

Typical Hybrid Dysgenesis is Absent from the Natural Population of *Drosophila melanogaster* in Japan

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Hybrid dysgenesis was investigated in a natural population of Japanese *Drosophila melanogaster*. Hybrid females with rudimentary ovaries emerge from some interstrain crosses, when they are developed under high temperature, e. g., 29°C. These gonadal dysgenesis are observed in one of the two reciprocal crosses, in which paternal strains are called "P" strains and maternal ones are referred to as "M" strains. Most strains from natural populations in U. S. A. and Australia were judged P by Kidwell *et al.* (1977), since males of them caused dysgenic daughters when they were mated with females from the M strain.

However, 46 isofemale strains from Katsunuma, Japan (strains kept in our laboratory for 6 months at 18°C), did not cause dysgenesis both when males of them were mated with the M strain and females with the P strain. Then, all of these strains were judged "Q" strains (Engels and Preston, 1981) and the nature of the wild population at Katsunuma differed apparently from the populations in U. S. A. and Australia.

Among 11 long-established laboratory strains (8 to 30 years) derived from Japan, 6 were M strains and others were Q or possibly in the intermediate state between Q and M. Therefore, Q strains discovered at Katsunuma will turn into M when they are kept in the laboratory.

Biochemical Phylogeny of the *Drosophila montium* Species Subgroup

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The *D. montium* species subgroup to which 61 species belong is the biggest subgroup in the *D. melanogaster* species group (Tsacas, 1979). Recently, Baimai (1980) surveyed karyotypes of twenty species including new species such as *D. leontia* and *D. bocki*, and found much variation in the fourth and Y chromosomes, showing that most of the species can be distinguished by the karyotypes. Although morphological characters (sexcombs and genitalia of males) as well as karyotypes are useful tools for the qualitative identification of these species, quantitative relationships (e. g. genetic distances) between these species have never been shown in this subgroup.

In this study, a phylogenetic tree among 21 members (14 different species) of the subgroup was constructed, based on the data set obtained by two-dimensional electrophoresis (2DE). The results are as follows; The 21 members were classified into four groups. The first group is the *D. kikkawai* complex to which six species belong (*D. bocki*, *D. pennae*, *D. kikkawai*, *D. leontia*, *D. lini* and *D. barbarae*). The second one includes three species, *D. jambulina*, *D. punjabiensis-like* and *D. punjabiensis*, whose systematics was reported in Jap. J. Genet. (in press) in more details. The third one is the *D. auraria* complex including four species (*D. auraria*, *D. biauraria*, *D. triauraria* and *D. quadraria*). The last one is *D. rufa* which is distantly related to the other species. However, an analysis of starch gel electrophoresis showed that *D. rufa* was more closely related to the *D. kikkawai* complex, and that only *D. jambulina* was classified into a separate group. In the 2DE analysis, it was found that *D. quadraria* was very similar to *D. triauraria*, although these two species are different in geographical distribution. It suggests that *D. quadraria* seems to be a variation of *D. triauraria*. In addition, an unclassified species which had been collected on Iriomote Island (Japan) in 1979 was found to be the same as *D. bocki* in the 2DE analysis. This was confirmed by an interspecific hybridization between them. Thus, it was evidenced that these electrophoretic techniques are useful as adjunctive tools in the study of systematics.