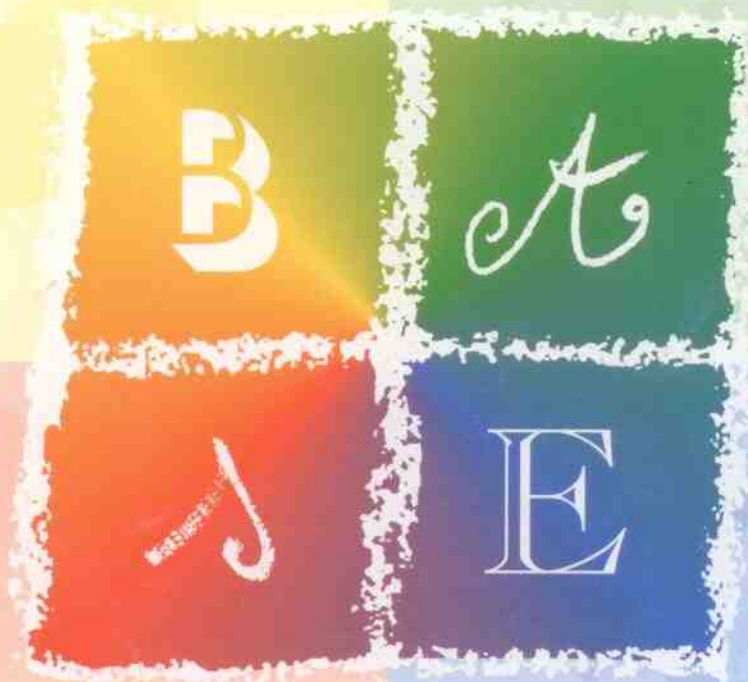


Biotechnologie, Agronomie  
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**LG3 K-CASEIN,  $\beta$ -LACTOGLOBULIN AND GROWTH HORMONE GENES POLYMORPHISMS IN ITALIAN BOVINE BREEDS.** M. Messina, E. Vrech, P. Pezzi\*, A. Prandi, *Faculty of Agronomy, I-33100 Udine, Italy and \*Faculty of Veterinary, I-40064 Bologna, Italy*

The polymorphisms of  $\kappa$ -casein is utilised to improve milk quality as genetic marker in the selection of dairy cattle breed.  $\beta$ -lactoglobulin polymorphisms seems to be related with milk yield and milk protein composition. Growth hormone (GH) affects milk production and plays a key role in nutrient utilisation, mammary control and growth. GH polymorphism could be related to its plasma levels and utilised in a selection program (Lucy *et al.*, 1993; Yao *et al.*, 1996). The aim of this work was to investigate a polymorphism of GH gene,  $\kappa$ -casein gene and of  $\beta$ -lactoglobulin gene to improve the early identification of genetic value of dairy cattle in terms of quantity and quality of milk yield. We have examined 182 Italian Friesian (IF) cows, 118 Brown Mountain (BM) and 157 Italian Simmental (IS) animals (91 cows and 14 bulls). Genomic DNA was extracted from blood of the cows and from the semen of the bulls. Genotyping of animals was determined by AS-PCR for GH gene and by PCR-RFLP for  $\kappa$ -casein and  $\beta$ -lactoglobulin. The site of the mutation investigated for the GH gene corresponding to the base n° 2291 of the sequence of Gordon *et al.* (1983).

K-casein genotypic frequency (%) was: AA=41.2, AB=27.5, BB=4.9, AE=17.6, BE=7.7 and EE=1.1 in IF, AA=15.2, AB=40.7, BB=43.2 and BC=0.8 in BM and AA=42.9, AB=39, BB=12.4, AC=5.7 in IS.

$\beta$ -lactoglobulin genotypic frequency (%) was: AA=21.4, AB=51.6, BB=26.9 in IF, AA=16.1, AB=55 BB=28.8 in BM and AA=35.2, AB=33.3, BB=31.4 in IS.

GH genotypic frequency (%) was: AA=84.1, AC=12.6, CC=3.3 in IF, AA=96.6, AC=3.4 in BM and AA=82.9, AC=13.3 and CC=3.8 in IS.

These previous results confirm the higher frequency of BB genotype for K-casein in BM instead of IS and IF. The allele C is present only in IS while it is absent the allele E. On the contrary, in the IF is present the allele E and the allele C is missing. In the  $\beta$ -lactoglobulins the distribution of the genotype is similar in the three breeds with a clear prevalence of the genotype AB. In the GH homozygote for C has been found in IF (3.3%) and IS (3.8%), and in the IS the genotype AC is more frequently present than in the IF. The frequency of AC in BM is lower (3.4) instead of IS (13.3) and IF (12.6). The genic frequency of AA and AC in the IF breed is in accordance with what already found by Yao *et al.* in the GH gene. The obtained results will be utilised in the study of the correlations between the genotype and the production quali-quantitative of the milk.

*References:* Yao *et al.*, 1996, *Genetics*, **144**, 1809-1816; Gordon *et al.*, 1983, *Mol. Cell. Endocrin.*, **33**, 81-95; Lucy *et al.*, 1993, *Domest. Anim. Endocrinol.*, **10**, 325-333

**Key word:** GH, milk proteins, polymorphism, PCR-RFLP, AS-PCR.

**LG4 SINGLE-STRAND CONFORMATION POLYMORPHISM (SSCP) ANALYSIS OF EXON 4 AND 5 OF GROWTH HORMONE GENE IN SERRANA TRANSMONTANA GOAT BREED.** M.C. Varejão, E. Bastos, R. Chaves, A. Cravador\*, J. Azevedo\*\*, H. Guedes-Pinto, *Dept. de Genética e Biotecnologia; \*\*Departamento de Zootecnia, Universidade de Trás-os-Montes e Alto Douro, P5000 Vila Real, Portugal. \*Unidade de Ciências e Tecnologias Agrárias, Universidade do Algarve, Campus de Gambelas, P8000 Faro, Portugal.*

The origin of Serrana goat breed is lost in time; however the wild goat *Capra pyrenaica*, from the Serra da Estrela, is probably its ancestor. The Serrana is the most representative of Portuguese breeds and is considered to have great productive potentialities and considerable expansion possibilities due to its productive and reproductive indices, high degree of ruggedness and high quality products: cheese and meat (1).

The aim of this study was to examine the genetic variability of this portuguese breed at the molecular level for exon 4 and 5 of growth hormone (GH) gene and to try to correlate specific DNA polymorphism with zootechnical parameters of interest with a view to improving future molecular assisted selection.

The single strand conformation polymorphism (SSCP) method depends on the conformation of the single strand DNA fragment and its base sequence, under non-denaturing conditions. One base difference molecule can lead to a different conformation, which can result in different mobilities in polyacrylamide gel (2).

The goat genomic DNA was obtained from blood taken from flocks owned by members of the "Associação Nacional de Caprincultores da Raça Serrana" (ANCRAS). The DNA extraction was carried out by the high salt method (3). The PCR products of the exon 4 and 5, 214 and 364 bp size respectively, were denaturated and loaded in a polyacrylamide gel. The gel was silver stained.

Six conformation patterns for exon 4 of the GH gene were found. However for exon 5, so far two patterns have been detected. The correlation between those results and milk production parameters are also being evaluated, in order to find molecular markers suitable for molecular assisted selection. (Supported by PRAXIS 3/3.2/CA/1991/95 Project.)

*References:* (1) Almendra, 1994, Edição da Associação Nacional de Caprincultores da Raça Serrana (ANCRAS) 28p; (2) Orita *et al.*, 1989, *Genomics* **5**, 874; (3) Montgomery *et al.*, 1990, *New Zealand J. of Agricultural Res.* **33**, 437.

**Key words:** SSCP, Goat, GH, Polymorphism