'obstruction' (e.g., the bristle or socket) and the area of reoriented trichomes. This is precisely what was found. The anterior dorso-central bristles were smaller in our strains than the posterior dorso-centrals. As predicted, the affected area around the anterior dorso-centrals was also smaller, in some instances including only the single row of trichomes surrounding the socket. Similarly, the normal bristle and socket set is smaller in basal area than the double socket cell complex in the mutant sv^n. The area of affected trichomes around normal bristles is also smaller.

Our second prediction was that mutations, such as inturned, that alter the orientation of bristles will also have an effect upon the orientation of trichomes. To test this prediction we examined flies which had patches of inturned bristles. Within each patch of normal and inturned bristles, the trichomes were found to point in the same direction as the bristles. Where differently-oriented patches touch, however, the trichome pattern is disrupted. An example of this is shown in the figure, c. The bristles on the left and right of the picture point in different directions, and the trichomes are disoriented in the area where direction changes. This is shown even more dramatically in the large disoriented region in the figure, d. The distortion of trichomes in the area between 2 patches might be due to local diffusion interactions similar to the gradient smoothing inferred from cuticular patterns in other organisms[6].

Finally, an interesting conclusion from the local similarity of bristle and trichome orientation is that both bristles and trichomes seem to be responding to the same information gradient. Thus, trichome patterns may be a useful fine structure marker of the gradients determining orientation of major cuticular structures in *Drosophila*.

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An electrophoretic polymorphism that mimics a true genetic polymorphism in *Triturus cristatus carnifex* (Amphibia, Urodela)

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Summary. Phosphoglucomutase electrophoretic patterns have been studied in 60 tail homogenates of *Triturus cristatus carnifex*. Our results show that the same sample produces a different electrophoretic pattern with homogenate ageing; a new band of intermediate mobility appears, together with the one produced by the fresh preparation. The phenomenon can mimic a true genetic polymorphism when differently stored samples are analyzed.

In the course of a study on the genetic variability of the Italian species of the genus *Triturus* (Amphibia, Urodela)[1], phosphoglucomutase (PGM) has been tested by means of horizontal starch gel electrophoresis. PGM (EC 2.7.5.1) is a phosphotransferase catalyzing the interconversion of glucose-1-phosphate and glucose-6-phosphate. It appears to be polymorphic in a great number of populations of the species considered[2].

Experiments have been carried on *Triturus cristatus carnifex* fresh tail homogenates, prepared according to Brewer[3] and then centrifuged at 13,000 rpm for 15 min to discard organelles and debris. Aliquots of each individual homogenate were immediately stored both at −20 °C and at −80 °C. The results obtained on 60 fresh samples from a natural population electrophoresed following the method of Spencer et al.[4], have shown the same pattern in all the homogenates, consisting of a main band and other 2 fainter bands migrating more rapidly towards the anode. The samples have also been tested by means a different method[5]. Aliquots a) fresh, b) stored at −80 °C, c) stored at −20 °C, frozen and thawed some times before electrophoresis, from each homogenate, have been run in parallel both with the method of Spencer et al.[4] and with that of Hedgecock[5]. Figure 1 shows that the same sample, if treated in different ways, produces a different electrophoretic pattern with the homogenate ageing.

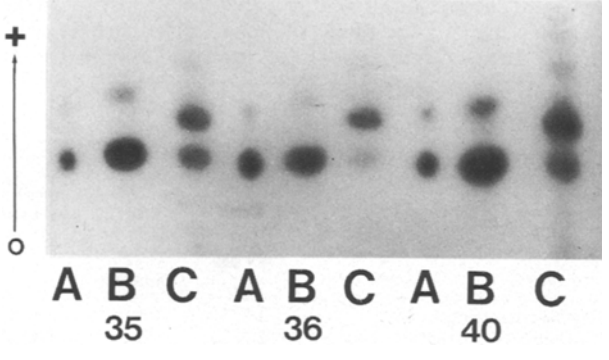

Fig. 1. Phosphoglucomutase electrophoretic pattern of comparison among tail homogenates A) fresh; B) stored at −80 °C; C) stored at −20 °C, frozen and thawed. 3 individuals out of a batch of 60 are examined (Nos 35, 36, 40).

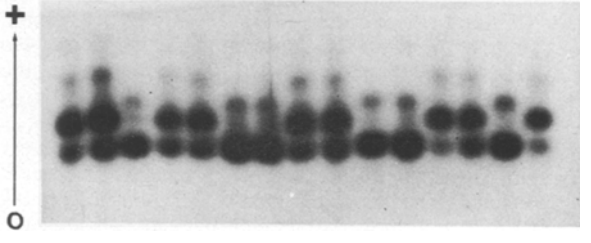

Fig. 2. Comparison among tail homogenates from 15 animals, subjected to different storage conditions and very closely resembling a true genetic polymorphism.

Indeed, 1 band of intermediate mobility, which is absent in the fresh sample, appears in the pattern of the samples stored at −20 °C and frozen and thawed. The pattern of the sample stored at −80 °C is indistinguishable from the pattern produced by the fresh ones.

Another enzyme, glucose-6-phosphate dehydrogenase (G6PD), which is monomorphic using the method[6] we have employed for its analysis has been studied in blood samples. In this case the sample showed the same electrophoretic pattern regardless of the storage conditions. Such a result suggests that in the PGM isozymic bands array, the slower isozyme is the primary form to be synthesized while the others derive from this form through secondary structural changes occurring during the sample ageing.

Our results on PGM show that if samples from different individuals are stored in different ways, such as those described above, and then compared by starch gel electrophoresis, a pattern is obtained that mimics a true genetic polymorphism. This effect is due to the appearance of a new sharp intermediate migrating band in the frozen and thawed homogenates that, together with the band given by the fresh preparation and still active, produces a phenotypic pattern which closely resembles the pattern one could expect from an heterozygote (figure 2).

Our observations indicate that some care should be used in the analysis of genetic polymorphisms, a topic which is at present acquiring increasing importance both in evolutionary and in population studies[7,8].

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Karyotypes and nuclear DNA contents of Polypteridae (Osteichthyes)[1]

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Summary. Calamoichthys calabaricus, Polypterus palmas, P. weeksii, P. delhezi and *P. ornatipinnis* have the same amount of DNA per erythrocyte nucleus. The karyotype of *P. weeksii* has 38 chromosomes and differs from the karyotypes of the other species, all with 36 chromosomes, by a Robertsonian chromosomal rearrangement. The karyotype condition is regarded as derived for vertebrates.

In recent work, *Polypterus* and *Calamoichthys* have been placed either in the Actinopterygii as derived chondrosteans[2,3] or outside the actinopterygians in a group of their own, the Brachiopterygii[4,5]. Papers on karyotypes[6-9] and DNA contents[10,11] of Polypteridae stressed the differences from actinopterygians - chondrosteans in particular - and noted some resemblances with Dipnoi and Amphibia.

The Polypteridae exhibit remarkable chromosomal homogeneity; the 6 species reported *(C. calabaricus, P. palmas, P. delhezi, P. ornatipinnis, P. senegalus* and *P. endlicheri congicus)* had 36 chromosomes, all with median (m) or submedian (sm) centromeres[7-9]; the papers, however, disagreed over the number of m and sm chromosomes. The karyotype similarity seems to be accompanied by marked differences in DNA contents: values of 8.54 pg *(C. calabaricus)*[10], 11.7 pg *(P. palmas)*[11] and 13.67 pg *(P. bichir)*[10] were reported.

Materials and methods. Relative DNA amounts of 5 species (table) were determined from erythrocytes by Feulgen cytophotometry in a Zeiss UMSP I[12]. Blood films were fixed in ethanol:acetic acid (3:1) for 30 min; 4 separate series, which included 2 slides from each species, were hydrolyzed with 1 N HCl at 60 °C for 6 min and stained following the procedure of de Tomasi[13]. 240 cells per species (30 cells from each slide) were measured.

The specimens of *C. calabaricus* (from Cameroun) and of *Polypterus* (from the Zaire river near Kinshasa) listed in the table as well as 3 males and 1 female of *P. delhezi* from lake Tumba (Zaire) were karyotyped. For each fish at least 4 metaphase spreads[7] were analyzed. Nomenclature for centromeric position, determined from chromosome arm ratios (r = long arm/short arm), follows Levan[14].

Results. The table shows the similarity between the DNA amounts of the 5 species studied here; no statistical difference (0.05 level) was found between *C. calabaricus* and each of the 4 *Polypterus* species.

No differences were found between the karyotypes of *C. calabaricus, P. palmas, P. ornatipinnis* and *P. delhezi.* Figure 1 shows a karyotype of *P. delhezi* with the 36 chromosomes divided in 3 size groups: a) large chromosomes: 4 pairs were clearly m but the 5th pair, with r = 1.6 ± 0.23 (SD from 32 metaphases), varied around the m-sm borderline (r = 1.7); b) medium-sized chromosomes: 4 m and 4 sm pairs but 2 pairs classified as sm were also borderline cases; c) small chromosomes: 5 msm pairs, which arm ratios could not be determined more precisely. Only the large pairs 1 and 5 could be identified in all metaphases. The karyotype of *P. weeksii* (figure 2), with 2n = 38, differs from the karyotypes with 2n = 36 by the

DNA contents in Polypteridae

Species	Specimens	DNA content in % of *C. calabaricus*	SD in % of mean
C. calabaricus Smith, 1865	3♂, 1♀	100	6.8
P. palmas Ayres, 1850	2♂, 2♀	98	8.3
P. delhezi Boulenger, 1899	2♂, 2♀	107	7.9
P. ornatipinnis Boulenger, 1902	2♂, 1♀	105	10.1
P. weeksii Boulenger, 1898	2♂, 2♀	108	8.4
P. bichir[10]		164	