

systems on heterozygosity of the gene were also assessed using the GLM procedure of SAS. The polymorphic information content (PIC) values ranged from 0.43 (for marker TGLA68) to 0.76 (marker BMS2580) with an average value of 0.54, showing that the microsatellite panel used was polymorphic. The overall observed and expected heterozygosity values were 0.46 and 0.54, respectively. Higher heterozygosity ($H_e = 0.76$) was observed in the BMS2508 marker whereas lower heterozygosity ($H_e = 0.43$) was observed in the TGLA54 marker. Sheep managed under mixed crop-livestock system showed significant heterozygosity ($P < 0.05$) at BM1329, TGLA68 and OarAE101 loci compared to those sheep breeds managed under pastoral and agro-pastoral production systems. The current result indicated that fecundity gene polymorphism has a positive relationship with the production systems where the sheep were managed. However, further study will be required to substantiate the presence fecundity genes and associated factors in the three indigenous sheep breeds. The fecundity gene polymorphism found in the current study would be used as baseline information for further study in the relationship of reproductive trait and fecundity gene in indigenous sheep of eastern Ethiopia.

Key Words: Booroola FecB, FecX gene and microsatellite marker

P4059 Origins and genetic structure of Creole cattle inferred from Y-chromosomal variation.

C. Ginja (CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal), C. Penedo (Veterinary Genetics Laboratory, School of Veterinary Medicine, UC Davis, Davis, CA), O. Cortés (Universidad Complutense de Madrid, Madrid, Spain), I. Martín-Burriel (Laboratorio de Genética Bioquímica, Universidad de Zaragoza, Zaragoza, Spain), A. Egito (Embrapa-Laboratório de Genômica e Melhoramento Animal, Campo Grande, Brazil), L. T. D. Gama (Faculdade de Medicina Veterinária, Universidade Técnica de Lisboa, Lisboa, Portugal), J. V. Delgado Bermejo, B. Consortium, and A. Martínez-Martínez (Departamento de Genética, Universidad de Córdoba, Córdoba, Spain)

American Creole cattle originated from animals brought from the Iberian Peninsula in the early years of discovery and colonization (15th century), with additional influences of cattle from other regions over the centuries. The paternal lineages of Creole cattle were investigated by using a comprehensive sample of American Creole populations and a broad representation of the breeds that may have influenced

them. Y-chromosome markers are useful to detect recent demographic events, such as founder effects, population expansions and bottlenecks. The study included DNA samples from a total of 1758 males belonging to 95 breeds representative of the following geographic groups: Creole ($N = 31$ breeds), Iberian ($N = 32$), Continental European ($N = 6$), British ($N = 6$), Atlantic and Balearic Islands ($N = 5$), African ($N = 10$), and Indicine cattle ($N = 5$). Genetic polymorphisms located on the non-recombining region of the Y-chromosome were genotyped, including five STRs (*DDX3Y1*, *BM861*, *INRA189*, *UMN0103* and *UMN0307*), two *indels* (*ZFY10*, *USP9Y*) and one SNP (*UTY19*). Multiplex PCR was done using the QIAGEN multiplex PCR kit, and the fragments analyzed on ABI 3730 instruments (Applied Biosystems). A negative and a female DNA controls were included in all assays. Allele sizes were standardized via known fixed alleles from several samples or breeds to match published data. SNP and STR alleles were combined into haplotypes. GENALEX v6.5 was used in Excel to determine distributions of haplotype frequencies and diversities. Median-joining (MJ) networks were constructed to investigate phylogenetic relationships among haplotypes with NETWORK v4.2.0.1. The markers allowed to identify major Y-haplogroups among the 1758 bulls analyzed, such as Y1 (587) and Y2 (824) which are known to be predominant in Northern and Southern European cattle, respectively, and the Y3-lineage (347) of Indicine cattle. Y-STRs allowed to detect the genetic diversity of paternal lineages within major haplogroups, *i.e.* at the breed level, with a total of 58 haplotypes (Y1 = 12; Y2 = 35; and Y3 = 11) detected. African cattle contained unique paternal lineages, with 13 and four exclusive Y2 and Y3 haplotypes, respectively. Y-haplotype diversity in Creoles was high, with several Y1 (7), Y2 (9) and Y3 (7) haplotypes represented. The sharing of specific patrilineages corroborates influence of Iberian (two Y1 and one Y2 haplotypes) and African (one Y2 haplotype) cattle in American Creoles, even though the major influence was from Indicine haplotypes.

Key Words: American Creole cattle, genetic diversity, Y-chromosome

P4060 Runs of homozygosity reveal natural selection footprints of some African chicken breeds and village ecotypes.

A. R. Elbeltagy (Department of Animal Science, Iowa State University, Ames, IA; Department of Animal Biotech. Animal Production Research Institute, Cairo, Egypt), D. S. Fleming, F. Bertolini, A. G. Van Goor (Department of Animal Science, Iowa State