



**ANIMAL GENOMICS: Synthesis of Past,  
Present, and Future Directions**

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**Detection of origin between two bloodlines of Romosinuano cattle using microsatellite screening.**A. BRENNEMAN<sup>1</sup>, C.C. CHASE, JR.<sup>1</sup>, T.A. OLSON<sup>2</sup>, G.A. ROHRER<sup>3</sup>, S.W. COLEMAN<sup>1</sup>

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Two primary bloodlines of Romosinuano cattle exist (i.e., a Costa Rican [COR] and a Colombian [COL] bloodline) and have been imported for evaluation at STARS near Brooksville, Florida. The two bloodlines are phenotypically indistinguishable except for occasional scurs or rare white spotting observed in the COR bloodline. The objective of this study was to determine whether or not the genetic variation between the two bloodlines was significant and how accurately an individual's bloodline of origin could be determined based on genetic markers. The COR bloodline originated through upgrading from Hereford dams at the University of North Carolina from 1948-50's and was imported in 1990-92 as frozen embryos from the Centro Agronomico Tropical de Investigacion y Enseñanza (CATIE), Turrialba, Costa Rica. The COL bloodline was imported in 1996 from Venezuela as frozen embryos with no evidence of outcrossing from the pedigrees tracing to Colombian origins. Forty-seven individuals from each bloodline were identified and screened across 46 microsatellite loci selected by proximity to published carcass merit QTL, usefulness in previously published genetic distance studies, or chromosomal location maximizing genomic coverage. Unique alleles (n=66, COR and n=47, COL) were detected in 41 of the microsatellite systems comprising up to an allele frequency of 0.511 for a single system. Polymorphism information content values (both maximum and average) and average heterozygosities for the 46 systems were (COR) 0.891, 0.752, 0.571 and (COL) 0.918, 0.705, 0.579, respectively, facilitating correct bloodline assignments.

D030

**The use of microsatellites for measuring genetic diversity of European local beef cattle breeds for conservation purposes**J. CAÑON<sup>1</sup>, P. ALEXANDRINO<sup>2,3</sup>, A. BEJA-PEREIRA<sup>2</sup>, I. BESSA<sup>2</sup>, C. CARLEOS<sup>4</sup>, Y. CARRETERO<sup>1</sup>, S. DUNNER<sup>1</sup>, N. FERRAND<sup>2</sup>, D. GARCIA<sup>1</sup>, J. JORDANA<sup>5</sup>, D. LOLOË<sup>6</sup>, A. SANCHEZ<sup>3</sup>, K. MOAZAMI-GOUDARZI<sup>6</sup>

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This study was undertaken to determine the genetic structure, the genetic relationships, and the genetic diversity of a set of 18 local cattle breeds from Spain, Portugal and France using 16 microsatellites. Heterozygosities, estimates of *F<sub>st</sub>*, genetic distances, dendrograms, multivariate, diversity analyses and assignment tests were performed. Heterozygosities ranged from 0.54 in the Pirenaica breed to 0.72 in the Alentejana breed. Seven per cent of the total genetic variability could be attributed to differences among breeds (mean *F<sub>st</sub>* -0.07; *P*<0.01). The six computed genetic distances have been compared and no correlation was found to be significantly different from 0 between distance based on population effective size and those which use the sizes of the alleles. Support for internal nodes in phenograms estimated by bootstrapping was, in general, low, except for the Alistana/Mirandesa and the Salers/Aubrac groups, which appeared with an occurrence of 94% and 96% respectively. Multivariate analysis distinguished 4 breed groups. The diversity of the

breeds was measured by the Weitzman's recursion approach which suggests that the most important breeds to be preserved are those included into two clusters: the one formed by Mirandesa and Alistana breeds, and the other one composed of the Sayaguesa and Tudanca breeds. The hypothetical extinction of one of those clusters presents a 17% of loss of diversity. In addition, the variation between breeds was sufficiently high as to assign individuals to their breed of origin with a probability of 99% for simulated samples.

D031

**Homozygosity mapping approach for the Chondrodysplasia gene in Dexter Cattle**J.A.L. CAVANAGH<sup>1</sup>, I. TAMMEN<sup>1</sup>, P.A.W. HARPER<sup>2</sup>, H.W. RAADSMA<sup>1</sup> & F.W. NICHOLAS<sup>3</sup>.

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Dexter cattle are a dwarf breed of cattle originating in Ireland which have been bred in Australia for several decades. There have been reports of mutant, aborted fetuses in this breed of cattle, described as chondrodysplastic fetuses. The affected fetuses display disproportionate dwarfism, a short vertebral column, marked micromelia, a relatively large head with a retruded muzzle, cleft palate and protruding tongue and a large abdominal hernia. Dexter chondrodysplasia is considered to be inherited in an incompletely dominant manner. As part of an approach to controlling the disease in Australia, the Australian Dexter Association has chosen to support research to develop a DNA test to prevent carrier/carrier matings. A homozygosity mapping approach is being used to localise the disease gene. Firstly, 12 candidate genes were identified by searching for diseases with similar phenotype in other species. Using comparative mapping, nine regions on the cattle genome were selected. A total of 90 microsatellite markers were used to cover these regions. A selection of animals was genotyped and the results analysed by searching for regions of homozygosity in the affected samples. Of the 90 selected markers, one demonstrated a homozygous pattern amongst the affected samples, but not among the parents and unrelated animals. A gene in this region is currently being screened for mutations. If a mutation is found, a DNA based heterozygote test can be developed.

D032

**Genetic polymorphism of Goat k-casein**E. BUDELLI<sup>1</sup>, P. BOLLA<sup>1</sup>, A. CAROLI<sup>2</sup>, S. JÄGER<sup>2</sup> & G. ERHARDT<sup>2</sup>.

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Investigation on milk protein polymorphism in goat mainly concerns *CSN1S1* fraction, which is characterized by a high qualitative and quantitative genetic variability. Isoelectric focusing (IEF) in ultrathin polyacrylamide gels with carrier ampholytes was used to demonstrate *CSN3* polymorphism in milk samples of Italian (Orobica n=36; Saanen n=60) and German goat breeds (Weisse Deutsche Edelziege n=85; Bunte Deutsche Edelziege n=25; Thüringer Waldziege n=57). A genetic polymorphism resulting in three phenotypes (A, AB, B) could be demonstrated at *CSN3* locus in addition to the already described polymorphism in *CSN1S1*, *CSN1S2* and *CSN2*. The further *CSN3* casein band exhibited a more cathodic migration than *CSN3<sup>A</sup>*. *CSN3<sup>B</sup>* can only be resolved using an ultranarrow pH range pH 4-5.5. Otherwise there is an overlapping by *CSN1S2* C and other protein fractions. After chymosin action, the genetic polymorphism was also observed in the para-k-casein fraction. Thus, the further allele might correspond to the B variant described by Di Luccia *et al* (1990). The genetic basis of *CSN3<sup>B</sup>* was confirmed by genetic studies. The frequency of *CSN3<sup>B</sup>* ranged from 0.36 (Orobica) to 0.26 (Bunte Deutsche Edelziege). The populations were in