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European autochthonous pig breeds are very relevant as a local resource. They have common characteristics as good environmental adaptation, high adipogenic potential, rusticity and excellent meat quality products. However, some of them are in great danger of becoming extinct and development of conservation policies and promotion of their sustainable use are needed. One key factor for the conservation of these breeds consists in their genetic characterization. In the current study, we assessed the genomic diversity of 20 European local pig breeds (Alentejana, Apulo-Calabrese, Basque, Bísara, Majorcan Black, Black Slavonian, Casertana, Cinta Senese, Gascon, Iberian, Krs?kopolje, Lithuanian indigenous wattle, Lithuanian White Old Type, Mora Romagnola, Moravka, Nero Siciliano, Sarda, Schwäbisch-Hällisches Schwein, Swallow-Bellied Mangalitsa and Turopolje) from 7 countries (Croatia, France, Germany, Italy, Lithuania, Portugal, Serbia, Slovenia, Spain) and wild pigs sampled in the Iberian Peninsula. A total of 992 DNA samples were genotyped with GGP Porcine HD Genomic Profiler v1 chip (68,528 SNPs). Different SNP sets were used according to the analyses performed to compute: genetic diversity parameters, genetic distances, population structure, linkage disequilibrium and effective sample size. The results revealed that several breeds as Apulo Calabrese, Casertana, Mora Romagnola and Turopolje have low genetic diversity exhibiting low heterozygosity and very small population effective size, therefore, strategies of conservation should be applied in these breeds. Principal component analyses showed individuals belonging to the same breeds cluster together with overlapping between several breeds, particularly marked for Iberian and Alentejana breeds, which suggests genetic closeness. In addition, few breeds were clearly isolated from the rest. These findings provide relevant information for the implementation of further conservation and selection strategies. This project has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement No 634476. The content of this abstract reflects only the author's view and the European Union Agency is not responsible for any use that may be made of the information it contains.

Key Words: genomic diversity, pig breeds, SNP chip, conservation

OP148 IMAGE: Innovative Management of Animal Genetic Resources. O. Cortes^{*1}, L. T. Gama², S. Dunner¹, IMAGE Consortium³, and M. Tixier-Boichard³, ¹*Veterinary Faculty, University Complutense of Madrid, Madrid, Spain, ²CIISA, Faculdade de Medicina Veterinária, Universidade de Lisboa, Lisboa, Portugal, ³INRA, France.*

IMAGE is a project funded by the Horizon 2020 Research and Innovation Programme of the European Union. The ultimate goal of the project is to demonstrate the benefits brought by gene banks to the development of more sustainable livestock farming systems. Thirteen EU countries are involved, together with Switzerland and 4 non-European countries (Argentina, Colombia, Egypt and Morocco), in a project that unites 28 partners including 3 SMEs, 3 NGOs, FAO, 9 research institutions, 11 higher education and research, and INRA Transfert. Image has still one year to go (2016–2020) and significant progress has been achieved on innovative approaches for animal gene banks. The IMAGE Dialogue Forum, a platform designed to involve all stakeholders in the discussion about the future of genetic management of animal gene banks, has covered important topics such as sanitary regulations, data/material sharing, ethics and standardization of gene bank management in the 3 sessions celebrated so far, encompassing more than 50 participants from different origins. IMAGE surveys have obtained a detailed information about the diversity of germplasm and genomic col-

lections across Europe from 61 organizations representing 20 different countries. Improvement of cryopreservation of germplasm, strategies toward breed conservation using genomic tools, genomic selection or introgression of specific characteristics into another breed are some of the topics of the papers already published with 15 articles in peer-review journals and 2 book chapters based on avian, horse, pigs, goats and cows species. New sequencing data are being produced that will significantly improve the knowledge and attractiveness of gene bank collections for research and breeding. Three post-graduate courses were organized in Argentina, Colombia and Netherlands which gathered students from Europe, America and Africa. The presence of the IMAGE project in social-media is wide and diverse. It has a youtube channel, and is represented in twitter (@imageh2020) and periodically the projects news are disseminated through Newsletters fully available, as all the documentation of the project, in the webpage (www.imageh2020.eu).

Key Words: H2020, gene banks, genomic, livestock

OP149 Sequencing of reindeer (*Rangifer tarandus*) genomes: Insights into evolution, domestication, and adaptation. M. Welde-negodguad^{1,2}, K. Pokharel¹, Y. Ming³, M. Honkatukia^{1,4}, J. Peippo¹, T. Reilas¹, K. H. Røed⁵, and J. Kantanen^{*1}, ¹*Natural Resources Institute Finland, Jokioinen, Finland, ²Department of Environmental and Biological Sciences, University of Eastern Finland, Kuopio, Finland, ³BGI-Tech, Guangdong, China, ⁴NordGen Nordic Genetic Resources Centre, Ås, Norway, ⁵Norwegian University of Life Sciences, Oslo, Norway.*

Semi-domesticated reindeer (*Rangifer tarandus*) have pivotal economic, societal and cultural value for indigenous people and pastoralists in northern and subarctic regions in Eurasian. Currently, there exist several semi-domesticated and wild *Rangifer*-populations, the taxonomic status of which has been actively debated. To examine genetic diversity, domestication history, taxonomy and adaptation, we deep-sequenced and de novo assembled one reindeer genome, resequenced 23 other *Rangifer* sp. samples. Genomic DNA of a 1-year-old Finnish male reindeer was sequenced at high coverage (100X) on the Illumina HiSeq2500 and 4000 platforms. Seven paired-end DNA libraries with insert sizes ranging from 170bp to 20kb were constructed. The genome assembly, annotation, and orthology analysis were conducted using a robust bioinformatics pipeline. In the resequencing approach, 23 semi-domesticated and wild reindeer and caribou were sequenced (10X) using Illumina HiSeq2500 platform. The data were subjected e.g., for the principal component analysis. A total of 300.5 Gb of clean data was assembled using SOAP denovo resulting into 256,454 scaffolds (N50 = 502 Kb) with cumulative scaffold length of 2.66 Gb and spanning 90% of the estimated (2.9 Gb) genome size of reindeer. Using a homology based approach the reindeer genome was predicted to harbor 27,332 protein coding genes, 98% of which were functionally annotated. The resequenced animals grouped into 2 main clusters: northern European and northern Russian/northern American. The draft quality of the reference genome along with the annotations will provide important insights into the evolution and demographic history of the reindeer and taxonomy of *Rangifer* sp. Our findings suggest that there have been at least 2 domestication events in the history of reindeer.

Key Words: de novo sequencing, domestication, reindeer, resequencing, taxonomy