



SNP detection for QTL analysis of social behaviour and production traits in quail

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macaque from 82 selected human Y-chromosomal microsatellites referred to the published studies. Polymorphism was detected at 6 loci in the first panel consisted with 23 animals from 23 subpopulations. In the second panel of 163 animals from 23 subpopulations, we detected the 23 alleles and 28 haplotypes in 6 loci. The haplotype diversity of Y-chromosomal microsatellites was 0.925 in 163 animals. These results showed that the developed Y-chromosomal microsatellites makers would be valuable for investigation of the genetic features of the Fukushima population before or after of earthquake, tsunami and Fukushima nuclear crisis.

Key Words: Y-chromosomal, microsatellites, Japanese macaque

P3055 Leptin and leptin receptor gene expression profiles across different porcine tissues. D. Pérez-Montarelo^{*1}, A. Fernández¹, J. M. Folch², R. Pena³, C. Rodríguez¹, L. Silió¹, C. Óvilo¹, and A. I. Fernández¹, ¹*Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Madrid, Spain*, ²*Universitat Autònoma de Barcelona, Barcelona, Spain*, ³*Institut de Recerca i Tecnologia Agroalimentàries, Lleida, Spain*.

The leptin hormone drives food intake and energy expenditure through the interaction with its receptor (LEPR). Despite their relevant role in porcine growth and fatness, their expression profiles have not been characterized so far in pig. In the present study we analyzed by Q-PCR the expression levels of the LEP gene and different isoforms of the LEPR gene across 4 porcine tissues: backfat, liver, longissimus dorsi and diaphragm muscles. Samples from 20 males of an (Iberian × Landrace) × Landrace backcross were analyzed. The primer pairs were designed between exons 2 and 3 of the LEP gene, and between exons 8 and 9 for the short isoforms and exons 19 and 20 for the long isoform of the LEPR gene. Q-PCR reactions were carried out in a LightCycler device, using SYBR Green. Two housekeeping genes (B2M and ACTB) were used for normalization. Significant differential expression of LEP gene was detected between tissues. Backfat LEP expression was around 100 times higher than in the other tissues. In contrast, liver showed the highest short LEPR isoforms expression, > 10-fold higher than in the other tissues. The long LEPR isoform showed very low, almost undetectable, expression in all the analyzed tissues. Moreover, we investigated their expression differences conditional on the genotypes for the LEPg.1387C>T and LEPRc.1987C>T polymorphisms, previously associated with porcine growth and body composition. We observed LEP expression differences in backfat conditional on LEPg.1387C>T genotype (C > T). As well, short LEPR isoforms expression differences conditional on LEPRc.1987C>T genotype were observed in liver (T < C).

Key Words: LEP, LEPR, expression

P3056 Genome-wide characterization of Italian ovine biodiversity. E. Ciani¹, F. M. Sarti², F. Napolitano³, A. Carta⁴, D. Matassino⁵, P. Crepaldi⁶, R. Ciampolini⁷, S. Bordonaro⁸, P. Modesto⁹, N. P. P. Macciotta¹⁰, P. Ajmone Marsan¹¹, B. Portolano¹², and F. Pilla^{*13}, ¹*Dipartimento Fisiologia Generale Ambientale Uniba, Bari (BA) Italy*, ²*Dipartimento Biologia Applicata Unipg, Perugia (PG) Italy*, ³*Consiglio Ricerca Agricoltura, Centro Produzione Carni e Miglioramento Genetico, Monterotondo Scalo, Roma, Italy*, ⁴*DiRPA – AGRIS, Olmedo (SS) Italy*, ⁵*ConsDABI, San Giorgio del Sannio, Benevento, Italy*, ⁶*Università degli Studi di Milano, Milano, (MI) Italy*, ⁷*Dipartimento di Produzioni Animali, Pisa (PI) Italy*, ⁸*DACPA-Unict, Catania (CT) Italy*, ⁹*Istituto Zooprofilattico Sperimentale PLV, Torino (TO) Italy*, ¹⁰*Dipartimento Agraria-Uniss, Sassari (SS) Italy*, ¹¹*Istituto Zootechnia-Unicatt, Piacenza (PC) Italy*, ¹²*Demetra-Unipa, Palermo (PA) Italy*, ¹³*AAA Unimol, Campobasso (CB) Italy*.

Genome-wide SNP panels provide an affordable tool to assess within-breed genetic diversity and between breed relationships, also among closely related populations. A set of 496 animals, representative of 20 local and cosmopolite sheep breeds from different geographic and agro-ecological areas of Italy were genotyped with the Illumina Ovine SNP50 BeadChip. On average, 97% of the loci were polymorphic within breed, with slight differences among breeds. SNP with MAF < 0.01, outside H-W equilibrium, with too many missing data and carrying signatures of selection were excluded from the working data set that comprised 41953 of the original 45068 markers Sardinian Ancestral Black is the breed displaying the highest proportion of monomorphic loci (0.05) and among the lowest gene diversity values (0.33), likely resulting from a combination of genetic isolation and demographic events. Cluster and Network analysis, Multi Dimensional Scaling (MDS), Structure analysis and haplotype sharing analysis highlighted known and unexpected relationships between breeds. MDS also revealed a clear geographical component of Italian sheep genetic diversity. Comparison with a panel of international breeds (International Sheep Genome Consortium) revealed a clear geographical component of genetic diversity only in non Merino-derived breeds.

Key Words: sheep, biodiversity, single nucleotide polymorphisms

P3057 SNP detection for QTL analysis of social behaviour and production traits in quail. F. Pitel^{*1}, S. Leroux¹, P. Dehais¹, A. Vignal¹, O. Bouchez², D. Gourichon³, S. Rivière³, A. Bertin³, B. Bed'hom⁴, F. Minvielle⁴, J. Recoquillay⁵, E. Duval⁵, C. Beaumont⁵, C. Arnould³, C. Leterrier³, ¹*INRA, ENVT, LGC, Castanet-Tolosan, France*, ²*GeT-PlaGe, Genotoul, INRA*

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Social behavior is critical when rearing animals in large groups as observed in poultry production. This project aims at finding QTL responsible for social motivation in birds and to decipher the genetic relationships between social behavior characteristics and the main production parameters. It is carried out in quail to take advantage of 2 experimental lines which have been selected divergently for social reinstatement (motivation to join flockmates) over 47 generations. An F2 design has been produced, and 940 individuals were measured for production traits (body weight, laying traits), and behavioral traits between 1 and 12 weeks of age (social reinstatement, response to social isolation, general activity, response to human, sexual behavior...). For a species without million of polymorphisms available, a way to obtain SNP informative in a specific cross is to directly develop these markers by sequencing the parental individuals of the population. Whole genome sequencing was thus performed on F0 parents of each line, to observe line-specific SNPs. From 2 HiSeq2000 lanes, more than 42 billion bases were obtained. Analyses were performed using the chicken genome as a reference for sequence alignment. From the most discriminating SNPs between the 2 lines, 6,000 markers were selected to perform individual genotyping through an Infinium iSelect beadchip.

Key Words: quail, SNP, social behaviour

P3058 Mitochondrial DNA lineage sorting from one diverse founder population can explain extant domestic sheep haplotypes. S. Hiendleder¹, A. Javadmanesh¹, P. L. Hind², M. R. Nassiri³, M. Pirastru⁴, P. Mereu⁴, B. Masala⁴, and Y. Plante^{2*}, ¹JS Davies Epigenetics and Genetics group, School of Animal and Veterinary Sciences and Robinson Institute, University of Adelaide, Roseworthy Campus, Roseworthy, SA 5371, Australia, ²Canadian Animal Genetic Resources Program - Programme Canadien des Ressources Genétiques Animales, AAFC - AAC, and Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada, ³Department of Animal Science, Faculty of Agriculture, Ferdowsi University of Mashhad, Mashhad, PO Box 91775-1163, Iran, ⁴Università degli Studi di Sassari, Dipartimento Scienze Biomediche, Via Muroni, 25 - 07100 Sassari, Italy.

Domestic sheep (*Ovis aries*) display major mtDNA haplotypes originally assumed to reflect multiple domestication events, involving different subspecies of Eurasian wild sheep, including mouflon (*O. orientalis*), urial (*O. vignei*) and argali (*O. ammon*). Subsequent analyses excluded mtDNA contributions, from urial and

argali, and pointed to domestication of mouflon subspecies. However, mtDNA lineage sorting from a highly diverse population could provide an alternative explanation for the 5 major haplotypes. We sequenced the complete mtDNA control region (CR) of mouflon from Sardinia (n = 5) and Cyprus (n = 3) - both now classified as feral Neolithic domesticates of *O. orientalis* -, of domestic sheep from these islands (n = 4), and of urial (*O. vignei arkal*, n = 23) from a single location in north-east Iran, Tandoureh National Park. We combined these 35 novel sequences with complete CR sequences from the database, including Anatolian mouflon (*O. orientalis anatolica*, n = 8), other mouflon with Sardinian/Corsican ancestry from Central Europe (n = 5) and domestic sheep from Eurasia (n = 33). Pair-wise nucleotide differences for domestic sheep, mouflon and urial were 26.9 ± 12.1 , 27.6 ± 12.6 and 26.6 ± 12.1 , respectively. Phylogenetic analyses (MEGA) revealed 2 major clusters formed by *O. vignei arkal* and *O. orientalis/O. aries* with similar deep branching. Anatolian, Cyprus, Sardinian/Corsican mouflon grouped with or near all 5 major domestic sheep haplotypes: A, C, D and E were found in or close to Anatolian and Cyprus mouflon, while haplotype B was only found among Sardinian/Corsican mouflon. The position of Cyprus mouflon and Sardinian/Corsican mouflon is consistent with the expansion of *O. orientalis* from mainland Asia Minor to Cyprus, Sardinia and Corsica.

Key Words: sheep, mtDNA lineage sorting, domestication

P3059 Mitochondrial genome haplogroups associated with Thoroughbred racing performance. Aladaer Qi^{1*}, Li Wen³, Shi Zhou², Bin Liu¹, Yong Zhang³, and Allan Davie², ¹Center of Systematic Genomics, Xinjiang Institute of Ecology and Geography, Chinese Academy of Sciences, Urumqi, China, ²School of Health and Human Sciences, Southern Cross University, Lismore, Australia, ³Tianjin Key Lab of Exercise Physiology and Sports Medicine and Department of Health and Exercise Science, Tianjin University of Sports, Tianjin, China.

Mitochondria are the powerhouse in cellular energy metabolism and breeding evidence suggested matrilineal inheritance has strong influence on aerobic endurance of racing horses. The aim of this study is to examine the association between the mitochondrial genomes and the elite racing performance of Thoroughbred horses. Blood samples were collected and the mitochondrial genome sequences were obtained to determine the haplogroup structures. Case and control groups were set up among 160 thoroughbred horses. The racing performance is ranked by the value of lifetime earnings divided by life time wins: horses with zero life time wins were selected as poor performance group and top ranking 30 horses were selected as elite performance group.