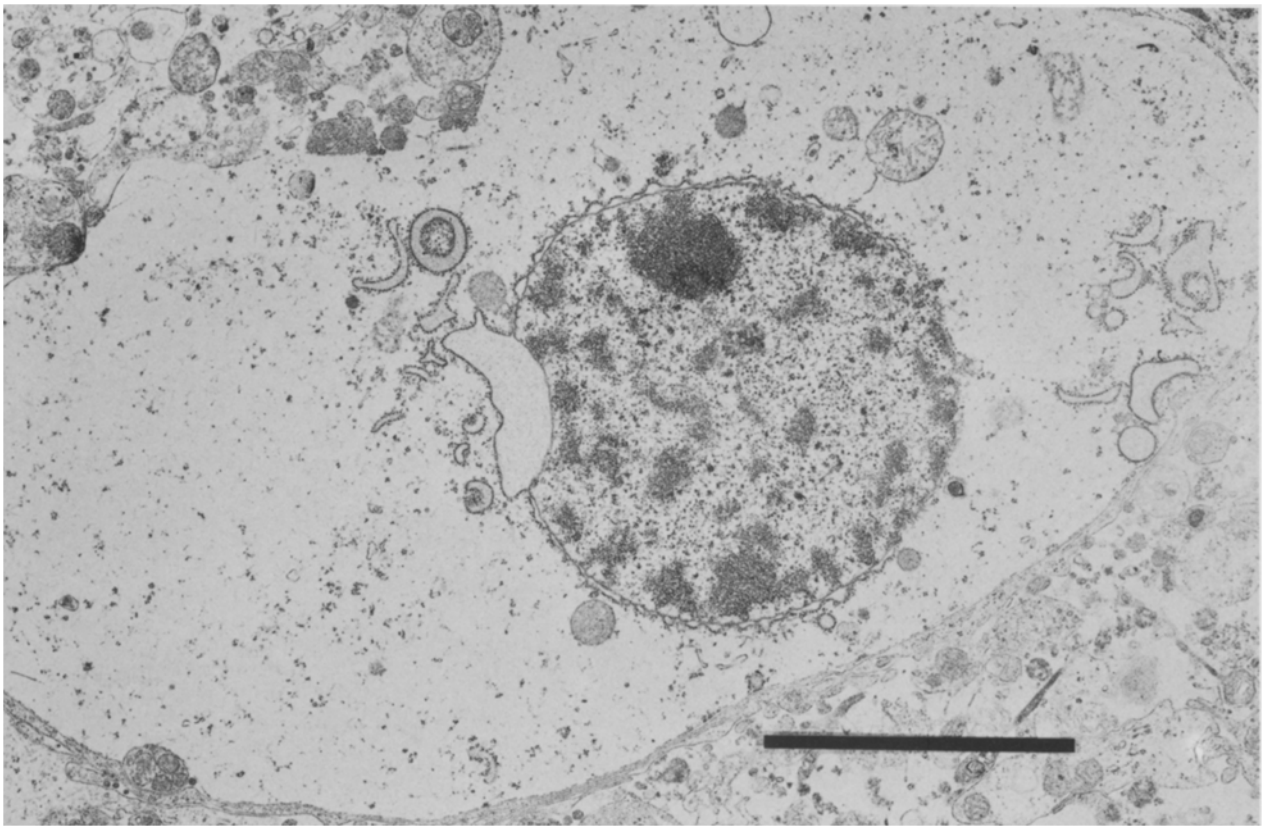

Fig. 2. Electronmicrograph of neuronal cell, 4 after gestation, in cerebral cortex of mouse. Addition of 0.01 AFS from control to feeding medium results in normal appearance. × 800. Bar = 2 µm.

addition, variability of donors contributing amniotic fluids, should give caution at oversimplified interpretations of the foregoing report.

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3 M.R. Murray, in: Handbook of Neurochemistry, vol. 5, p. 373. Ed. A Lajtha. Plenum Press 1972.
4 W.O. Whetsell, Jr, J. Schwartz and E. Elizan, J. Neuropath, exp. Neurol. *363*, 547 (1977).
5 F. Proctor-Bowen, Abstract, March of Dimes, 1976.
6 M. Abercrombie and J.F.M. Haysman, J. nat. Cancer Inst. *19*, 561 (1976).
7 G.M. McKhann, W. Ho., Ch. Raiborn and S. Varon, Archs Neurol. *20*, 542 (1969).

Lactate dehydrogenase polymorphism in *Mus musculus* L. and *Mus spretus* Lataste[1]

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Summary. First variation at the *Ldh-A* locus and a new allele at the *Ldh-B* locus are reported in a *M. musculus* population dimorphic at the *Ldh-A* locus and in a *M. spretus* population trimorphic at the *Ldh-B* locus.

Biochemical population genetics of Southern European mice appear promising in solving recurrent problems in systematics and in providing new variants needed for research. For instance, lactate dehydrogenase (LDH) was used to demonstrate reproductive isolation of *Mus musculus* and *Mus spretus* in nature. In Southern France, the latter species has a new allele fixed at the LDH B chain locus (*Ldh-B*); this was the 1st report of allelic variation of this outstanding enzyme in the genus *Mus*[4,5]. Extending this investigation geographically, we are now able to assert that LDH variation in *Mus* occurs not only at the interspecific level but also at an intrapopulation level and that the LDH A chain locus (*Ldh-A*) is involved as well as *Ldh-B*.

Material and methods. This report deals with the electrophoretic survey of 2 mice populations, one from Southern Spain (18 individuals trapped in cultivated fields at Santa Teresa, Province of Granada), the other from Hungary (9 individuals trapped inside houses at Farkasgyepü, Veszprem County). Allelic variation was investigated at 20 loci by starch gel electrophoresis. Techniques and symbols used are indicated in Britton and Thaler[5].

Results. The following loci for which no variation is known

in *M. musculus* or *M. spretus*, are also monomorphic for the same alleles in both populations: *Got-1, Id-2, Mor-2, a*-Gpd and *Sdh*. The following alleles are fixed in both populations: *Ldr-1*^{a}, *Es-5*^{a} and *Got-2*^{b}. The remaining 12 loci are either polymorphic or have different alleles fixed in the 2 populations (table 1).

All the alleles present in these populations have already been recorded in other populations of either *M. musculus* or *M. spretus* except for the *Ldh* loci which exhibit 2 new alleles: *Ldh-B*^{m} in the Spanish population and *Ldh-A*^{l} in the Hungarian one. *Ldh-B*^{m} (*m* for 'moyenne'), if compared to the previously recorded alleles *Ldh-B*^{r} (*r* for 'rapide') and *Ldh-B*^{l} (*l* for 'lente') codes for a LDH B chain of intermediate electric charge. *Ldh-A*^{l} is the 1st variant reported at this locus for which the only allele previously known is now designated as *Ldh-A*^{r} and codes for a LDH A chain of lesser charge.

Table 1. Allelic variation at 12 enzymatic and non-enzymatic loci in the Spanish *Mus spretus* and Hungarian *Mus musculus* populations

Locus	Allele	Spanish population *(Mus spretus)*	Hungarian population *(Mus musculus)*
Ldh-A	*r*	1.00	0.90
	l	0.00	0.10
Ldh-B	*r*	0.76	1.00
	m	0.11	0.00
	l	0.13	0.00
Id-1	*a*	1.00	0.00
	b	0.00	1.00
Adh-1	*a*	0.00	0.33
	b	1.00	0.67
Mod-1	*160*	0.74	0.72
	200	0.26	0.28
Es-1	*a*	0.00	1.00
	91	1.00	0.00
Es-2	*a*	0.90	0.00
	b	0.05	0.13
	98	0.05	0.00
	c	0.00	0.87
Es-3	*b*	0.92	0.50
	c	0.05	0.50
	71	0.03	0.00
Alb-1	*a*	0.00	1.00
	98	1.00	0.00
Hbb	*s*	1.00	0.39
	d	0.00	0.61
Mor-1	*b*	1.00	0.83
	c	0.00	0.17
Ipo	*a*	1.00	0.00
	b	0.00	1.00

Table 2. Nei's coefficients of proteic identity (I) and genetic distance (D)

D/I	1	2	3	4
1	-	0.951	0.640	0.679
2	0.051	-	0.664	0.726
3	0.446	0.410	-	0.974
4	0.387	0.320	0.027	-

The following loci were used: *Ldr-1, Es-1, Es-2, Es-3, Es-5, Id-1, Id-2, Ldh-A, Ldh-B, Mor-1, Mor-2, Ipo, Alb-1, a-Gpd* and *Adh-1*. The populations used in computing the coefficients are the following: *1 M.m.brevirostris*, St Clement, indoors, France[5]. *2 M.m.domesticus*, South-West Jutland, Denmark[6]. *3 M.m.spicilegus*, Veszprem County, Hungary. *4 M.m.musculus*, North of Limfjorden, Denmark[6].

The observed distribution of genotypes at the *Ldh-B* locus in the Spanish population is the following:

rr	*mm*	*ll*	*rm*	*rl*	*ml*
12	0	1	2	2	1

No polymorphism had been recorded at this locus until now. All populations of *M. musculus* were monomorphic for the *Ldh-B*^{r} allele, whereas *Ldh-B*^{l} was fixed in Southern French populations of *M. spretus*, which so far had only been investigated in this region.

The observed distribution of genotypes in the Hungarian population at the *Ldh-A* locus is the following:

rr	*rl*	*ll*
7	1	1

This, of course, is the 1st report of a polymorphism at this locus for which no variation had been recorded previously in *Mus*.

Discussion. As the Spanish population exhibits the 2 *Ldh-B* alleles, which are respectively fixed in previously studied populations of *M. musculus* and *M. spretus*, one may wonder if it may not represent a hybrid population. However, the *Alb-1*^{98}, *Es-1*^{91} and *Adh-1*^{b} alleles are fixed in the Spanish population, as they are in French populations of *M. spretus* with which it also shares habits (never found in houses) and morphology (short tail).

Moreover, in the same Spanish locality, several mice were captured in houses. They are long-tailed and homozygous for *Alb-1*^{a}, *Es-1*^{b} and *Adh-1*^{a}, as are all *M. musculus brevirostris* populations in Southern France. Therefore, since no heterozygote at any of these 3 loci was observed among indoor or outdoor mice in the Spanish locality, we may consider that, there also, *M. musculus* and *M. spretus* occur sympatrically without hybridizing. We may then conclude that the polymorphism involves only *M. spretus*, and that the *l* and *m* alleles at the *Ldh-B* locus are specific to this species. The Hungarian mice are usually referred to as *M. musculus spicilegus*, a subspecies never yet studied by electrophoresis. The Hungarian population which we have analyzed is biochemically quite similar to *M. musculus musculus* populations from Denmark[6,7]. The genetic distances computed according to Nei's formula[8] indicate that they belong to the same East European semi-species (table 2).

Conclusion. Both *Mus musculus* and *Mus spretus* exhibit LDH polymorphism in certain areas and not in others. The study of this enzymatic system on a geographical basis will contribute to the understanding of the genetic structure of these species.

Since fertile hybrids have been obtained under laboratory conditions between *M. musculus* and *M. spretus*[9], one has at last the opportunity to study the formal genetics of LDH in mice for both the A and B chain loci.

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2 Catedra de Zoologia, Facultad de Ciencias, Granada, España.

3 Museum of Natural History, Budapest VIII, Muzeúm Körut 14-16, Hungaria.

4 J. Britton, N. Pasteur and L. Thaler, C.r. Acad. Sci., Paris *283*, 515 (1976).

5 J. Britton and L. Thaler, Biochem. Genet. *16*, 213 (1978).

6 R.K. Selander, W.G. Hunt and S.Y. Yang, Evolution *23*, 379 (1969).

7 W.G. Hunt and R.K. Selander, Heredity *31*, 11 (1973).

8 M. Nei, Am. Nat. *106*, 283 (1972).

9 F. Bonhomme, S. Martin and L. Thaler, Experientia *34*, 1140 (1978).