Table 1. Electrophoretic mobility of albumin and alpha-globulin proteins within serum and fluids from small (FF-S) and large (FF-L) follicles.

Item		Albumin	Alpha-globulin band number 1	2	3	4	5
Serum	(18)[a]	0.887 ± 0.004[b]	0.799 ± 0.004	0.726 ± 0.004	0.676 ± 0.005[c]	0.656 ± 0.019	-
FF-S	(62)	0.892 ± 0.003	0.803 ± 0.002	0.728 ± 0.002	0.671 ± 0.002[c]	0.657 ± 0.005	0.639 ± 0.002
FF-L	(66)	0.892 ± 0.002	0.803 ± 0.002	0.733 ± 0.002	0.687 ± 0.003[d]	0.656 ± 0.004	0.639 ± 0.002

[a]Denotes total number of samples observed electrophoretically - all samples did not possess the entire profile of the alpha-globulin proteins; [b]mean value ± SE; [c,d]mean values within a column with no superscript in common are significant ($p < 0.01$) different.

Results and discussion. Mean protein concentration (including fibrinogen) for serum (n = 18), FF-S (n = 62) and FF-L (n = 66) was 84.2, 63.1 and 66.9 mg/ml, respectively. Serum protein was greater ($p < 0.05$) than FF protein, which agrees with previous reports for the bovine[2,3]. Electrophoretic mobility data are presented in table 1. Mobility of albumin in serum was not faster than in FF, as suggested in a previous report employing paper electrophoresis[2]. Alpha-globulin 3 migrated faster ($p < 0.01$) in FF-L than in serum or FF-S.

As shown in table 2, the percent of serum, FF-S and FF-L samples possessing more than 3 alpha-globulin bands was 16.7, 29.0 and 51.5%, respectively. This percent value for FF-L was greater ($p < 0.05$) than values for serum and FF-S, suggesting some protein specificity for FF-L. A fast alpha-globulin 3 and a greater percent of alpha-globulin bands in FF-L as compared to FF-S has not been previously reported. Mean serum progesterone concentration (8.3 ng/ml; range of 0.9 to 12.7 ng/ml) indicated that all but 2 pairs of ovaries contained a functional CL. It appeared that the CL exerted no influence on either albumin or alpha-globulin mobilities or numbers between ipsilateral and contralateral ovaries within FF-S and FF-L groups. In pig FF obtained from pooled FF-S and pooled FF-L samples, FF-S consistently possessed 3 alpha-globulins while FF-L had 4. Mobility differences in 2 alpha-globulins were observed between FF-S and FF-L[4].

Although little is known of the nature and activity of alpha-globulin FF proteins, activities of specific human serum alpha-globulins have been noted, i.e. antiplasmin, antitrypsin, thyroxine binding, cholinesterase and antichymotrypsin activity[11]. The possibility that specific differences in the alpha-globulin profile of bovine FF-S and FF-L are related to oocyte maturation, the ovulation process, or both certainly must be considered.

Table 2. Number and percent of samples of bovine serum and fluids from small (FF-S) and large (FF-L) follicles possessing varying numbers of alpha-globulin bands

Item			Number of alpha-globulin bands/sample < 3	3	> 3
Serum	(18)	No.[a]	3	12	3
		%[b]	16.7[c]	66.7[c]	16.7[c]
FF-S	(62)	No.	4	40	18
		%	6.5[d]	64.5[c]	29.0[c]
FF-L	(66)	No.	3	29	34
		%	4.6[d]	43.9[d]	51.5[d]

[a] Number of samples containing the designated number of bands; [b] percent of samples containing the designated number of bands; numbers in parentheses denote total number of tested samples; [c,d] percent values within columns with no superscript in common are significantly different ($p < 0.05$).

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Muscle specific structural differences in piscine muscle glycogens

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Summary. Piscine red muscles are rich in glycogen content. Structurally white muscle glycogens have one glucosidal unit more in their external branches than the red muscles.

It is widely known that distinct molecular species of glycogen exhibiting different susceptibilities to glycogen breakdown may occur in a given muscle[3]. In order to examine this in case of fish, wherein the concentration of muscle glycogen has been recognized as an aspect of functional specialization[4], the present investigation has been undertaken.

The red and white muscles of the lateral line musculature and the heart muscles were excised in bulk, pooling the

Table 1. Glycogen levels in the piscine muscles

Fish	mg glycogen/kg wet weight White muscles	Red muscles	Cardiac muscles
Catla catla	586 ± 42	218 ± 36	198 ± 21
Clarius batrachus	546 ± 34	198 ± 28	189 ± 19

Values are $\bar{x} \pm$ SD of 5 observations.

Table 2. Chain lengths of piscine muscle glycogens

Source fish	Cardiac muscle			Red muscle			White muscle		
	Total unit	External branch unit	Internal branch unit	Total unit	External branch unit	Internal branch unit	Total unit	External branch unit	Internal branch unit
Catla catla	10.57 ± 0.07	8.3 ± 0.10	2.27 ± 0.07	10.5 ± 0.11	8.17 ± 0.07	2.32 ± 0.08	12.52 ± 0.11	10.1 ± 0.11	2.42 ± 0.07
Clarias batrachus	9.37 ± 0.15	7.8 ± 0.21	1.57 ± 0.07	9.3 ± 0.09	7.72 ± 0.14	1.6 ± 0.13	11.12 ± 0.20	9.57 ± 0.08	1.5 ± 0.10

Values are $\bar{x} \pm$ SE of 4 observations.

tissue from 10 freshly killed riverine carp *Catla catla* (1–1.5 kg) and 10 catfish *Clarias batrachus* (300–350 g). Glycogen was extracted and purified from pulvarized muscles according to Kjólberg et al.[5] and Somogyi[6]. Glycogen chain lengths were investigated by Kjólberg et al.[5] and Sayre et al.[7].

White lateral muscles of both species have more glycogen than the red and cardiac muscles. The content does not vary in red and cardiac muscles (table 1).

In general, the muscle glycogens of *Catla catla* have greater chain lengths than those of *Clarias batrachus* (table 2). In an individual species, the red and cardiac muscle glycogens resemble each other in chain lengths (table 2). The length of internal branch unit of glycogens of conspecifics remains the same. White muscles of both species are characterized by having one glucosidal unit more in their external branches (table 2).

The results obviously support the view of Lawrie et al.[3] and show that the molecular species of glycogen reflect the functional aspects of metabolic specializations, since the cardiac and red muscles are geared to oxidative metabolism and the white muscles are anaerobic[8]. Another noteworthy observation is that the red and heart muscles of one species resemble each other in glycogen concentration and structural aspects of glycogen. Probably these muscles are not differentiated further than that of white muscles embryonically[9]. Unlike the mammalian glycogens, the fish muscle glycogens[10,11] of the present study show a constant internal chain length. The little variation in the degree of branching in different species of fish could be discernible from their genetic characteristics.

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Genetic variation in natural populations: Morphological traits in *Drosophila melanogaster*[1]

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Summary. In a wild population of *Drosophila melanogaster* located near Madrid (Spain), it has been found that the frequency of morphological mutant phenotypes is 0.36 per captured female. The study of these females shows that they carry 3.6 recessive mutants in heterozygous condition per female. The genetic variability found is higher than the frequencies observed by other authors in other natural populations.

The evolutionary potential of a population is measured by the amount of genetic variation in the population: The more genetic variation there is, the greater the opportunity for evolution to occur[2]. Evolutionary geneticists have, therefore, attempted to ascertain levels of genetic variation in natural populations. Early studies of genetic variation investigated variants with morphological effects[3–8]. The discovery of the giant polytene chromosomes of Diptera later made possible the investigation of natural variation for chromosomal inversions[9]. More recently, the techniques of gel-electrophoresis have provided a wealth of data concerning polymorphisms in enzymes and other proteins[10].

However, the increase in knowledge brought about by the new methods has not been accompanied by additional research using the old, complementary methods of investigating genetic variation. In particular, the last 3 decades have seen the publication of few systematic studies of genetically determined morphological variation[8]. Yet, different kinds of variation are uncovered by morphological studies rather than by electrophoretic or other methods of investigation. This is particularly relevant to the issue whether the variation is adaptatively significant - it has been questioned whether enzyme variation has any adaptive relevance, while many morphological traits are clearly adaptive. This paper reports a study of morphological variation in 3 samples of a natural population of *Drosophila melanogaster*.

Material and methods. The collections of *Drosophila melanogaster* flies were made in a small (387 × 13 m) isolated forest near Vallecas on the outskirts of Madrid. The forest, in the centre of the Spanish plateau, is characterized by typical continental climate and contains several *Drosophila* species that oscillate in relative abundance depending on the season[11]; *melanogaster* flies do not appear in the samples between November and April, but become extremely abundant in the summer months, with peaks between July and August.

2 sets of data are obtained for each sample: a) detectable morphological variation in the wild-collected females; b) variants manifested in inbred F_2 progenies. 7 separate brother-sister matings were made with the F_1 progeny of