Two hundred flies were hydrolyzed and the heads placed in lactophenol on microscope slides. Camera lucida drawings depicting the head were made using a wild-M8 stereoscopic microscope X80. For each group of head bristles emcompassing the eye, average number of bristles was determined from the drawings. An optical comparator (reticle graduated to 0.1 mm) was used to determine distances between diverse groups of bristles and those within a group. Data from 200 heads were averaged to produce a "typical" eye. Conversion factors were applied to each tuh eye to adjust its dimension to that of the model eye and the locations of the defects determined. The 200 tuh abnormalities selected for analysis were prescreened to insure that appropriate bristle markers were represented for accurate spatial mapping.

Camera lucida drawings are shown in Fig. 1a-f for the abnormalities. A compositie of defects seen in Fig. 1b,c,f and a group of abnormalities surrounding the entire eye are presented in Fig. 1a. Three restrictive margins were found. Figure 1a,b and c indicate that a large number of irregularities are confined to either the anterior or posterior side of a dorso-ventrally oriented restriction line that lies slightly posterior to the medio-lateral axis of the eye. Those abnormalities exhibited in half-heads demonstrating extensive reductions of the ommatidial number fail to observe this line. At about 130 µm down the longitudinal axis from the dorsal-most eye a region of high activity (HA) was observed (Fig. 1b). It lies on the anterior-posterior restriction line slightly above the horizontal bisector of the eye and expresses numerous abnormalities. Approximately 40 µm ventral to the top of the eye, there is a rather nebulous horizontal restriction line inasmuch as abnormalities more frequently exceed it than the previously described line (Fig. 1b,c,d and f). In the lower quadrant, roughly 50 µm from the bottom of the eye, there is another weak restrictive region (Fig. 1b,c and e). Small, isolated abnormalities circumscribed by ommatidia were occasionally documented in this area. The abnormalities in Fig. 1d and 1e exceed the dorsal and ventral restriction lines. Deviations in this neighborhood generally border a reduced eye.

Some previously described restriction lines correspond to regions frequently observed by the tuh defects. However, no specific abdominal tergite was confined to any of these regions although 8th tergite was expressed only in the anterior eye.

Supported by NIH Grant AGO-1846, NSF Grant PCM-8403124, ACS-Fla. Div. summer research fellowship to JLC.

References: Baker, W.K. 1978, Dev. Biol. 62:447-463; Campos-Ortega, J.A. & M. Waitz 1978, Wilhelm Roux's Arch. 184:155-170.

De Frutos, R. and L. Pascual. University of Valencia, Spain. Weak points and ectopic pairing in polytene chromosomes of **Drosophila subobscura.**

Intercalary heterochromatin in polytene chromosomes has been related to different biochemical and cytological features, such as ectopic pairing, tendency to break, late replication, etc. In a first attempt to detect intercalary heterochromatin sites in polytene chromosomes of **Drosophila subobscura**, the tendency to break (weak points) and ectopic pairing, were analyzed.

A total of 1152 slightly squashed nuclei of larval salivary glands were observed by optic microscopy analysis. 714 breaks and 374 ectopic contacts were detected. Centromeric contacts were not included because most nuclei showed centromeric pairing. Only ectopic contacts between not-centromeric or between non-centromeric and centromeric regions were taken into account. Weak points and ectopic contact sites are indicated in Fig. 1. Their location is based on the standard salivary gland chromosome map of Kunze-Mühl & Müller (1958). The map includes the situation of weak points or ectopic pairing sites only, but not their frequencies. A total of 63 weak points and 151 contact sites were identified. The number of weak points is clearly lower than ectopic contacts. In general, break points coincide with sites of ectopic pairing. The distribution of both features does not seem to be erratic. Clusters of them are found in some regions, for instance, the proximal half of the J and U chromosomes. On the other hand, weak points do not coincide with the boundaries of inversions. These chromosome arrangements are very frequent in **Drosophila subobscura.** The various types of weak chromosome points described by Zhimulev et al. (1982): breaks, semibreaks, constrictions and shifts, were found in polytene chromosomes of this species. Depending on the regions, they tend to show one or another type of break. For instance, 23E site generally shows constrictions, 27C shifts, etc. With respect to the regions involved in each of the ectopic contacts, they tend to take place between neighbouring zones of the same chromosome. Most of them occur between strong bands. Chromatin threads arise from either intact or broken large bands. However, in a few cases a tangle of threads arise from a whole interband, for instance, the whole of section 47. Also, threads arise from active puffs or the Balbiani ring with a very low frequency. Furthermore, in many cases

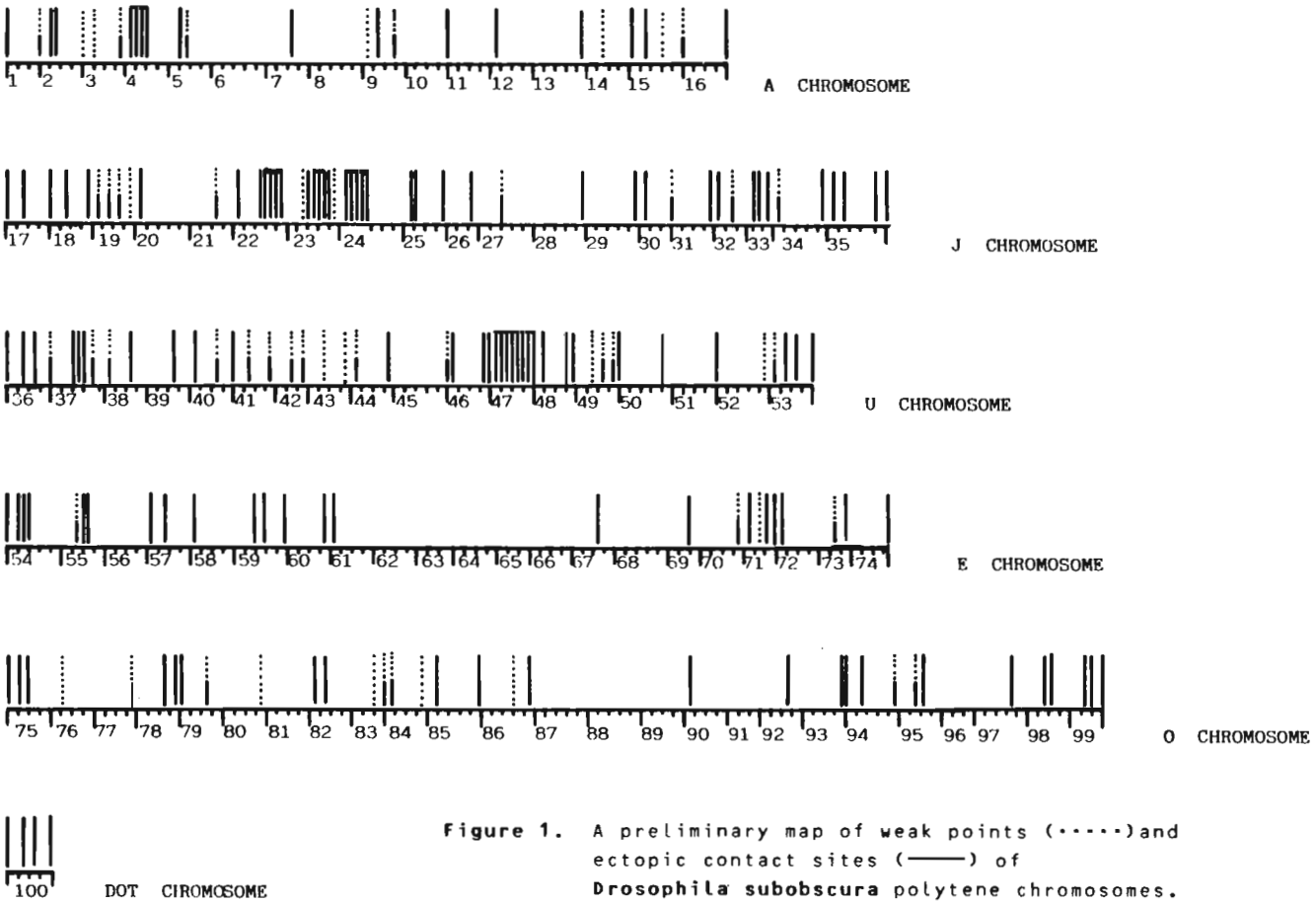

Figure 1. A preliminary map of weak points (·····)and ectopic contact sites (——) of **Drosophila subobscura** polytene chromosomes.

breaks, constrictions and ectopic contacts, are located close to active puffs. If both features could be taken as an indication of intercalary heterochromatin, it can be suggested that intercalary heterochromatin does not affect the gene expression of neighbouring regions.

References: Kunze-MÜhl, E. & E. MÜller 1958, Chromosoma 9:559-570; Zhimulev, I.F. et al. 1982, Chromosoma 87:197-228.

Del Puerto, G.A., J.J. Culich and C.J. Chihara.
University of San Francisco, California USNA.

Last larval instar cuticle protein patterns and their use for the identification of twenty-one species of Drosophila.

Ten different third instar larval cuticle proteins have been described for **D.melanogaster** and have been labelled as L3CP 1-9 (Figure 1). Genetic studies have shown that the production of each of these proteins is under the control of a different locus. L3CP 1-4 have been located on the second chromosome, whereas L3CP 5, 6, and 8 have been placed on the third chromosome (Fristrom et al. 1978; Snyder et al 1981, Chihara et al. 1982; Chihara & Kimbrell, unpubl.). Studies have shown that in related species some of the cuticle proteins seem to be shared among species in so far as the amino acid constitution of the proteins is concerned (Hackman 1971, 1976; Willis et al. 1981). Recently, electrophoresis has become an invaluable tool for insect systematics. Most of these studies have focused on genetic variation of enzymatic loci and have helped in the description and identification of different species (Avise 1974; Berlocher 1984).

Twenty-one different species of Drosophila belonging to the groups **melanogaster, obscura, virilis,** and **repleta** were studied for their urea soluble, last instar larval cuticle proteins using P.A.G.E. Each species was found to have a unique cuticle protein pattern that can be used to establish larval species identity. In addition, we have also developed consensus on last larval instar cuticle protein patterns for four species: **D.simulans, D.persimilis, D.pseudoobscura,** and **D.virilis.** Our results suggest that it is possible to identify a particular species of Drosophila based on its last instar larval cuticle protein pattern.