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ready access to domesticated pigs. The samples, a molar and a humerus, were processed in rooms dedicated to aDNA procedures, following established stringent protocols. DNA was extracted by a magnetic bead-based technology. The *MC1R* gene was enriched using array capture technology, and sequencing was performed on an Illumina HiSeq2500 instrument using HiSeq v3 chemistry. Libraries treated with uracil–DNA–glycosylase (UDG) to remove deaminated cytosine as well as untreated libraries were analyzed. Reads were mapped against the porcine genome assembly Sscrofa 10.2. With non-UDG libraries, 100% and 91% of the ORF were covered in the two samples with a mean depth of 10.9X and 2.9X, respectively. Typical damage patterns were observed. The analysis of the *MC1R* ORF revealed a pattern matching previously described European wild-type haplotypes for one of the samples. The results for the other sample were also consistent with a wild-type allele, but that animal was heterozygous for two variants that have previously been observed only in present-day Asian haplotypes. This finding indicates that the population structure of the suids in the Meso-/Neolithic and their domestication history might be more complex than inferred from modern pig data. In future studies, more ancient samples will be analyzed and further genes will be included.

Key Words: aDNA, pig, *MC1R*

P4032 Polymorphism of 10 microsatellite DNA used for parentage control in pigeons in Poland.

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The aim of this study was to test the polymorphism of 10 microsatellite markers and their usefulness for parentage verification in pigeons. Samples were collected from 69 individuals of Polish, German and Belgian breeds from different locations in Poland. The assay involved the following 10 loci: CliμD01, CliμD16, CliμD32, CliμT13, CliμT17, PG2, PG3, PG 5, PG 6, PG 7 and the bird sex marker CHD. We used genomic DNA extracted from feathers and buccal swab samples. DNA extracts were amplified by PCR for the all microsatellite and CHD marker together in one multiplex reaction. Each of the forward primers was labeled with fluorescent dye (6-Fam, Vic, Ned, Pet). Markers were amplified using the QIAGEN Multiplex PCR Kit, the amplified products were separated on a ABI PRISM® 3100xl Genetic Analyzer and genotyped using GeneMapper software (Applied Biosystems). In the study of 10 microsatellite markers we detected 60 alleles, which number per locus ranged from 2 (PG5) to 8 (CliμD01 and CliμT17). Based on the frequency of identified alleles expected heterozygosity (He) and observed (Ho) were determined as Ho = 0.88 and He = 0.78, respectively. The average negative inbreeding coefficients was Fis = -0.03. The lowest polymorphism in the present study was noted at the PG5 (PIC = 0.34 and H = 0.47) where two alleles identified and PG6 (PIC = 0.43 and H = 0.59) for which two of three alleles occurred with higher frequency in excess of 94%. The average power of discrimination (PD) was 0.83. The combined power of discrimination values for all 10 loci reached the high value as 0.9999999. The cumulative probabilities of parentage exclusion, when one parent is known, and two parents is known (PEc1 and PEc2) were 0.9726 and 0.9982, respectively.

Key Words: pigeon, microsatellite DNA, parentage control

P4033 Characterization and diversity analysis of European local pig breeds and production systems under Treasure project framework.

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Treasure is a multidisciplinary European Union H2020 funded project focused on the research and development of activities for the benefit of sustainable pork chains based on European local pig breeds and their production systems. One of the main objectives of the project is to demonstrate singularity of about 20 untapped local pig populations from nine European countries (Portugal, Spain, France, Italy, Slovenia,

Croatia, Serbia, Germany and Lithuania) through phenotypic, genomic and transcriptomic activities. Genomic approaches include the use of high density SNP data, candidate gene analyses and whole genome sequencing (WGS). Untapped breeds are first characterized at the production system level through a specific survey addressed to collect census data, breed distribution and phenotypic traits and information on breed organizations and production chains. Genomic data analyses bring the possibility for the estimation of different population genetics and population genomics indicators, such as relative homozygosity and observed and expected genetic diversity of the studied local pig breeds, as well as the definition of the structure of meta-populations through the proportion of shared alleles/haplotypes among animals and population admixture parameters. Comparative analyses including commercial pig populations in Europe identify genome regions with evidence of selective sweeps or signatures of demographic events across breeds. WGS analyses are focused on population adaptation and resilience signatures. To complete the local pig breed characterization, identification of population-specific biological processes responsible for specific production traits and product quality will be achieved through transcriptomic and metagenomic assays under specific production systems and management conditions. Together all these analyses are expected to provide useful methods and DNA markers for authentication and traceability of mono-breed products, conservation of local pig genetic resources and development of specific breeding programs for sustainable pork production chains in Europe. The Treasure project is funded under European Union's Horizon 2020 research and innovation program, Grant No. 634476

Key Words: Treasure, Europena local pig breeds, genomics, transcriptomics, metagenomics

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P4034 Milk protein polymorphisms in African indigenous cattle: Opportunity for Sustainable Breeding Program. I. Houaga* (Jomo Kenyatta University Of Agriculture And Technology, Juja-Kenya, Kenya; University of Abomey-Calavi, Abomey-Calavi, Benin)

Milk protein polymorphisms in cattle are important tools for genetic diversity studies, breed characterization, gene evolutionary studies with many applications in human nutrition and animal breeding. Unfortunately, few studies have focused on African indigenous cattle compared with Western dairy breeds. This paper summarizes the available information about the genetic polymorphism of major milk proteins in African indigenous cattle and discusses the opportunity to increase their milk production by implementing a sustainable breeding program using both quantitative and molecular approaches. Moreover, news proteins variants have been discovered in African indigenous cattle, but their effects on milk traits have never been investigated. This strongly suggests the necessity of genetic associative studies on major milk proteins polymorphism, which is deemed necessary for the implementation of rapid and effective genetic improvement program for African indigenous cattle adapted to local environment to avoid loss of genetic diversity.

Key Words: African indigenous cattle, polymorphisms, genetic diversity

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P4035 Exploiting Genomic Data of Spanish Atlantic salmon to identify genes involved in sex determination and to estimate effective population size. M. Saura* (INIA, Madrid, Spain), A. Chtioui (INIA, Madrid, Spain; Universidad Politécnica de Valencia, Valencia, Spain), A. I. Fernández (Departamento de Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid, Spain), P. Morán (Universidad de Vigo, Vigo, Spain), M. P. Kent (Center for Integrative Genetics (CIGENE), Department of Animal and Aquacultural Sciences (IHA), Norwegian University of Life Sciences (NMBU), Ås, Norway), B. Villanueva (INIA, Madrid, Spain)

Advances in salmon genomics in recent years have led to the development of high-density single nucleotide polymorphism (SNP) chips opening thus new opportunities for investigating the evolutionary history of populations. In particular, they can be used for detecting genes affecting life history traits and to infer ancestral and current population sizes. In this study, the 220K high-density Affymetrix SNP genotyping array (Aquagene/CIGENE) has been used for identifying genes involved in sex determination and to estimate effective population size in Spanish Atlantic salmon populations. Samples from six rivers covering all the distribution area of the species in Spain were genotyped. After quality control, 187 fish and more than 150,000 SNPs were available for the analyses. A total of 317 significant associations with sex determination were detected representing nine putative QTL regions on Ssa2, Ssa6, Ssa9, Ssa10, Ssa21 and Ssa22. Giving these results, powerful candidate genes to be responsible of the QTL effects are proposed: the *sdY* gene, which is the master male-specific sex-determining gene, maps within our QTL intervals on Ssa2, and the estrogen receptor gene, *esr1*, which is essential for sexual development and reproductive function in females, maps close to our QTL region