), pied, and rosy also are autosomal recessives. The colors show various interactions. As expected, albino is epistatic to the other color mutants. The blond-rosy combination = "peach"; the white-pied combination = "black eye white"; ivory-rosy = "cream"; and cream-pied = "peaches and cream". Combinations of silky, lectin reactivity, and the plumage color mutants show no unusual interactions.

The agglutination reactions of the peanut-Maakia lectins with red cells form a closed, mutually exclusive system, peanut negative = Maakia positive being dominant. Monohybrid ratios fit Mendelian expectations well, except for rosy and ivory, rosy being considerably deficient. Differential mortality is not evident.

Dihybrid testcross data indicate no linkage among the 7 loci.