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## SELECTIVE SWEEPS AND SIGNATURES OF SELECTION IN THE DOMESTICATION OF THE CHICKEN

C.-J. RUBIN<sup>1</sup>, M.C. ZODY<sup>1,2</sup>, J. ERIKSSON<sup>1</sup>, J.R.S. MEADOWS<sup>1</sup>, E. SHERWOOD<sup>3</sup>, M.T. WEBSTER<sup>1</sup>, L. JIANG<sup>1</sup>, M. INGMAN<sup>4</sup>, T. SHARPE<sup>2</sup>, S. KA<sup>5</sup>, F. HALLBÖÖK<sup>5</sup>, F. BESNIER<sup>6</sup>, Ö. CARLBORG<sup>6</sup>, B. BED'HOM<sup>7</sup>, M. TIXIER-BOICHARD<sup>7</sup>, P. JENSEN<sup>8</sup>, P. SIEGEL<sup>9</sup>, K. LINDBLAD-TOH<sup>1,2</sup> AND L. ANDERSSON<sup>1,6</sup>

<sup>1</sup>Department of Medical Biochemistry and Microbiology, Uppsala University, SE-751 23 Uppsala, Sweden. <sup>2</sup>Broad Institute of Harvard and MIT, Cambridge, Massachusetts 02142, USA. <sup>3</sup>Department of Cell and Molecular Biology, Karolinska Institutet, SE-171 77 Stockholm, Sweden. <sup>4</sup>Department of Genetics and Pathology, Uppsala University, SE-751 85 Uppsala, Sweden. <sup>5</sup>Department of Neuroscience, Uppsala University, SE-75124 Uppsala, Sweden. <sup>6</sup>Department of Animal Breeding and Genetics, SLU, SE-751 24 Uppsala, Sweden. <sup>7</sup>INRA, UMR1313 Animal Genetics and Integrative Biology, F-78350 Jouy-en-Josas, France. <sup>8</sup>IFM Biology, Linköping University, SE-58183 Linköping, Sweden. <sup>9</sup>Virginia Polytechnic Institute and State University, Department of Animal and Poultry Sciences, Blacksburg, VA 24061-0306, USA  
Corresponding Author: leif.andersson@imbim.uu.se

We used massively parallel sequencing to identify selective sweeps of favourable alleles as well as candidate mutations that have played a prominent role during chicken domestication and subsequent specialisation into broiler (meat-producing) and layer (egg-producing) chickens. We generated 44.5x coverage of the chicken genome using pools of genomic DNA representing eight different populations of domestic chickens as well as red junglefowl, the major wild ancestor. We report more than seven million SNP, about 1 300 deletions and a number of putative selective sweeps. One of the most striking selective sweeps found in all domestic chickens occurred at the locus for thyroid stimulating hormone receptor (TSHR), which has a pivotal role for metabolic regulation and photoperiod control of reproduction in vertebrates. Several of the selective sweeps detected in broilers overlapped genes associated with growth, appetite and metabolic regulation. We found little evidence that selection for loss-of-function mutations played a prominent role during chicken domestication, but we detected two deletions in coding sequences that we suggest are functionally important. This study has direct application in animal breeding and enhances the importance of the domestic chicken as a model organism for biomedical research.

2-SA08

## GENOME-WIDE ASSOCIATION STUDY FOR PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME (PRRS) VIREMIA IN COMMERCIAL PIGS

S. BOTTI<sup>1,3</sup>, S. BIFFANI<sup>1,3</sup>, A. CAPRERA<sup>1</sup>, A. ANSELMO<sup>1</sup>, B. LAZZARI<sup>1</sup>, S.C. BISHOP<sup>2</sup>, A. STELLA<sup>1</sup> AND E. GIUFFRÀ<sup>1</sup>

<sup>1</sup>Parco Tecnologico Padano – Loc. Cascina Codazza, Via A. Einstein, 26900 Lodi Italy. <sup>2</sup>The Roslin Institute and R(D)SVS, University of Edinburgh, Roslin, Midlothian EH25 9PS Scotland, UK. <sup>3</sup>*Equal contributors*  
Corresponding Author: elisabetta.giuffra@tecnoparco.org

Porcine reproductive and respiratory syndrome (PRRS) is a major cause of economic loss for the swine industry worldwide. This study was aimed at identifying and characterizing chromosomal regions with significant effects on PRRS resistance, paving the way for genomic selection to complement existing management procedures. We have created a long-term resource database combining pedigree data and phenotypes for health and production traits, and an extensive biorepository (MISAGEN) of about 5 000 purebred animals from 18 genetically connected commercial farms in Northern Italy. Here we report a genome-wide association study (GWAS) for the PRRS viremia measured by PCR in sera of weaning piglets. The selected population comprised 1 208 pigs across four breeds (Large White, Landrace, Duroc and Pietrain) genotyped with the Illumina PorcineSNP60 BeadChip. After editing, 47 446 markers and 1 127 individuals were available. The GRAMMAR methodology was used for the analyses. Firstly, a mixed model was fitted to the phenotypes with a random effect of sire and fixed effects of sex, breed and herd-year-season of sampling. Residuals for each individual were then regressed on each SNP, assuming an additive model. This GWAS analysis identified seven SNP well above the genome-wide 5% significance threshold, of which five could be mapped to known chromosomal locations of the pig genome sequence (Build9). Furthermore, the genome-wide analysis of positive samples using an additional quantitative phenotype (PRRSV viremia by qPCR) confirmed the most significant associations previously identified. Further research will exploit the LD among adjacent SNP and evaluate models including multiple marker and haplotype associations. Supported by Regione Lombardia (Regional Program in Agriculture 2001-2003 and 2004-2006) and SABRE EU-FP6 Integrated project (Demonstration Funds).