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**Simultaneous characterization of genomic regions associated with two feather traits and two eggshell colors in domestic Japanese quail (*Coturnix japonica*)**

Bertrand Bed'Hom, Frederique Pitel, Patrice Dehais, Sophie Leroux, David Gourichon, Sandrine Riviere, Nicolas Bruneau, Christine Leterrier, Céline Chantry-Darmon, Marie-Noelle Rossignol, et al.

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We have also surveyed several goat populations from Europe (Carpathian and Saanen, N=30) and Africa (Tunisia, Djallonké and Sahel, N=50). A multidimensional scaling plot analysis revealed three well separated clusters: one containing European goat breeds (Spanish and non-Iberian populations), another one encompassing breeds of African origin and the third one represented by the Palmera breed from the Canary Islands. The remarkable differentiation of Palmera goats is consistent with a scenario of founder effects combined with prolonged geographic isolation. Notably, genetic variation and geography were closely associated, with North (Bermeya, Blanca de Rasquera and Mallorquina) and South Spanish (Florida, Murciano-Granadina and Malagueña) breeds forming distinct subclusters. The analysis of the data with Admixture revealed the same trends reported above. We are currently genotyping five ovine Spanish breeds (Ripollesa, Xisqueta, Canaria de Pelo, Gallega and Roja Mallorquina, N=132) with the 50K Ovine Bead-Chip in order to achieve a more comprehensive perspective about the genetic variation of small ruminants in Spain.

**P4079 Simultaneous characterization of genomic regions associated with two feather traits and two eggshell colors in domestic Japanese Quail (*Coturnix japonica*).** Bertrand Bed'Hom (INRA, AgroParisTech), Frédérique Pitel, Patrice Dehais and Sophie Leroux (INRA, ENVT, ENSAT), David Gourichon and Sandrine Rivière (INRA), Nicolas Bruneau (INRA, AgroParisTech), Christine Leterrier (INRA, CNRS, Université François Rabelais), Céline Chantry-Darmon and Marie-Noëlle Rossignol (LABOGENA) and Francis Minvielle (INRA, AgroParisTech)

As in many domestic animals, and particularly in chicken, the domestic Japanese Quail (*Coturnix japonica*) has accumulated many visible traits since domestication. In order to understand the genetic mechanisms governing such traits, the

genomic regions associated with four autosomal recessive mendelian traits (two feather phenotypes and two eggshell colors) have been characterized. Feather phenotypes are Curly (CU) and Rusty (RU). CU chicks have calamus of adjacent growing wing feathers not independent but connected through the follicle walls which appear to be joined together. The plumage of RU chicks is rusty, with down underneath having the usual wild-type dark-slaty color. A similar color pattern is present in RU adults. Eggshell colors are Celadon (CE) and White (WE). CE color is glossy pale blue, WE color is pure white, whereas the wild-type eggshell is brownish, with spots. Two F2 crosses have been organized, each one segregating for one eggshell color and one feather phenotype. 425 animals, i.e. 12 F0, 16 F1 and 397 F2 (females only) have been produced and phenotyped. With DNA extracted from blood, all animals have been genotyped using a genome-wide Illumina iSelect 6K SNP panel. SNP information has been obtained from whole genome sequencing of individuals from several INRA experimental populations. Genomic SNP coordinates are based on the relatively close chicken (*Gallus gallus*) reference genome. After quality filtering, 2090 informative SNP have been used for association analysis using PLINK. RU, CU and WE phenotypes are associated with high significance ( $p$ -value  $< 1E-20$ ) to quail genomic regions corresponding to parts of GGA1, GGA5 and GGA6 respectively. The CE phenotype is weakly associated ( $p$ -value  $< 1E-5$ ) to a quail genomic region corresponding to a part of GGA16.

**P4080 Genetic Diversity of Korean Native Chicken Using Microsatellite Marker.** JooHee Seo (Genomic Informatics Center, Dept. of Animal Life and Environment science, The General Graduate School, Hankyong National University) and Jong Jin Kim and Hong Sik Kong (1 Genomic Informatics Center, Hankyong National University)