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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 Genetiques 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, ⁴Universita 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.