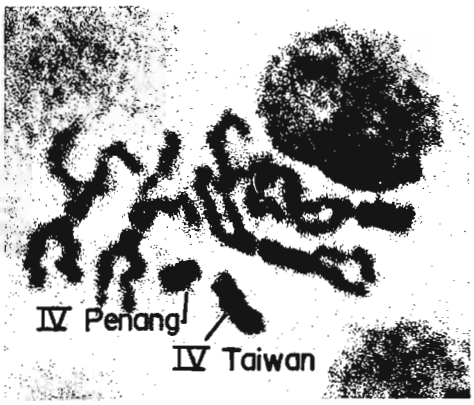

Fig. 1. Different fourth chromosomes in D. albomicans from Penang and Taiwan.

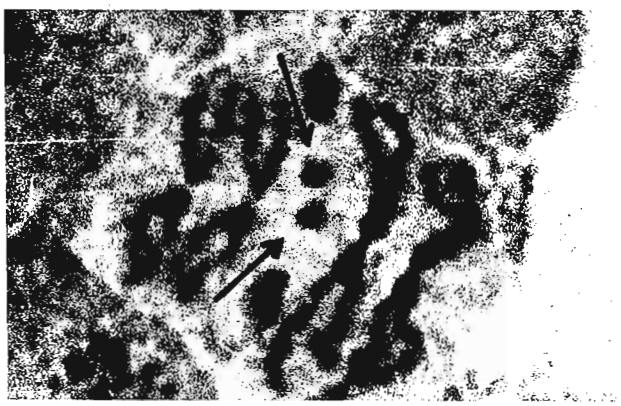

Fig. 2. Two extra "dots" of heterochromatin in D. albomicans from Chiang Mai.

The isofemale lines used in this study were collected and established by Dr. Wharton B. Mather, University of Queensland. The work reported was part of a Ph.D. thesis accepted by the University of Queensland in 1978.

Creus, A. and R. Marcos. Autonomous University of Barcelona, Bellaterra, Spain.
Relationship between mating speed and duration of copulation in D. melanogaster.

From a survey of published data on the genus Drosophila, it is clear that in various species, D. gaucha, D. melanogaster, D. persimilis, D. pseudoobscura and D. robusta, the mating speed is an important component of fitness. However, the relation between mating speed and duration of copulation has been the subject of very few studies. As a part of a wider analysis we present in this note the preliminary results.

The lines used in these experiments were derived from a wild type stock of D. melanogaster designated AR, isolated by R. Marcos in 1973 from a strain collected at the mouth of the Llobregat River, Barcelona. The flies were cultured and the experiments conducted at 25±1°C under standard light conditions. Samples of 50 males and 25 virgin females aged for 3 days were placed together in glass bottles of 500 ml. As soon as a pair commenced mating, they were sucked out. Mating speed and duration of copulation were scored in minutes. In each experiment the matings were scored only during the first hour. Ten replicas were done at each line.

The regression coefficients of duration of copulation with respect to mating speed were calculated. The results are summarized in the table.

Line	N (mated)	$b_{yx} \pm e_b$	F	t	d.f.
AR1	108	-0.108 ± 0.030	12.55***	3.54***	106
AR2	182	-0.138 ± 0.061	4.98*	2.23*	180
AR3	145	-0.128 ± 0.041	11.29***	3.13***	143
AR4	132	-0.133 ± 0.052	6.98**	2.58**	130

***- significant at 0.001 level; **-sigificant at 0.01 level; *- significant at 0.05 level.

From these results we can infer that there is a negative and significant regression; that is, the flies taking a long time to mate have a shorter duration of copulation. These results are in contrast to those obtained by Spiess (1968) in D. pseudoobscura.

Reference: Spiess, E.B. 1968, Amer. Nat. 102:363-379.

Comendador, M.A. University of Oviedo, Spain.
Abnormal bristles that show maternal inheritance in D. simulans.

During a routine analysis of a population of D. simulans recently captured in the Azores Islands, we observed an unusual proportion of flies that lack some dorsocentral and scutellar

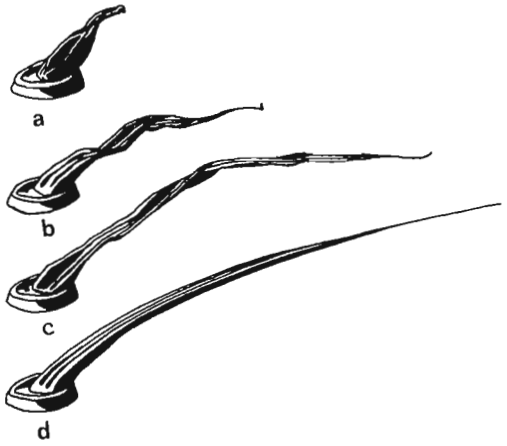

Fig. 1. Various types of bristle structures altered in size and/or shape in relation to the normal one (d), as seen under the scanning electron microscope (see text).

bristles. The 50 females with higher number of missing bristles were selected for individual mating to males from the same population. In all the progenies but one, a very small proportion of flies showed a low number (one or two) of missing bristles, as is often found in many natural populations. The progeny of a female, however, comprised an unexpectedly high number of individuals with most or even all dorsocentral and scutellar bristles either wholly suppressed or variously altered in their structure. This deviant phenotype (S) is most apparent in the dorsocentral and scutellar regions, although it shows up also in other bristle regions; our data will refer only to both dorsocentral and scutellar regions taken together.

The following types of altered bristles are observed: (1) bristle structures wholly suppressed; (2) only the basal ring left (which under scanning electron microscope appears as in Fig. 1a); (3) shortened and distorted bristle; (4) shortened, distorted and light-colored bristle; (5) normally large but distorted and light-colored bristle (Fig. 1). For the time being and in order to clear up its mode of inheritance, we assume that all these five graded types of altered bristles result from the variable expressivity of one and the same phenotype.

The first noteworthy feature of S strain is its sex dimorphism: there are more deviant males (45.12%) than females (30.20%), and the mean number of abnormal bristles per affected fly is also significantly higher in males (2.32±0.06) than in females (1.66±0.07). This is contrary to most known cases of Drosophila strains with missing bristles, where both penetrance and expressivity for bristle suppression are greater in females than in males.

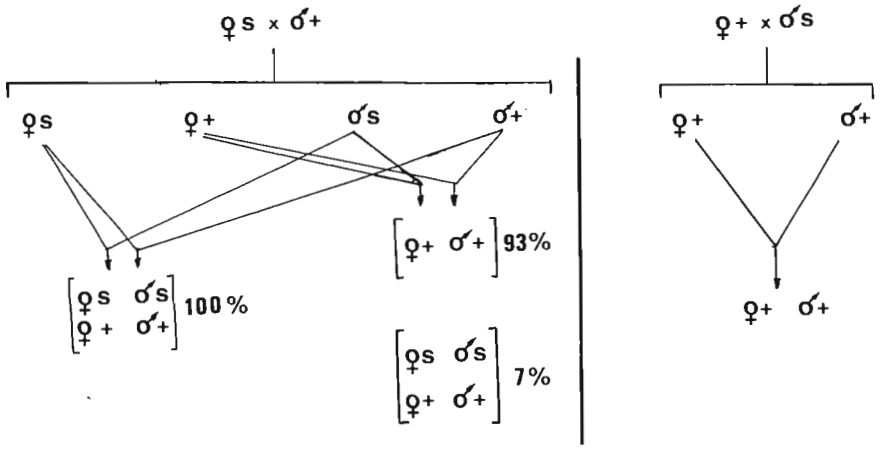

Fig. 2. Phenotypic segregation in F_1 and F_2 from mating S females to wild type (+) males and loss of the character in the progeny of the reciprocal cross. In percentage is given the proportion of single pair mating having each type of progeny.

A second intriguing feature of the S phenotype appears in the spatial bristle pattern shown by flies with two altered bristles: both tend to be located more often than expected in the null hypothesis of equal probability for any location of two bristles ($\chi^2_{\frac{1}{2}}=20.95$, $p < 0.01$) on the same side of the body. That is, there is an appreciable strong tendency toward bilateral asymmetry. And it is so regardless of whether the two altered bristles are dosocentral or both are scutellar.

In order to establish the type of inheritance of S phenotype, 100 females and males with well expressed S phenotype were individually mated to wild type males and females taken from a natural population of Asturias. The results of these reciprocal crosses and their F_2 are given in Fig. 2. Clearly no Mendelian segregation would fit these F_1 and F_2 segregations restricted to one type of mating. Despite the small percentage (7%) of females F_1+ that, irrespective of the male parent (crosses ♀+ X ♂S and ♀+ X ♂+), give F_2 segregant progenies,

there is every reason to suggest that the trait is controlled by an extranuclear factor.

Most facts here reported might be explained if such a factor were scarce and its replication rate were slower than the cellular division rate, so that it could be lost in certain cellular lines but not in others within an individual. Further tests to probe the hypothesis are already in progress.

David, J.R., M. de Scheemaeker-Louis and E. Pla. Laboratoire de Biologie et Génétique Evolutives du CNRS, Gif-sur-Yvette, France. Evolution in the seven species of the Drosophila melanogaster subgroup: comparison of the electrophoretic mobility of the enzymes produced by the Adh locus.

Alcohol dehydrogenase (Adh) of Drosophila melanogaster is an extensively studied enzyme for several reasons. It has been possible to relate the enzymatic function with a physiological trait, ethanol tolerance. This phenotypic property has a strong adaptive significance in the ecology of wild populations. Finally the worldwide polymorphism known at the Adh locus seems to be maintained by natural selection. The F allele, producing a fast migrating protein, has a higher activity than the S allele and is most frequent in temperate countries where the alcohol tolerance is higher (see David, 1976 for a review). Apart from the two widespread Adh^F and Adh^S alleles, three other rare ones have also been found in natural populations.

At the present time six other species are known in the D. melanogaster taxonomic subgroup; these include the cosmopolite D. simulans and five others, endemic in the Ethiopian region. Up to now only the Adh of D. simulans has been studied and the species is known to be generally monomorphic for a very slow allele, having some analogy with the US allele found in an African population of D. melanogaster. It seemed therefore interesting to compare the mobility of Adh found in the different species with that of the five alleles available in D. melanogaster.

Results are presented in Fig. 1. In order to improve electrophoretic discrimination, the various alleles were ordered according to their decreasing anodal mobility. In all cases, the electrophoretic pattern was the same: for a homozygous strain, we observe two isozymes which correspond to conformational differences of the dimer molecule; the activity of the slower isozyme is always higher. Moreover, treatment of flies with acetone (not shown) resulted in all cases in the disappearance of the slow migrating isozyme and in the increase of a third, still faster migrating, band. There is therefore almost a complete certitude that the enzymes shown in Fig. 1 are the product of the same, homologous locus, in all species.

It is well known that a single electrophoretic technique reveals only part of the effective genetic variability. In the present case, it is striking that ordinary starch gel electrophoresis was sufficient for showing a significant difference between all alleles. In some cases, the difference of migration is very small (1 mm) but it proved to be always the same in different runs.

Five alleles were found in D. melanogaster, the most extensively studied species. By contrast, all the other species were observed to be monomorphic. This last conclusion, however, cannot be considered as being strongly established because only a small number of laboratory strains were studied. Present data seem, however, to allow several conclusions.

First the Adh locus, at least in that group of species, can be considered as a fast evolving gene. As previously stated, the enzyme produced is involved in ethanol detoxification and big differences are observed in ethanol tolerance of the various species (David et al. 1974). Perhaps this diversification of the ecological niche with respect to environmental alcohol is related to the occurrence of different alleles in the different species.

Second, a proportion of 100% of unique alleles is observed here so that the enzyme seems to have an absolute diagnostic value for a specific identification. In a recent paper (Throckmorton, 1978) indicated that, when studying phylogenetic relationship between related species, an average of 30% of unique alleles was observed. The much higher proportion found here is probably a singularity of the locus here studied.

Third, a general problem in speciation studies is to establish whether the electrophoretic alleles occurred before or after the specific divergence. In the present case we can state that the apparition of the new alleles and their fixation almost certaintly occurred after the specific separation.