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Cytological localization of the *Drosophila melanogaster* *Dhr38* gene.

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The *Dhr38* gene codes for a protein belonging to superfamily of steroid hormone receptors and plays an important role in regulation of metamorphosis processes at late developmental stages in *D. melanogaster*

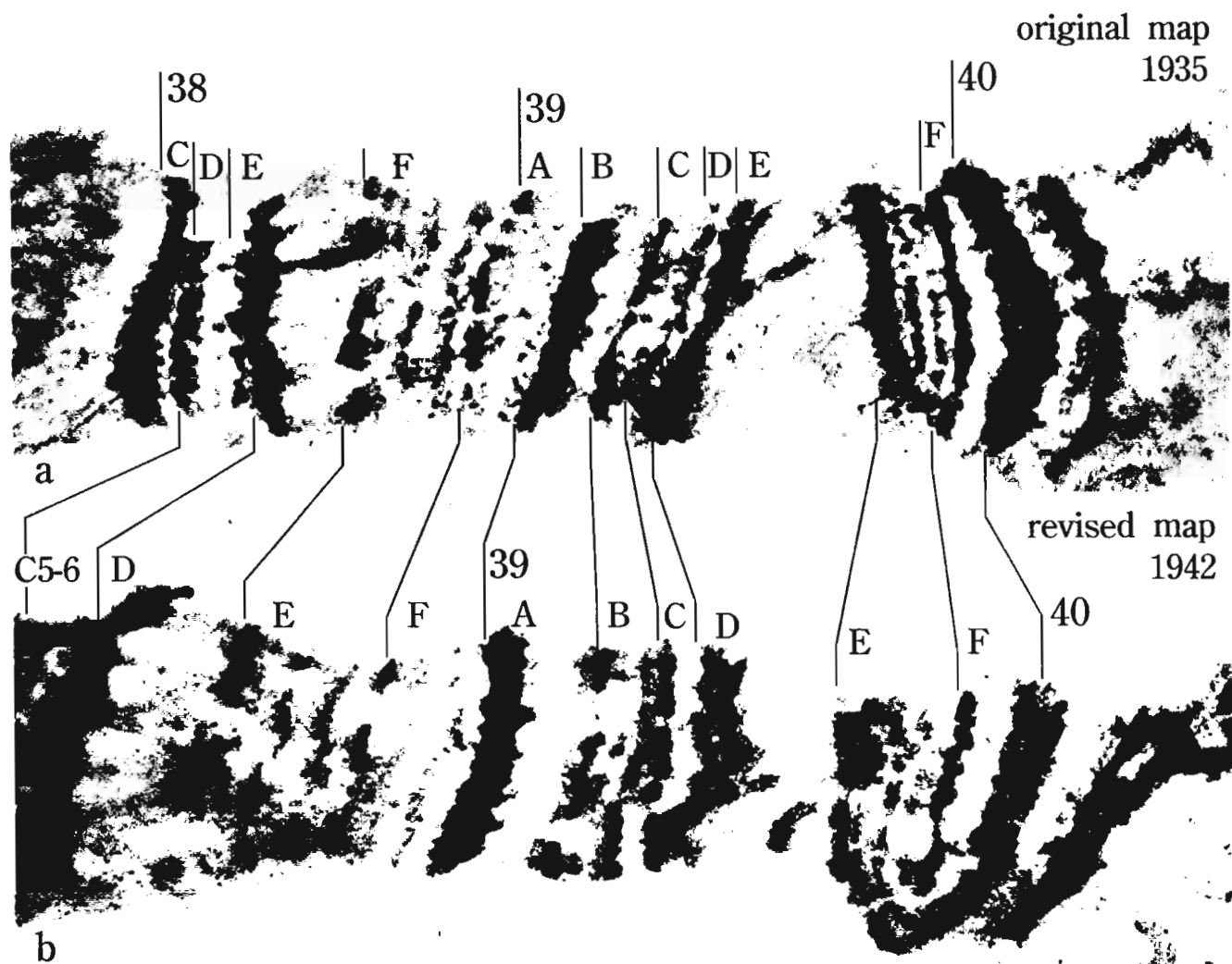


Figure 1. Electron microscopical map of 38C-39F region. Batumi L strain. Sections and subsections are designated according to C.B. Bridges, 1935(a) and P.N. Bridges, 1942(b).

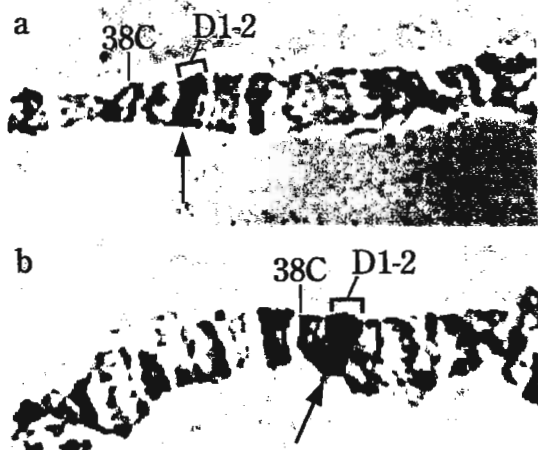


Figure 2. *In situ* hybridization of λ TD31 DNA (a) and P-element DNA (b) labeled by biotin with polytene chromosome salivary glands of *l(2)02306* strain. Arrows indicate label localization.

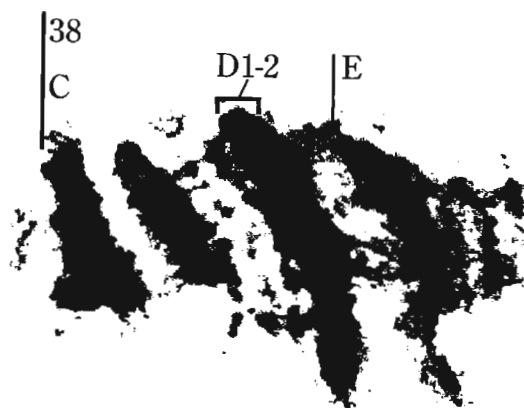


Figure 3. EM photography of the 38C-38E region in *l(2)02306* strain.

(Figure 2b), containing insertion of PZ construction in the TATA box region of the *Dhr38* regulatory zone (Kozlova *et al.*, 1998). PZ construction contains material of *lacZ* and *ry* genes and its length is about 17kb. That is why it could be proposed that insertion of such construction to *l(2)02306* strain close to the 38D1-2 band leads to formation of a new band, while its absence witness to joining of transposon material with the band as it was observed in analysis of other transposed DNA fragments (Semeshin *et al.*, 1989). As it is shown in Figure 3 EM analysis of the 38D region in *l(2)02306* strain does not reveal a new morphological structure (for comparison see Figure 1a). Insertion material probably joins to the 38D1-2 band and is incorporated into the band structure. From the data obtained we conclude that the *Dhr38* gene is localized in the dense single 38D1-2 band of the 2L chromosome.

(Fisk and Thummel, 1995; Sutherland *et al.*, 1995; Kozlova *et al.*, 1998). According to *in situ* hybridization data, *Dhr38* is localized in the 38 region of 2L chromosome (Sutherland *et al.*, 1995). When mapping the 38-39 region some confusion takes place connected with divergences in subsection boundary designations in original (C.B. Bridges, 1935) and revised (P.N. Bridges, 1942) maps (see as well Lefevre, 1976; Lindsley and Zimm, 1992). In detail, this difference was described earlier (Saura and Sorsa, 1979) and is connected with shifts of subsection boundaries in the revised map of 1942, where subsections 38C and 38D (1935) are combined into a single one, 38C (1942), and on the contrary, subsection 39E (1935) is divided into two, 39D and 39E (1942).

To make the gene location clear, new electron microscopic (EM) mapping of the 38C-38F region was performed. The material and methods used were the same as previously described (Semeshin *et al.*, 1985a). Hereinafter we will use designations of the revised map of P.N. Bridges (1942) which were used earlier for EM mapping of this and other chromosome regions (Saura and Sorsa, 1979; Semeshin *et al.*, 1985b).

The data obtained by EM mapping of the region are given in Figure 1. The banding patterns found in EM studies correspond well to the original Bridges map (1935), if "doublets" in 38E, 39B and 39F sections, as well as "triplets" in 38C and 39E regions, are considered as single bands. Divergences of the revised Bridges map (1942) and previously obtained EM data (Saura and Sorsa, 1979; Saura, 1983) follow: the 38C5-6 band consists of two single bands; all other bands designated as double look like single ones, and fine bands, such as 38C4, 10, 38F2, 6, 39A6, 39C3, 4, 39D4, 5, 39E5 were not revealed in this study.

For localization of the *Dhr38* gene on the new EM map *in situ* hybridization of biotinylized DNA probe of λ TD31 clone containing cDNA of this gene was carried out with polytene chromosomes. A signal was observed in the region of the large 38D1-2 band (Figure 2a). A similar pattern was obtained after *in situ* hybridization of P-element DNA with chromosomes of *l(2)02306* strain

Several deletions in the 38-39 region were mapped in the study. The new data on the break points of the deletions are given below.

Df(2) DS8: 39A6-7 – 39D3

Df(2) DS9: 38D1-2 – 39B

Df(2) TW1: 38B3 – 39D

Df(2) prA14: 37D – 39B2

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Ontogenetic profiles of male accessory gland secretory proteins in a few species of *nasuta* subgroup of *Drosophila*.

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Seminal fluid molecules critical for many of the mating induced changes in *Drosophila* are produced in the male's accessory gland (Chen *et al.*, 1988; Kalb *et al.*, 1993; Harshman and Prout, 1994; Chapman *et al.*, 1995). These secretory proteins are sex specific, stage specific, and tissue specific (Chapman and Wolfner, 1988). Their transcripts and translational products can be detected right from the time of adult eclosion (Chen, 1985).

Stumm-Zollinger and Chen (1985) have shown that the accessory gland secretory proteins in *D. melanogaster* comprise 40 fractions in one-dimensional gels and 85 in two dimensional gels. It has been documented that in unmated males 7 days after eclosion, the secretory proteins that accumulated in the gland lumen amounts to nearly three quarters of the total soluble protein (Chen, 1991).

The *nasuta* subgroup of *Drosophila immigrans* group consists of a cluster of morphologically almost identical, related species having varying degrees of reproductive isolation (Wilson *et al.*, 1969). Shivanna and Ramesh (1995) working with the male accessory gland secretory proteins in two *nasuta* subgroup species, namely, *D. n. nasuta* and *D. s. neonasuta*, have shown that the patterns are much simpler and the accumulation of secretory proteins reaches maximum in about a week of post eclosion in the unmated males. However, the information pertaining to developmental changes in the male accessory gland secretions of both *D. melanogaster* and *nasuta* subgroup is confined to quantitative measurements. Thus the qualitative studies involving the developmental patterns of the secretory protein fractions are lacking. Present investigations were undertaken to study the pattern of accessory gland secretory protein profiles during the development of the imago in seven species of *D. nasuta* subgroup, to compare the extent of variation if any, in this tissue specific, sex specific, and stage specific protein among closely related species.

In the present study, we have used *D. nasuta nasuta* (201.001), *D. n. albomicans* (202.001), *D. n. kepulauan* (203.001), *D. kohkoa* (204.001), *D. sulfurigaster sulfurigaster* (205.001), *D. s. albostrigata* (207.001) and *D. s. neonasuta* (206.001). All these stocks were obtained from *Drosophila* stock centre, University of Mysore, Mysore, India. All these cultures were maintained at $22 \pm 1^\circ\text{C}$ under uniform conditions. For the experimental purposes, synchronized eggs were collected following the modified method of Delcour (Romachandra and Ranganath, 1988). 50 eggs thus collected were allowed to develop in $3'' \times 1''$ vials containing equal quantities of food medium, maintained at a temperature of $22 \pm 1^\circ\text{C}$. The adult males, within 3 hours of their emergence from such cultures, were isolated from females and placed in fresh culture vials and were also maintained under the said environmental conditions.