



HAL
open science

Transcriptome-wide investigation of genomic imprinting in chicken

Laure L. Fresard, Sophie S. Leroux, David Gourichon, Magali San Cristobal,
Nathalie N. Marsaud, Olivier O. Bouchez, Patrice Dehais, Catherine C.
Beaumont, Tatiana Zerjal, P. P. Kaiser, et al.

► To cite this version:

Laure L. Fresard, Sophie S. Leroux, David Gourichon, Magali San Cristobal, Nathalie N. Marsaud, et al.. Transcriptome-wide investigation of genomic imprinting in chicken. 33. Conference of the International Society for Animal Genetics, Jul 2012, Cairns, Australia. pp.75. hal-01000657

HAL Id: hal-01000657

<https://hal.science/hal-01000657>

Submitted on 3 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



ISAG
2012

33rd CONFERENCE
CAIRNS, AUSTRALIA
July 15 – 20, 2012



**33rd Conference of the
International Society for Animal Genetics**

July 15–20, 2012, Cairns, Australia

Programme and Abstract Book



P3019 Mitochondrial DNA sequencing detected additional variability in tench (*Tinca tinca* L.).

R. Lo Presti¹, K. Kohlmann², P. Kersten², C. Lisa¹, and L. Di Stasio*¹, ¹*Dept. Animal Science, Turin University, Grugliasco, Italy*, ²*Dept. Aquaculture and Ecophysiology, Leibniz Institute, Berlin, Germany*.

Previous RFLP studies on ND1, ND6, cytb and D-loop segments of mtDNA revealed the existence of 9 haplotypes, H1-H9, with H1 corresponding to the RefSeq. With the aim of analyzing in more detail the genetic variability in tench, the same 4 segments were sequenced in 14 individuals covering all the composite haplotypes found with the RFLP procedure. Eighty-four polymorphic sites were identified, 42 located in the coding regions and 42 in the control region. All the differences were single nucleotide substitutions, except for 3 indels found in the D-loop. Compared with the RFLP technique, the sequencing revealed additional variability, with the H2 haplotype subdivided into 4 different haplotypes (named H2a-H2d), so that a total of 12 composite haplotypes were found. Moreover, the sequencing showed that the H1 haplotype differed from the reference sequence for 3 base substitutions in the D-loop. The Neighbor-joining tree confirmed the existence of 2 deeply differentiated haplogroups, one including H1, H3, H4, H5 and H6 haplotypes (haplogroup A), and the other including H2a, H2b, H2c, H2d, H7, H8 and H9 haplotypes (haplogroup B). The Median-joining network, illustrating the evolutionary branching of the observed haplotypes and the potential connecting haplotypes, showed a star-like phylogeny for the haplogroup A and a less clear situation for the haplogroup B.

Key Words: tench, mtDNA, sequencing

P3020 Identification of shared epitopes in the light chain of avian immunoglobulins.

Mateja Bancina, Ivanka Cizelj, Mojca Narat, Dusan Bencina, and Peter Dovc,* *University of Ljubljana, Biotechnical Faculty, Domzale, Slovenia*.

Immunoglobulins (Ig) play the essential role in the vertebrate immune defense system. In the phylum Aves, the Ig structures have been determined for several species at molecular level only. In the present study, we report the genomic DNA sequence encoding Ig light chain (LC), namely joining LC (jLC) and constant LC (cLC) regions in turkey (*Meleagris gallopavo*), ring-necked pheasant (*Phasianus colchicus*) and gray partridge (*Perdix perdix*). Their deduced amino acid (aa) sequences of jLC (13 aa) and cLC (103 aa) contain the same number of aa as homologous regions in chicken (*Gallus gallus*). However, comparison with chicken cLC revealed deletion of an asparagine (N 19) and extension for an additional Serine. The LC of *P. colchicus* is most similar to that of *G. gallus*, with 99% and 94% nucleotide sequence identity in jLC and cLC region,

respectively. The N-terminal and internal sequences obtained by direct aa sequencing of *P. colchicus* LCs were identical to the chicken sequences. The high level of similarity between different avian species was also confirmed using monoclonal antibodies (3C10/F6 and CH31 recognizing chicken LC, which also reacted with LCs from 7 species belonging to the phylum Aves. The highest similarity was found among LCs of 3 genera of pheasants and *Tragopan melanocephalus*.

Key Words: immunoglobulin, light chain, avian species

P3021 Transcriptome-wide investigation of genomic imprinting in chicken.

L. Fresard*¹, S. Leroux¹, D. Gourichon², M. San Cristobal¹, N. Marsaud³, O. Bouchez³, P. Dehais¹, C. Beaumont⁴, T. Zerjal⁵, P. Kaiser⁶, S. Lagarrigue⁷, A. Vignal¹, M. Morisson¹, and F. Pitel¹, ¹*INRA, ENVT, LGC, Castanet-Tolosan, France*, ²*INRA, PEAT, Tours, France*, ³*GeT-PlaGe, Genotoul, INRA Auzeville, Castanet-Tolosan, France*, ⁴*INRA, URA, Tours, France*, ⁵*INRA, GABI, Jouy-en-Josas, France*, ⁶*The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, United Kingdom*, ⁷*INRA, Agrocampus Ouest, PEGASE, Rennes, France*.

The question of evolution of imprinting in vertebrates and its existence in birds is evoked in the literature, but not yet definitely answered. Genomic imprinting is an epigenetic modification leading to parent-of-origin-specific expression of certain genes. It has been observed in eutherian mammals and marsupials, but not in birds. So far, the allelic expression of imprinted gene orthologs has been analyzed in the chicken, without any reliable evidence of imprinting. Several imprinted QTL have been found in poultry; as some of them may finally be considered as not relevant to genomic imprinting, others appeared to be consistent, when using appropriate animal design and methodology. Our main objectives are to detect genes for which variation in expression is observed according to the allele, either because of an allele-specific expression or a parent-of-origin dependent expression. We screened the entire genome for allele-specific differential expression on whole embryonic transcriptomes by using high-throughput sequencing. Two chicken lines were used, as inbred and as genetically distant as possible, to unquestionably identify the parental origin of each observed haplotype. Two families from 2 reciprocal crosses were produced and transcripts from 20 embryos (4.5 d) have been tagged and sequenced through 6 HiSeq2000 lanes. About 200 Gb have been generated and are under analysis.

Key Words: imprinting, chicken, RNAseq

P3022 Direct resequencing reveals further variability within the bovine casein genes.

J. L. Gallinat*¹, S. Quanbari², C. Drögemüller³, E. Pimentel⁴, G. Thaller¹, and J. Tetens¹, ¹*Institute of Animal Breeding*