chromosome. Southern blot analysis using DNA probes spanning the *m-dy* complex indicates that the m^{MR} mutation is a 19-25kb chromosomal deletion in the *m-dy* interval. Our unpublished molecular analysis of this region indicates the existence of separable *m* and *dy* transcription units, and we postulate that m^{MR} removes part or all of both transcription units.

Mutation Notes - Other Species

Report of E. Solé. Dept. Genètica, Facultat de Biologia, Universitat de Barcelona, Spain.
Spontaneous *yellow* mutation in the *ch cu* strain of *Drosophila subobscura.*

Two *yellow* male flies spontaneously arose in a homokaryotypic stock of *D. subobscura* kept in the laboratory for a long time. This stock bears the recessive mutations ch (*cherry*, bright red eyes) and *cu* (*curled*, wings curled concave upwards), both located on chromosome O. Another *yellow* male fly arose after some generations in a cross between a wild male and five *ch cu* females. Only the right half of this mutant individual was *yellow*; his half left was wild type. It was fertile and no mutant flies appeared either in the F1 or F2 of a cross with *ch cu* females.

The *yellow* mutation is recessive, located in the A (sexual) chromosome and has been previously described in *D. subobscura* (Krimbas, 1993; Mestres, 1996).

References: Krimbas, C.B., 1993, Drosophila subobscura: *Biology, Genetics, and Inversion Polymorphism.* Verlag Dr. Kovac, Hamburg; Mestres, F., 1996, Dros. Inf. Serv. 77: 148.

Report of Albert Kamping and Wilke van Delden. Department of Genetics, University of Groningen, P.O. Box 14, 9750 AA Haren, The Netherlands.
A rare *α-Gpdh* allele in *Drosophila simulans.*

In contrast to many other allozyme loci, *α-Gpdh* is remarkably invariable in *Drosophila.* The *α-Gpdh* locus is monomorphic for electrophoretic variation in almost all *Drosophila* species. Some species show alleles at very low frequencies and in only two out of almost 200 species that have been analyzed, the *α-Gpdh* locus is classified as polymorphic (*D. melanogaster* and *D. subarctica*). The low level of variation is ascribed to the important functions in energy metabolism of the enzyme. New mutants at this locus are assumed to be deleterious, and only under conditions without biochemical or physiological constraints new mutants may be maintained. Allele substitutions have taken place in the evolution of *α-Gpdh* in *Drosophila*, because different species carry different alleles. Alleles with identical electrophoretic mobility are restricted to certain species or species groups. The distribution and uniformity in alleles within and between species cannot be explained without the action of natural selection, where metabolic function of the enzyme and ecological niches of the species are assumed to be main factors in the evolutionary process of *α-Gpdh.*

Table 1. Changes of the rare $\alpha Gpdh^{S}$ allele frequency in laboratory *D. simulans* populations, started with different initial frequencies at 20°C and 29.5°C and raised under uncrowded conditions.

Temperature	Initial frequency	Generations 1	5	10	15
20°C	.25	.24	.25	.16	.14
	.50	.53	.52	.37	.31
	.75	.74	.69	.59	.59
29.5°C	.25	.28	.29	.21	.19
	.50	.51	.49	.41	.36
	.75	.72	.69	.65	.68

D. melanogaster is one of the exceptions concerning the level of variation at the *α-Gpdh* locus. Almost every wild population of *D. melanogaster* is polymorphic for two common alleles, Slow (*S*) and Fast (*F*). The sibling species *D. simulans* is monomorphic and carries an allele with identical electrophoretic mobility as the *D. melanogaster F*-allele. In consecutive years we observed an additional *α-Gpdh* variant in a wild population of *D. simulans* in The Netherlands. Electrophoretic mobility of this allele is comparable with the *S* allele of *D. melanogaster*, and its frequency reaches the level of polymorphism. Four out of 21 captured *D. simulans* females produced progeny (no hybrids) carrying the *S* allele in a frequency not significantly different from .25. We derived homozygous *S* and *F* strains, and laboratory populations with different