Forward, K. J. and B. P. Kaufmann. University of Michigan, Ann Arbor, Michigan. The bipartite nature of the salivary-gland X chromosome.

When Drosophila melanogaster females are mated with D. simulans males, the adult hybrid progeny are ordinarily female, although exceptional (non-disjunctional) males are obtainable (Sturtevant, Genetics 5, 1920; Morgan, Bridges and Sturtevant, Bibliog. Genet. 2, 1925). A cytological examination of third-instar larval salivary-gland chromosomes from the cross, D. melanogaster, Sw-b ♀ x D. simulans ♂ revealed that most individuals were female, although occasional males, having a single unpaired X chromosome, were detected. The diameter of this X usually equals or surpasses that of the paired autosomal homologues within the complex (as is shown on the accompanying photomicrograph), and may be assumed - as noted by Dobzhansky in Chromosoma 8, 1957, following a study of hybrids from the cross D. insularis x D. tropicalis - to present a "visible counterpart of the genetic phenomenon of dosage compensation." Spectrophotometric studies by Aronson, Rudkin, and Schultz (J. Histochem. & Cytochem. 2, 1954) indicated that in D. melanogaster the amount of DNA in the salivary-gland X chromosome of the male is about half as much as in the paired homologous X's of the female. A similar quantitative relationship is suggested by the faint stainability with acetic-orcein of the X in the melanogaster-simulans hybrid as compared with the more intense colorability of the arms of the autosomes (see photograph).

We have observed that unpaired X chromosomes in third-instar salivary gland cells of malanogaster-simulans hybrid males vary greatly in length, breadth, and puffing pattern. The significance of these variations with respect to developmental processes will be discussed in another paper. What we would like to point out here is that the X, when well extended as shown in the accompanying photomicrograph, often reveals with striking clarity a bipartite structure (see intertwining strands at arrows). The X of the male fly has sometimes been designated as "unipartite." but it is apparent that a subsidiary order of organization can be recognized at the level of resolution afforded by the light microscope. By analogy, chromosomes composed of paired homologues should at times reveal a quadripartite structural pattern. That this is indeed the case was reported, for example, by Frolova for D. robusta (Biolog. Zhurnal 6, 1937), by Melland for a chironomid (Proc. Roy. Soc. Edinb., B, 1942),

and has been observed occasionally by us in squash preparations of salivary-gland chromosomes of D. melanogaster (although more commonly the limits of the subsidiary units are masked by the close apposition of the strands that constitute the giant chromosomes). These microscopically discernible subunits assumedly reflect the basic pattern of organization of the chromosomes in the mitotically-active cells from which the salivary-gland progenitors are derived, and they undergo pari passu a series of endomitotic replications to produce the giant polytene chromosomes. (Supported by N.I.H. Grant GM-10499).

Miller, D. D., N. J. Westphal and R. A. Voelker. University of Nebraska, Lincoln, Nebraska. A preliminary note on gene sequence variation reinvestigation in the C chromosome of Drosophila athabasca.

Novitski (1946, Genetics 31:508) reported that the salivary gland chromosomes of D. athabasca revealed the C chromosome to be relatively variable and that certain of its sequences were restricted to the west, others to the east. Therefore, it seemed desirable to reinvestigate gene sequence variation in this chromosome for a possible relationship between structural heterozygote configurations and the partially isolated western-northern subdivisions of the species, distinguished by Y chromosome type, duration of copulation, and pigmentation (Miller and Westphal, 1965, Genetics 52:459). Numerous C chromosome configurations have been observed, all evidently based on one or more inversions. Their analysis is incomplete, but early results seem significant.

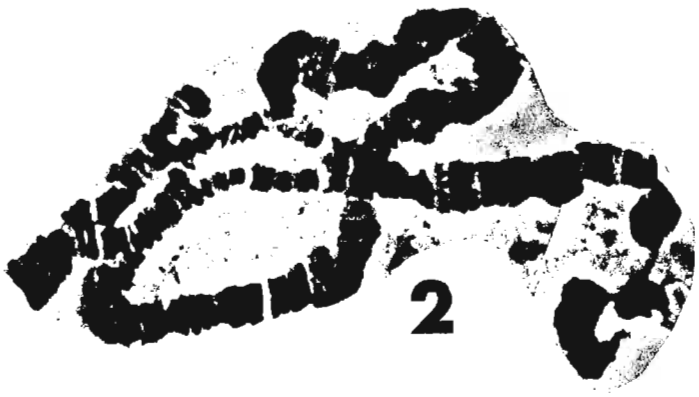

Figure 1 (Raton Pass, New Mexico) shows two configurations that appear to be widespread in the western strains at our disposal but have not been found in the eastern ones. The small subterminal double configuration (1A) has been encountered in strains from British Columbia (Okanagan), Idaho (Boise), Minnesota (Hallock), New Mexico (Raton Pass), Oregon (Eel Creek, Eugene), and Washington (Sequim Bay). This resembles the M/O heterozygote configuration of Novitski (1946, Fig. 5A); coexistence of the M and O sequences was reported by him him from British Columbia, Oregon, Washington, and Wyoming. The single submedian inversion configuration (1B) has been found in our strains from British Columbia (Okanagan), Minnesota (Duluth, Hallock), New Mexico (Raton Pass), Oregon (Eugene), and Washington (San Juan Islands). All these western strains are characterized by a Type I or Type V (Sequim Bay) Y chromosome, long copulation time, and dark pigmentation; they also demonstrated partial or complete failure to mate with laboratory strains of D. athabasca with Types II and III Y chromosomes. Other configurations found in these western athabasca strains were all relatively short and/or single inversion dependent.

None of the western configurations is clearly present in our eastern strains. Although these strains do have relatively small, simple inversion configurations, most also