

O025**Genetic improvement and population structure of Italian Limousine**Mauro Fioretti¹, Stefano Biffani¹, Riccardo Negrini¹, Riccardo Bozzi²¹Associazione Italiana Allevatori, Roma, Italy²Dipartimento di Scienze delle Produzioni Agroalimentari e dell'Ambiente, University of Firenze, ItalyContact: biffani.s@aia.it

The Limousine breed was firstly introduced in Italy in 1985 and since then has been experiencing an increasing and steadily growth. The herd book was officially recognized from the Italian ministry of the agriculture in 1999. In 2016 there were 1464 herds, 26,399 cows, 7425 heifers, 20,625 young animals and 1.273 bulls. The breed is well distributed across Italy, but the large number of herds/animals are in Sicily, Sardinia, Tuscany and Lazio regions. The objective of the present paper was to infer the population structure of the Italian Limousine and to implement a first genetic evaluation for average daily gain. Population structure was performed using the Endog program. Pedigree data included 275,083 animals born from 1950 to 2016. Base populations included 52,177 individuals. The effective number of founders was 1500 and the genetic contribution of 10, 50 and 302 most influent ancestors explained 10.2, 25.1 and 50% of the genetic variability in the population, respectively. Inbreeding and average relatedness coefficients were 0.68 and 0.21%, respectively. The effective number of ancestors was 468 and the effective population size was 360. Pedigree known (%) was 83, 67, 58 and 42% in generation 1, 2, 3 and 4, respectively.

Genetic evaluation for average daily gain (ADG) was performed using a single-trait repeatability test-day model. A total of 271,330 weights from 116,299 animals were included in the analysis. The pedigrees of the animals were traced back to 1950, and consisted of 276,518 animals. Genetic groups ($n=15$) were defined based on origin and year of birth. The fitted model included herd-test day, sex and twinning as fixed effects and age at weigh by sex and age of the dam as linear and quadratic covariates. A minimum number of 2 weights from 30 to 365 days were required for each individual. The software DMU was used to estimate variances and predict the breeding values. Heritability and repeatability were 0.30 and 0.26, respectively. The ADG EBV was obtained dividing liveweight EBV by 335 days. Breeding values were standardised with mean = 100 and standard deviation = 10. The genetic base was fixed as the average ADG EBV for weighted animals born in 2011. BLUE estimates for age at weight by sex covariate were 1079 and 0.965 kg/d for males and females, respectively. These results are the first step towards the development of a national genetic evaluation.

O026**Ancient distinctive migration routes suggested by the current mitochondrial gene pool of Podolic cattle breeds in Italy**Hovirag Lancioni¹, Piera Di Lorenzo², Simone Ceccobelli², Licia Colli^{3,4}, Irene Cardinali¹, Taki Karsli⁵, Marco R. Capodiferro⁶, Luca Ferretti⁶, Paolo Ajmone-Marsan^{3,4}, Francesca M. Sarti², Emiliano Lasagna², Alessandro Achilli⁶¹Dipartimento di Chimica, Biologia e Biotecnologie, University of Perugia, Italy²Dipartimento di Scienze Agrarie, Alimentari e Ambientali, University of Perugia, Italy³Istituto di Zootecnica, Università Cattolica del Sacro Cuore, Piacenza, Italy⁴BioDNA Research Center on Biodiversity and Ancient DNA, Università Cattolica del Sacro Cuore, Piacenza, Italy⁵Zootehni Bölümü, Akdeniz University, Antalya, Turkey⁶Dipartimento di Biologia e Biotecnologie "L. Spallanzani", University of Pavia, ItalyContact: hovirag.lancioni@unipg.it

Podolic cattle are a very ancient group of European bovine breeds, considered to be directly descendant of the aurochs (*Bos primigenius*). The aim of the present study was to assess the diversity of Podolic cattle breeds in order to obtain additional information on their genetic relationships and ancestral origin. Mitochondrial DNA (mtDNA) control-region sequences of 18 Podolic and 9 non-Podolic breeds have been analyzed: Piemontese (PI), Romagnola (RO), Marchigiana (MR), Chianina (CH), Maremmana (MA), Podolica Italiana (IP), Mucca Pisana (MP), Calvana (CA), Bianca di Val Padana (BP), Hungarian Grey (HG), Bulgarian Grey (BG), Istrian cattle (IC), Katerini (KA), Romanian Grey (RG), Slavonian Sarmian Podolian (SS), Turkish Grey (TK), Ukrainian Grey (UK), Podolsko (PO) and Valdostana (VA), Bruna Italiana (IB), Grigio Alpina (GA), Pezzata Rossa Italiana (RP), Modicana (MO), Reggiana (RE), Agerolese (AG), Cinisara (CI), Cabannina (CB). All sequences were aligned to the Bovine Reference Sequence and classified in haplogroups and sub-haplogroups. The analysis clearly highlighted the expected lack of maternal relationship between Podolic and non-Podolic groups. Intriguingly, two groups of the Italian Podolic breeds were genetically distinguished: the first clusters with other European Podolic cattle, and a second one more closely related to the Turkish Grey. Besides the possible explanation of a selection-driven effect, we propose the hypothesis of a dual ancestral origin among Italian Podolic breeds: a first group deriving from the Eastern European cattle, in agreement with historical records; a second directly