P 41 D. (D.) ezoana Takada et Okada
P 42 D. (D.) littoralis Meigen
P 43 D. (D.) lummei Hackman
N 44 D. (D.) borealis Patterson
H 45 D. (D.) montana Patterson et Wheeler
C 46 D. (D.) immigrans Sturtevant
H 47 D. (D.) testacea von Roser*
P 48 D. (D.) phalerata Meigen
N 49 D. (D.) rellima Wheeler
H 50 D. (D.) transversa Fallen
N 51 D. (D.) melanderi Sturtevant

* Takada & Toda (1981) reported D.putrida from MacKenzie Delta, but that was a misidentification of D.testacea.

The northernmost subarctic drosophilid fauna is characterized by the relative richness in species number of the following taxa: Chymomyza, Scaptomyza, the obscura group (Nos. 28-33) and the virilis group (Nos. 41-45). It is notew thy that the southernmost antarctic drosophilid fauna is monopolized by Scaptomyza (Brncic & Dobzhansky 1957). The relative percentages of the four chorological elements, calculated by excluding unidentified species, are as follows: Palaearctic (19 spp., 40.4%), Nearctic (12 spp., 25.5%), Holarctic (11 spp., 23.4%) and Cosmopolitan (5 spp., 10.6%). The relatively high percentage of Holarctic elements suggests that the intercontinental faunae exchange, possibly across Beringia, repeatedly occurred until relatively recent times in the northernmost subarctic region.

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The structure of two rearrangements resulting in the Pgd gene position effect in Drosophila melanogaster.

The study shows that the previously described rearrangements T(1;4)pn2 and Tp(1)pn3 (Ilyina et al. 1980) are pericentric inversions, designated In(1LR)pn2a and In(1LR)pn2b, respectively, with very similar genetic structurs.

Analysis of recombination in pn2a/y cv v f car females has shown the genetic map of the rearrangement to differ from that of the normal X chromosome. The pn2a rearrangement is characterized by the following order of the markers: cv-v-f-car-y (cf. y-cv-v-f-car in the normal chromosome). The distances between the y gene and the markers nearest to it, car and f, in the rearrangements are in good agreement with the reported (Schalet & Lefevre 1976) distances between these markers and the centromere. The easiest way to explain these results is to assume that the distal section of the X chromosome carrying the y^+ gene is transferred to the centromeric region of the X chromosome and not to the 4th chromosome, as formerly believed. The genetic maps of the rearrangements pn2a and pn2b do not differ. Analysis of the polytene chromosome shows the distal end of the rearranged chromosome to break off in the 2DE region. The telomere of the rearranged chromosome consists of heterochromatic material, as attested by its metachromasy (bluish staining with azure-eozine, as opposed to the violet staining of the bulk of the chromosomes) and the presence of highly repetitive sequences, probably satellite DNA, revealed by in situ hybridization with total labelled DNA in a set-up where the hybridization of highly repetitive DNA is selectively favoured. THe 1A-2DE region is associated with the chromocenter through the 2DE segment. The metaphase chromosomes show an enlarged XR the size of the 4th chromosome, which probably corresponds to the 1A-2DE fragment. Comparative analysis of the data on the recombination and structure of the polytene and metaphase chromosomes suggests that the rearrangements are pericentric inversions of the X chromosome (Figure 1).

The euchromatic break point of the inversions lies in the 2D-F region, whose fine genetic structure has been studied earlier (Gvozdev et al. 1973; Gvozdev et al. 1975). Genetic analysis has demonstrated that in both inversions the genes corresponding to

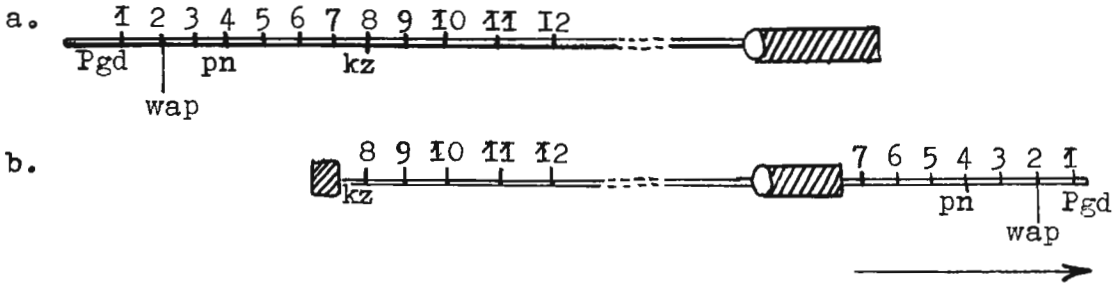

Figure 1. Structure of the normal X chromosome (a) and the rearrangements pn2a and pn2b (b). Numbers designate complementation groups for the region which has been studied earlier through saturation by lethals (Gvozdev et al. 1975). The shaded rectangle denotes the heterochromatin right arm of the X chromosome. The arrow shows the direction in which gene inactiviation proceeds.

complementation groups 1 (Pgd), 2 (wap), 3,4 (pn), 7 (groups 5 and 6 were not analyzed, as the corresponding lethals had been lost) of the 2D-F region were localized in the right arm, and complementation groups 8 to 12 in the left arm (Figure 1).

In the In(1LR)pn2a and In(1LR)pn2b inversions the 2D-F region is divided into two units, each finding itself close to the XR heterochromatin (Figure 1), which is known to cause the position effect for euchromatic genes that have been moved to it. Indeed, one observes a strong position-effect inactivation of the genes in the right arm of the inversions, while the left-arm genes are not inactiviated.

The inactivation of the Pgd gene in the pn2a rearrangement is sharply enhanced by the removal of the Y chromosome. In the females the Pgd gene activity in In(1LR)pn2a is about 50% of the normal level, as assessed by the 6PGD activity in crude extracts. The Pgd gene activity in XO males amounts to 25% of the normal level. The heterochromatic Y chromosome, which is known to suppress position-effect inactivation, normalizes the Pdg gene is observed in the pn2b rearrangement: in males it comes to only 15% of the normal level. The inactivation of the pn gene is also stronger in the pn2b rearrangement.

The inactivation of genes corresponding to complementation groups 2,3,7 sharply reduces the viability of females that carry the inversions in a heterozygote with lethals for those groups. Their viability does not exceed 3% of the normal value. The inactivation is stronger in the case of the pn2b inversion.

The above results show, within the accuracy of the methods used, that the two rearrangements have the same structure but differ considerably in the intensity of the position effect. The causes of the difference in inactivation intensity are not clear. This difference might be due to autosomal modifiers. However, the difference in the position effect intensity persists when the 1A-2DE region, associated with heterochromatin, is transferred to another genotypic environment. This result suggest that the factors responsible for the difference are linked to the centromeric regions of the rearrangement.

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