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Genetic and phenotypic fine characterizations of French porcine reference populations

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The SLA Nomenclature Committee was established in 2002 at the 28th ISAG Annual Conference in Göttingen, Germany. It currently comprises a total of 8 members from 3 continents, and its primary functions are: 1) to validate newly identified SLA sequences according to the guidelines established for maintaining high quality standards of the accepted sequences; 2) to assign appropriate nomenclatures for new alleles as they are validated; and 3) to serve as a curator of the IPD-MHC SLA sequence database which is the repository for maintaining a list of all recognized SLA genes and their allelic sequences. To date, there are 131 class I (SLA-1, SLA-2, SLA-3, SLA-6) and 174 class II (DRA, DRB1, DQA, DQB1, DMA) alleles officially designated. There are also 31 class I (SLA-1-3-2-6) and 26 class II (DRA-DRB1-DQA-DQB1) high-resolution (allele level) haplotypes designated, while designation of low-resolution (group level) haplotypes is in progress. The SLA system is among the most well characterized MHC systems in non-primate species. Continuous efforts on studying of SLA diversity in various pig populations will further our understanding of the allelic architecture and polymorphism of the SLA system, which may ultimately facilitate the research on swine immunology, vaccine development, and the use of swine as a large biomedical animal model.

Key Words: MHC, SLA, nomenclature

P3042 Withdrawn

P3043 Genetic and phenotypic fine characterizations of French porcine reference populations. M. Sancristobal¹, S. Boitard¹, M. I. Fariello-Rico¹, H. Gilbert^{1,5}, B. Laurent⁴, L. Liaubet^{*1}, A. Paris⁶, C. Rogel-Gaillard⁵, F. Rohart^{1,4}, J. Riquet¹, B. Servin¹, N. Villa-Vialaneix⁷, M. P. Sanchez⁵, T. Tribout⁵, D. Milan¹, ¹INRA, UMR444 Cellular Genetics, F-31326 Castanet Tolosan, France, ²INRA, UE450 Unité Expérimentale de Testage de Porcs, F-35653 LE RHEU, France, ³INRA, UMR1331 ToxAlim, F-31027 Toulouse, France, ⁴CNRS, UPS, UMR5219 Institut de Mathématiques de Toulouse & INSA Toulouse, F-31077 Toulouse, France, ⁵INRA, UMR1313 GABI, F-78352 Jouy-en-Josas, France, ⁶INRA, UR1204 Food Risk Analysis Methodologies, Mét@risk, F-75231 Paris, France, ⁷Université Paris I Panthéon-Sorbonne, EA4543 SAMM, F-75634 Paris, France.

Fine study of the porcine genome. The porcine industry has to face new societal stakes, and propose a more sustainable production. Genetics is one of the control levers. The objective of the DéLiSus project (ANR-07-GANI-001) was, based on recent developments in genomics, to improve our knowledge on the porcine genome structure, on genetic mechanisms controlling traits, but also connected to the development of new

systems of production (such as food efficiency, quality of meat). High throughput genotyping and phenotyping strategy laid on accumulating information on a large number of animals of various porcine breeds, from the gene to the phenotype, and looking for the links between these informations. Thereafter the main results: (1) Large-sized databases with genotypes, transcriptomic, metabolomic and phenotypic data; (2) Contribution to the improvement of the assembly of the porcine genome and to the mapping of 60K SNP; (3) QTL detection (25 phenotypes); (4) Revealing the genetic variability clearly structured; (5) New methodology to detect footprint of selection revealing of genomic regions presenting a strong local decline of variability; (6) Metabolomic profiles allow predicting phenotypes of interest, such as the rate of muscle; and (7) Differential expression between races of numerous genes in the post-mortem muscle (among 44K).

Key Words: diversity, genomics, haplotype

P3044 Diversity studies of SLA haplotypes by targeted high-throughput resequencing. Núria Mach^{*1}, Marco Moroldo^{1,2}, Sylvain Marthey^{1,2}, Asako Ando³, Jun-Heon Lee⁴, Chak-Sum Ho⁵, Joan Lunney⁶, Jordi Estellé¹, and Claire Rogel-Gaillard¹, ¹INRA, Laboratory of Animal Genetics and Integrative Biology, F-78350 Jouy-en-Josas, France, ²INRA, Biological Resources Centre for livestock genomics, CRB GADIE, Laboratory of Animal Genetics and Integrative Biology, F-78350 Jouy-en-Josas, France, ³Department of Molecular Life Science, Division of Basic Medical Science and Molecular Medicine, Tokai University School of Medicine, Isehara, Kanagawa, Japan, ⁴Department of Animal Science and Biotechnology, College of Agriculture and Life Sciences, Chungnam National University, Daejeon, Korea, ⁵Histocompatibility Laboratory, Gift of Life Michigan, Ann Arbor, MI, USA, ⁶Animal Parasitic Diseases Laboratory, BARC, ARS, USDA, Beltsville, MD, USA.

The swine MHC (SLA complex) is a gene-dense region that plays a key role in self versus non-self immune recognition. It consists of 3 major gene clusters (class I, III and II), and the diversity of the SLA class I and II genes has a fundamental role in susceptibility to infectious diseases. Characterizing and maintaining SLA diversity at the population level is crucial to maximize the capacity to face a large range of pathogens. Sequencing and annotation of the entire Hp-1a.1 haplotype, and of 2 class I haplotypes Hp-28.0 and Hp-62.0, revealed that haplotype variability relies also on copy number variation. Since genetic variation of other haplotypes is largely unknown we decided to analyze 11 SLA haplotypes by studying the genetic variability of the whole SLA region. A 385K solid phase array targeting a region of 2.8 Mb based on the Hp-1a.1 haplotype