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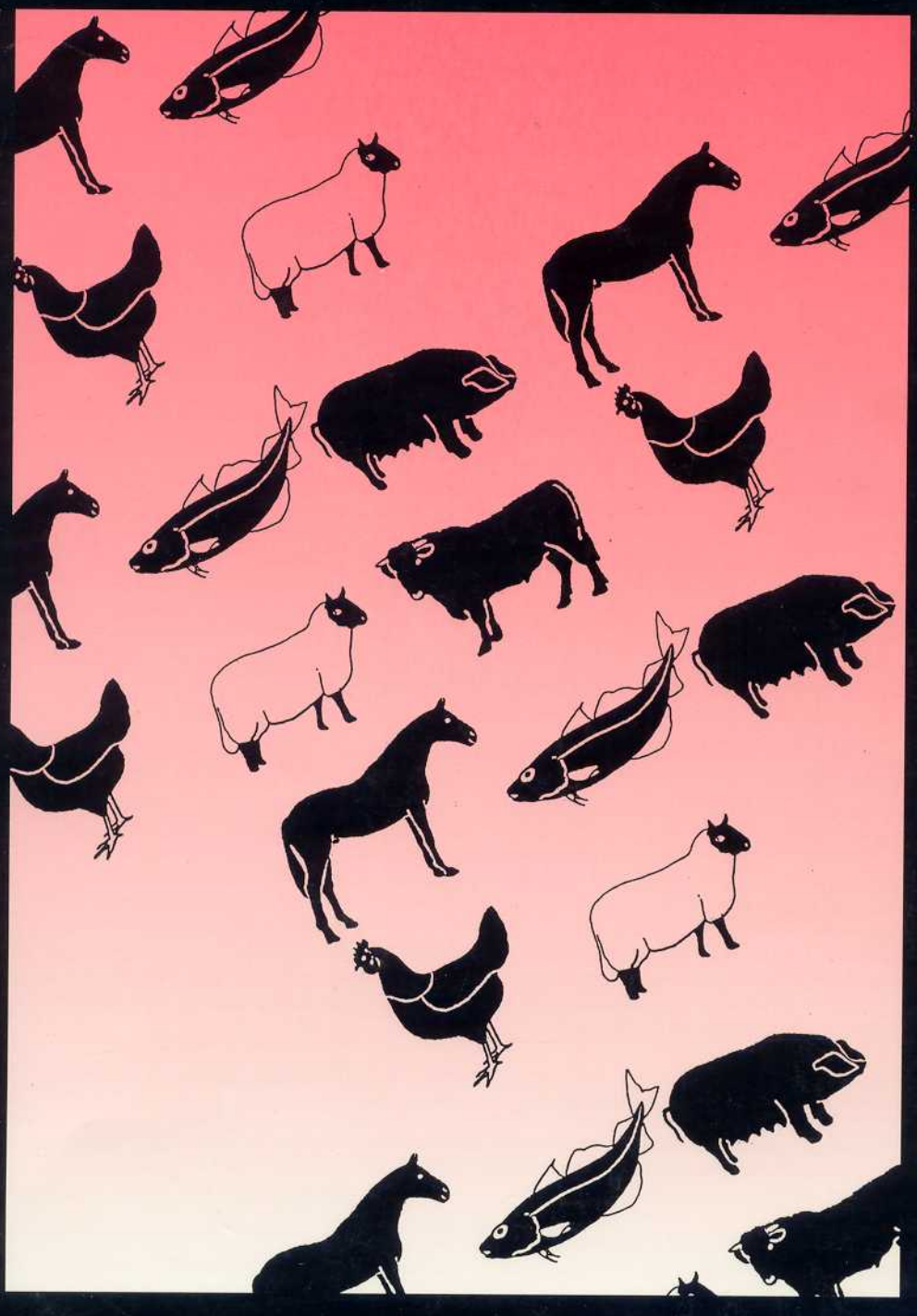

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detected clearly as mobility shifts. The best condition of detecting the point mutation was obtained by using the following conditions. Acrylamide concentration is 5%, a bis ratio is 49:1, glycerol is not necessary. Electrophoresis temperature is 5 C, running time is 5 hours (2W/plate). Furthermore, the *RYR1* genotypes observed by PCR-SSCP were identical to the results of RFLP in 175 pigs. The results indicate that the PCR-SSCP analysis for the *RYR1* mutation is easy and useful for large-scale screening in the field of pork industry.

B20
The distribution of kappa Cn alleles *A, B, E* in cattle

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Polymorphism of kappa casein has been studied for a long time in relation to technological properties of milk and to protein content. In the Czech Republic results were obtained from cows and bulls of the Bohemian Spotted and Black Pied cattle breeds. Polymorphism of the kappa Cn gene was determined using both the methods of biochemical genetics and of PCR and RFLP (Schlee *et al., Züchtungskunde* **64**, 312-322, 1992). The frequency of alleles in cows of Bohemian Spotted cattle was $Cn^A = 0.61$, $Cn^B = 0.39$; in bulls $Cn^A = 0.68$, $Cn^B = 0.32$. The frequency of alleles in the Black Pied cows was $Cn^A = 0.56$, $Cn^B = 0.44$; in bulls $Cn^A = 0.82$ and $Cn^B = 0.18$. No occurrence of the Cn^E allele has been recorded in the Czech Republic. Using the DNA test, the heterozygous *A/E* genotype was found in a bull of the Bohemian Spotted breed. The segregation of this allele in the progeny is being studied.

B21
Tf N, a partially deficient and atypical transferrin variant in the horse

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A new, partially deficient and phenotypically atypical transferrin variant, Tf N, was found in some Finnhorses. The variant was inherited codominantly. After electrophoresis of serum samples the zone of variant N migrated slightly faster in polyacrylamide gel than the main fast zone of variant M. Variant N contained a component with four sialic acid residues, while a component with two sialic acid residues, which is present in other Tf variants, was not observed after electrophoresis of sera.

B22
The genetic variation of an endangered breed: the Sorraia horse

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The Sorraia is believed to be the primitive ancestor of the Iberian saddle horse breeds and possibly one of the primitive ancestors of all the world's light saddle horses. The breed survives today in two populations located in Portugal (with 4 subpopulations) and Germany (the latter derived from the former). As it has been possible to maintain small numbers only and the breed was recovered from few founder individuals with no further introductions, both populations are highly inbred (mean of F_g of 0.416 and 0.306 for the Portuguese and German herds, respectively). Both populations were examined for genetic variation using blood group and biochemical genetic loci. Allelic diversity within the Sorraia is low with only 40 total genetic variants recognized for 17 loci compared to an average of nearly 65 for other domestic breeds (based upon 77 breeds). The effective number of alleles was 1.87 for the Sorraia compared to a mean of 2.06 for other domestic breeds. However, observed heterozygosity was near the average for other breeds (37.5% versus 37.7%, respectively). For both populations, there was no statistically significant relationship of individual heterozygosity with inbreeding coefficient. Genetic relationships of the Sorraia to other domestic breeds are also analysed. These analyses supported the primitive position of the Sorraia as it most closely clustered with the Exmoor Pony, another primitive horse breed.

B23
A new allele in the horse *GC* system

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Two alleles (*F* and *S*) are internationally recognized in the vitamin D binding serum protein system of the horse. By using PAGE and protein staining, an additional variant, tentatively designated GC D, has been found in 11 Moroccan horses (5 Arab-Barbs and 6 Barbs) out of 5416 Arab-Barb and 311 Barb horses analyzed. In all 11 cases the variant appeared as a heterozygote with *GC F*. Four cases included two mare-foal pairs of Arab-Barbs. The new variant migrates anodally to the GC F type to a position equidistant and symmetric to GC S. By conducting immunoblotting using antiserum to the human GC protein, we have confirmed the occurrence of the GC D variant. GC gene frequencies in Moroccan horses were as follows:

Allele	Arabian (N=538)	Arab-Barb (N=5416)	Barb (N=311)
GC D	0.0000	0.0005	0.0096
GC F	0.9452	0.9804	0.9759
GC S	0.0548	0.0191	0.0145

Since this new variant is not found in Moroccan Arabian horses, it seems to be a genetic characteristic of the Barb horse.

B24
A major familial hypercholesterolemia subphenotype in swine is inherited as an autosomal recessive trait and its gene is not linked to the *APOB* locus

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We report here results of genetic studies in swine on the mode of inheritance of a quantitative hypercholesterolemia variant dissected from a complex familial hypercholesterolemia (FHC) resembling closely human familial combined hyperlipidemia and to test whether the gene locus for this disorder is linked with the *APOB* locus. Genetic analysis of segregation data on cholesterol variations in plasma of 418 progenies from 58 designed matings has indicated that the isolated dyslipidemia represents a quantitative FHC subphenotype which showed a monogenic autosomal recessive mode of inheritance, designated FHC-r. Data were tested for goodness-of-fit to three genetic models (additive, dominant, recessive) and the recessive mode was significantly better fit (R2=0.91). Data from three mating types (FHC-r x FHC-r; N x N; FHC-r x N) resulted in the following means: 222.5±25, 98.8±12.5 and 103.4±13.3 mg/dL for the three genotypes *r/r*, *N/N* and *N/r*, respectively, determined by two alleles designated *r* for the recessive hypercholesterolemia and *N* for dominant normolipidemic phenotype. By comparison with other hypercholesterolemia the recessive expression of FHC-r is unique. Segregation data on the quantitative cholesterol phenotypes, specified by *r* and *N* alleles at the *FHC-r* locus and the Lpb5 allotypic marker determined by the *APOB* allelic gene were used for linkage analysis. A low lod