

Basden, E.B. Institute of Animal Genetics, Edinburgh, Scotland. *Drosophila mycethophila* Goureau and *D. testacea* Goureau.

In 1865 Colonel C.C. Goureau published a second supplement to his "Les Insectes Nuisibles aux Arbres Fruitières aux Plantes Potagères", a Paris pamphlet of 147 pages. On page 120 he described *Drosophila mycethophila* (spelt *mycethophila* on p. 141) from toadstools (champignons),

it differing from *D. transversa* Meigen (sic), i.e. *transversa* Fln., by having only two, not four black marks on each abdominal segment. This could be *D. histrio* Mg. (1830), or even *D. limbata* v. Ros (1840), or *D. kuntzei* Duda (1924); and less likely to be *D. phalerata* Mg. (1830), which frequently (φ) has four-spotted segments.

On page 119 he describes *D. testacea* Goureau, also from champignons, it differing from *transversa* by the black third-antennal joint and clear transverse veins. This species is most probably *D. cameraria* Hal. (1833), and not *D. testacea* v. Ros (1840).

Goureau's specimens need to be examined to confirm their identity but they probably no longer exist and it is unlikely that his two toadstool species had not already been described, as suggested above. Goureau's name *mycethophila* should be made known, however, as D.E. Hardy has described *D. mycethophila* from Oahu (1965, *Insects of Hawaii*, 12: 376), which should now be given a new name. An apposite one would commemorate the 100 years between the two.

Falk, R. The Hebrew University, Jerusalem, Israel. Evidence against the one-to-one correspondence between bands of the salivary gland chromosomes and genes.

The cytological location of a series of lethals that were induced in the proximal segment of the X-chromosome of *D. melanogaster* by Lifschytz & Falk (*Mutation Res.* 8: 147-155; 1969) was determined in an experiment in which various proximal segments of the X chromosome, of known

cytological length, were tested for their capability to cover lethal effects. The segments of the X-chromosome were obtained from X-Y translocations produced by Nicoletti and Lindsley (*Genetics* 45: 1705-1760).

Females heterozygous for lethals that were mapped in the proximal segment were mated to males with the X-Y translocations. The recovery of hyperploid sons with the lethal chromosome and the X^P element of the translocation indicated that the lethal was located proximally to the known breakage point of the translocation. Of three translocations T(1;Y)14, T(1;Y)132, and T(1;Y)151 that all have their breakage point in 19F, the first two did not produce viable hyperploid males with even the most proximal lethals Q464 and P19. T(1;Y)151, on the other hand, covered lethals Q463, P19, 3DES and Q464. It did not cover E54, Q414, w2, R-9-29 or AA33. This, its breakage point was at the "hot spot" at section 18 of the complementation map of Lifschytz & Falk (1969).

Since T(1;Y)14 and T(1;Y)132 give fertile males only in the presence of an additional free Y, the possibility had to be considered that T(1;Y)/Y males produced only gametes that carried either both elements of the translocation or only the free Y, i.e., that the translocation elements did not segregate.

To test this possibility the reciprocal mating FM4/T(1;Y)132 x 1/Y.mal⁺ was tried with different lethals. In the mating with 1^{Q463} 11 y B females were obtained among a total of 174 daughters. These y B females obtained from their mother the FM4 chromosome together with the X^D element of the translocation, i.e., they were due to non-disjunction of the translocation elements. They survived as they obtained from their father the Y.mal⁺ chromosome. No hyperploid males with the lethal chromosomes were obtained in these matings. This proves that the absence of 1^{Q463}/X^P.Y^S was indeed due to their lethality.

Since section 19F of the salivary gland chromosomes has at most six visible bands and since from the complementation map T(1;Y)151 and T(1;Y)132 are separated by at least 20 functional units (two more units were identified in this segment since the publication of the map) the minimum estimate of genes per band in this segment is three. These results exclude the possibility of a one-to-one correspondence between salivary gland chromosome bands and cistrons.

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