Mutation Notes — Other Species

Rediscovery of *spread* mutation in *Drosophila ananassae.*

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Drosophila ananassae has been recorded from all six geographical regions but is largely circumtropical in its distribution and is of common occurrence in India. This species is frequently found in and around the human habitats. The genetic research on *D. ananassae* was started by two eminent Japanese geneticists of their time, H. Kikkawa and D. Moriwaki, during the 1930's. A number of investigations have been carried out on different aspects like population, behavior and evolutionary genetics in *D. ananassae* in our laboratory since the 1960's (see review by Singh, 2000, for references).

H. Kikkawa had discovered the *spread* (*sd*) wing mutation in *D. ananassae* for the first time in 1935 (see Moriwaki and Tobari, 1975). The linkage map of *D. ananassae* constructed by Kikkawa (1938) shows that the spread mutation is located on chromosome II of *D. ananassae*.

Figure 1.

Because of World War II, research became impossible in many countries and valuable stocks were endangered. Almost all stocks maintained by D. Moriwaki (also of H. Kikkawa who had provided all his *Drosophila* stocks to D. Moriwaki in 1938 as he developed interest in silkworm genetics) had been lost even after his several efforts (Crow, 1989; Tobari, 1993) including the *spread* mutation stock of *D. ananassae*.

We have found two male and one female *spread* wing mutant flies (*spr*) in isofemale line of Seer (SG- 11) established in 2000, and a separate laboratory stock of this mutation has been established and is being maintained in our laboratory. The wings of flies are held out at 180^0 angle to the body axis (Figure 1) and droop in older flies. Both sexes are fertile and the flying capacity is very weak. The mutant stock was crossed reciprocally with the wild stock of SG- 11 and all the flies of both crosses irrespective of sex were normal for wing morphology in F_1 generation. In F_2 generation in both the crosses, nearly a 3:1 ratio between normal and *spread* wing flies was found, which indicates that the *spr* (we are suggesting this symbol for having similarity in phenotype with that of *D. melanogaster*) in *D. ananassae* is a recessive autosomal mutation. The linkage analysis with *cu e se* (on chromosome II) suggests that *spr* in *D. ananassae* is located on chromosome II as it was initially suggested by H. Kikkawa.

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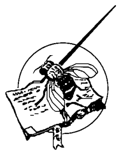
References: Crow, J.F., 1989, Genetics 122: 467- 469; Kikkawa, H., 1938, Genetica 20: 458-516; Moriwaki, D., and Y.N. Tobari 1975, *Drosophila ananassae*. In: *Handbook of Genetics* (King, R.C., ed.), Vol. 3, Plenum Pub., New York, USA, 513- 535; Singh, B.N., 2000, Current Science 78: 391-398; Tobari, Y.N., (ed.) 1993, *Drosophila ananassae*: Genetical and Biological Aspects, Japan Scientific Societies Press, Tokyo, Japan and Karger, Basel, Switzerland, xi- xii.



Detection of *yellow* mutation in North American *Drosophila subobscura.*

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Drosophila subobscura were collected in Port Hardy (British Columbia, Canada) on 8 and 9 June 2002. Several isofemales lines were founded and maintained in the laboratory. We detected a conspicuous yellow male in one line after several generations (October 2002). The mutation was confirmed as *yellow* by crossing male offspring of yellow-colored males with virgin females of the *y ch cu* (*yellow cherry curled* strain; Solé, 1997). All flies obtained in the next generation were *yellow* phenotype.

The *yellow* mutation is well known in Palearctic *D. subobscura* (Krimbas, 1993; Mestres, 1996; Solé, 1997; Solé and Mestres, 1999). However, it has never previously been detected in North America, including in prior collections from Port Hardy.

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References: Krimbas, C.B., 1993, Drosophila subobscura: *Biology, Genetics and Inversion Polymorphism*. Kovac, Hamburg; Mestres, F., 1996, Dros. Inf. Serv. 77: 148; Solé, E., 1997, Dros. Inf. Serv. 80: 105; Solé, E., and F. Mestres 1999, Dros. Inf. Serv. 82: 121.

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