Section A: Polymorphism and biodiversity

(Polymorphisme et biodiversité)

A001

Characterization of baboon (*Papio cynocephalus*) non-casein proteins

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The non-casein proteins of baboon milk (24h, 30 days and 60 days lactation) were characterized by native one-dimensional polyacrylamide gradient gel electrophoresis (10–15%T, pH 8.3) (1D-PAGGE), isoelectric focusing (pH 4–6), SDS-PAGE (15%T, pH 8.8), immunoblotting of 1D-PAGGE and SDS-PAGE gels with rabbit antisera to human α-lactalbumin, lysozyme, albumin and bovine β-lactoglobulin and N-terminal sequencing of proteins passively absorbed from SDS-PAGE gels to PVDF membrane.

The major proteins were identified as β-lactoglobulin (BLG), α-lactalbumin (αLA), lysozyme (LYZ), lactoferrin (LTF) and albumin (ALB). The first 30 N-terminal residues of baboon BLG (M_r 20750, pI 4.54) are identical to those of simian (*Macaca fascicularis*) BLG. This is the first report of the occurrence of BLG in the baboon and only the third primate species known to express BLG. αLA (M_r 14 500, pI 4.67) has an identical N-terminal sequence (25 residues) to the published sequences for baboon and human αLA. The N-terminal sequence of LYZ (M_r 16 000) is identical to that of olive baboon (*Papio anubis*) and differs from human LYZ in two residues (Ile/Val and Leu/Met at positions 2 and 17) in the first 21. There are four differences in 21 N-terminal residues of LTF (M_r 85700) compared to the human protein. Human and baboon ALB (M_r 67 000) have identical N-terminal sequences (15 residues).

A002

Comparison of electrophoretic and chromotographic methods for analysis of deer haemoglobins

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The growing international trade in dried deer parts (velvet antler, genitalia, tails and sinews) has made it necessary to identify protected species from material that may be compromised for morphological and sometimes even protein analysis. The need for an effective identification technique was the incentive for a collaborative study comparing isoelectric focusing (IEF) and high pressure liquid chromatography (HPLC) for the analysis of haemoglobin. IEF characterizes the intact tetrameric haemoglobin molecule, while HPLC separates the α and beta globin chains. Whole blood samples of European red deer and fallow deer, Asian sika deer, and elk, white-tailed deer and mule deer from North American deer populations were analysed by both techniques to determine haemoglobin characteristics. The results were consistent between methods and, when applied in the 1995 ISAG Deer Comparison Test, showed that two samples were from mule deer white-tailed deer hybrids.

A003

Evaluation of genetic diversity in Friesian cattle with the aid of AFLP™ markers

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We evaluated the genetic variability present in a sample of Italian Friesian cattle with AFLP technology (AFLP trademark, Keygene NV). The AFLP markers were produced through the double digestion of genomic DNA with *Eco*RI and *Taq*I restriction enzymes, ligated by synthetic adapters, PCR amplified using primers complementary to the adapters and carrying 1 additional nucleotide at their 3′ end and finally subjected to touch down amplification with a ^{33}P labelled *Eco*RI primer and an unlabelled *Taq*I primer, both carrying three additional nucleotides. The amplification products were separated on a sequencing gel and autoradiographed.

Sixteen primer combinations were utilized to evaluate a sample of 47 individuals (35 progeny tested sires and 12 dams). Approximately 1100 AFLP loci were assayed and 248 (23%) were found to be polymorphic. Independent experiments assessed the high reproducibility of the technique and two identical twins, included as a check, had exactly the same profiles.

We estimated an average heterozygosity value equal to 0.37 and an average polymorphism information content of 0.33. Genetic distances were calculated using Dice, Jaccard and Simple Matching coefficients. UPGMA clusters consistently clustered together related individuals.

The quite large number of polymorphic markers detected indicated that this AFLP technology is very promising for the evaluation of biodiversity, the organization of germplasm and the analysis of animal genomes and that it largely compensates, by the simultaneous assessment of a large number of loci, for the low information content carried by each single marker.

A004

Identification of bovine Y-specific random amplified polymorphic DNA markers by bulked segregant analysis

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