

alignments, and conserved and constrained elements. These updates will be released as part of Ensembl version 90, which is expected in July. All data are freely available through our website at <http://www.ensembl.org>, REST API (<http://rest.ensembl.org>) and our public MySQL server (ensemldb.ensembl.org) as well as tools such as the Ensembl Variant Effect Predictor (www.ensembl.org/Tools/VEP) and BioMart (<http://www.ensembl.org/biomart>). Ensembl also supports the upload and visualisation of data in multiple file formats such as BAM or GFF3. We have developed the Track Hub Reg-

istry (<http://trackhubregistry.org/>) to facilitate data sharing through discovery of publicly accessible track data hubs and viewing them alongside Ensembl data. Additionally, data can now be viewed in Ensembl even if the files are not hosted locally by submitting them in CRAM format to the ENA and registering a track hub with the ENA accession numbers.

Key Words: pigs and related species, genome annotation, Functional Annotation of Animal Genomes (FAANG), bioinformatics tools, databases/repositories

Novel, Groundbreaking Research/Methodology Presentation

150 Sheep parchment as a genetic resource. M. Teasdale*, *Trinity College Dublin, Dublin, Ireland.*

Before the mass production of paper, parchment was the major medium for codices and until the widespread adoption of typewriters, they were a clerk's preferred medium for many formal legal documents and records. Unlike modern parchment, which is typically made from goat or calf, ~1,000 English legal documents that we have analysed via peptide mass fingerprints (MALDI-TOF mass spectrometry), were made of sheepskin. Parchment has been shown to harbour sufficient concentrations of DNA to allow for

high-throughput sequencing and therefore offers tremendous scope for documenting the recent genetic history of British sheep breeds. Documents contained within the British archival collections span the transition from a wool- to a meat-based economy and the beginnings of intense artificial selection. We have sequenced a range of parchment samples from the county of Yorkshire (UK) that date from the 14th to the 19th century to low coverage. These animals were then compared to modern breeds from the Sheep HapMap and the Sheep Genomes Database and scanned for evidence of recent positive selection between the time points.

Key Words: genomics, ancient DNA, selection

Applied Genetics of Companion Animals

151 AgriSeq targeted sequencing panel for determination of canine parentage and genetic health. M. Karberg*¹, A. Burrell¹, P. Siddavatham¹, A. Allred¹, M. de Groot², and W. van Haeringen², ¹*Thermo Fisher Scientific, Austin, TX, USA;* ²*VHL Genetics, Wageningen, the Netherlands.*

The objective of this presentation is to show the performance of canine parentage and genetic health AgriSeq primer panels, and demonstrate how the panels can be combined, or otherwise modified, without detrimental effects to detection. Ensuring an accurate pedigree is particularly important for purebreds, having both economic and animal health implications. Historically, microsatellites (short tandem repeats or STRs) have been used for genetic identification, traceability and paternity. In recent years, other DNA based tests such as single nucleotide polymorphism (SNPs) detection have become increasingly used for this purpose. High-throughput targeted amplification and re-sequencing, using the Applied Biosystems AgriSeq target enrichment technology and the Ion S5 sequencing system, allows for the simultaneous and accurate genotyping of a large number of SNPs to interrogate the heritage and genetic health of an animal. In addition, the AgriSeq approach is very flexible, allowing panels to be combined or modified easily, thereby helping both breeders and diagnostic laboratories stay relevant with evolving content needs. Here, we describe the development of two AgriSeq panels targeting canine SNP markers: a parentage panel based on 200 ISAG canine targets, and a genetic health panel based on over 140 well characterised genetic markers. To demonstrate the modularity of the AgriSeq approach, the performance of the genetic health and parentage panels were analysed independently and also combined and analysed simultaneously using 192 samples pooled on an Ion S5 540 chip. Variant calling was performed using the Torrent Variant Caller (TVC) plugin as part of the Ion Torrent Suite software package. The data show that the two panels work similarly, regardless of whether they are used separately, or combined together on one sequencing chip. The mean sample call rate was

above 95% and the sample concordance between the separate and combined panels was over 99.9%.

Key Words: dogs and related species, DNA sequencing, parentage

152 Pedigree and genomic-based relationships in a dog population. A. Talenti*¹, D. L. Dreger², F. Danelli¹, S. Frattini¹, B. Coizet¹, S. P. Marelli¹, G. Pagnacco¹, G. Gandini¹, M. Polli¹, R. Caniglia³, M. Galaverni³, E. A. Ostrander², and P. Crepaldi¹, ¹*Department of Veterinary Medicine, University of Milan, Milan, Italy;* ²*National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA;* ³*Laboratorio di Genetica, Istituto Superiore per la Protezione e la Ricerca Ambientale, Ozzano dell'Emilia, Italy.*

In many dog breeds, small population sizes, associated with intense selection schemes, have led to considerable losses of genetic diversity. This complicates the production of accurate genomic estimates of parentage. The Lupo Italiano, with ~300 living dogs, is an Italian breed created in 1966 by crossing the Apennine grey wolf (*Canis lupus italicus*) with German Shepherd dogs (GSD). The aim of this work was to compare calculated relationships from genomic and pedigree data, using the Lupo Italiano as an example of a small population. The entire pedigree of the Lupo Italiano is known, consisting of up to 12 generations and dating to the founder animals. The pedigrees of 28 Lupo Italiano dogs (provided by AAALI) were used to build an additive relationships matrix (A) (CFC software). These 28 dogs were genotyped on the Illumina CanineHD 170K SNP chip (University of Milan and National Institutes of Health in Bethesda, MD), and the resultant genotypes were used for the estimation of the within-breed Genomic Relationships Matrix (GRMa) (GCTA64 software). The mean parentage values for GRMa (-0.02±0.05) and A (0.80±0.05) were not equivalent, however, they did display a significant positive correlation ($R = 0.75$; $P < 0.001$). Four additional populations, genotyped on the same panel, consisted of 20 Apennine grey wolves (ISPR), 30 GSDs, 14 grey wolves, and 31 village dogs (publicly available

in Dryad, Shannon et al. 2015). The GRM produced with the combined set (GRMb) led to a higher correlation with A ($R = 0.80$; $P < 0.001$) and to higher estimates of parentage between Lupo Italiano individuals (0.53 ± 0.05). The calculation was expanded a final time to include an additional 250+ GSDs (GRMc). This matrix showed a decrease in the correlation with A ($R = 0.76$; $P < 0.001$) balanced by a strong increase in the parentage values (0.82 ± 0.08), making it the closest to the A matrix. These results show that estimation of

genomic relationships from populations with greater allelic diversity can improve the correlation and accuracy with pedigree-derived estimates. Consideration of these implementations can allow for better management of mating schemes and conservation of genetic variation in dog breeds with small population sizes. The authors thank AAALI for the kind collaboration.

Key Words: dog, parentage, SNP

Applied Sheep and Goat Genetics

153 Introgression of wool-shedding genes into the Romane breed sheep. L. Drouilhet^{*1}, B. Pena¹, C. Huau¹, D. Marcon², Y. Bourdillon², and D. Allain¹, ¹*GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France*; ²*INRA UE0322, La Sapinière, Bourges, France*.

Wool production in Europe became unprofitable compared to the meat or milk productions. One major reason is that the wool income is lower than the cost of shearing. The Romane breed, a French composite breed between the Berrichon du Cher breed (meat breed) and the Romanov breed (prolific breed), showed little ability to shed. We decided to introgress in the Romane breed the phenotype of wool-shedding of the Martinik Hair breed. Indeed, the Martinik Hair sheep have the ability to annually naturally woolshed. The experimental trial of introgression was realised on 4 successive backcrosses from the Martinik Hair (MH) to the Romane breed (RM): F1 (MH*RM), then BC1 (F1*RM), BC2 (BC1*RM) and BC3 (BC2*RM). Two traits were considered: the ability to shed at least a part of the fleece or not, as a binary trait and the extent of shedding as the ratio of wool shed area to total body area. During those backcrosses, animals were measured and selected on their ability to shed at 7 months of age. The BC3 population represents the first generation (G1) of the introgressed population for the wool-shedding phenotype. This introgressed breeding stock ($n = 150$ ewes) was then selected using estimated breeding values based on shedding extension. A high heritability estimate (0.50 ± 0.09) and a large genetic gain (2.2 genetic standard deviations) on wool-shedding were observed after 6 generations of selection, without impairing the production fitness on the Romane sheep. We did not observe a bimodal distribution of wool-shedding extension phenotype, suggesting that not only one mutation is segregating in our population, but more probably a few major genes with large effects due to the large genetic gain observed. At the G6, 96 animals (9 family sires, 6 to 11 progeny per sire, 10 dams) with extreme phenotypes (total wool shedding or not) including some full-sibs and their dam were selected and genotyped on 50K SNP chip. This dataset is currently analysed using linkage analysis (LA), linkage disequilibrium (LD) and joint LD-LA mapping using QTLMAP software. The first results showed at least 3 different loci influencing the ability to shed on chromosome OAR3, OAR12 and OAR15. The analysis are in progress to precise those intervals of localization.

Key Words: sheep, genetic introgression, genome wide-association, wool shedding

154 Community-based sheep breeding programs in Ethiopia resulted in substantial genetic gains. A. Haile^{*1}, T. Mirkena³, G. Duguma², S. Gizaw², M. Wurzinger⁴, J. Solkner⁴, O. Mwai², T. Dessie², A. Abebe⁶, M. Mamiru⁸, T. Tadesse⁷, R. N. B. Lobo⁵, and B. Rischkowsky¹, ¹*International Center for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia*; ²*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia, and Nairobi, Kenya*; ³*FAO, Addis Ababa, Ethiopia*; ⁴*BOKU University, Vienna, Austria*; ⁵*EMBRAPA-goat and sheep, Sobral, Brazil*; ⁶*Debre Berhan Agricultural Research Center, Debre Berhan, Ethiopia*; ⁷*Bako*

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In small ruminants, centralized breeding schemes, entirely managed and controlled by governments – with minimal, if any, participation by farmers – were developed and implemented in many developing countries. Such programs have generally failed to sustainably provide the desired genetic improvements to small-holder livestock keepers. Community-based breeding Programs (CBBPs) have been suggested as an alternative and are being implemented in a few pilot countries. A team of international and national scientists designed and implemented sheep CBBPs in three sites/breeds (Bonga, Horro and Menz) in Ethiopia. The team developed an innovative methodological framework on how to design, implement and sustain CBBPs. Selection traits identified through participatory approaches were six month weights in all the three sites, and in Horro and Bonga, where resources, particularly feed and water, permit larger litter sizes, twinning rate was included. Eight years (2009–2016) performance data from the programs were analysed using WOMBAT (Meyer, 2007). The results indicate that the birthweight of lambs has not improved over the years in Menz and Bonga. In Horro, there is even a slight decrease. Given that we have not selected for birthweight in the community flocks we did not expect genetic change. However, there could have been an effect through correlated responses which was not the case in all the three breeds. Six months weight, the major selection trait in our CBBPs, increased over the years in all breeds. In Horro the average increase was 0.31 ± 0.060 kg per year, followed by average increase of 0.26 ± 0.058 kg per year in Bonga and 0.14 ± 0.006 kg for Menz. This is quite substantial in an on-farm situation. In Horro and Bonga sheep, where twinning rate was one of the selection traits, the litter size of lambs born increased over the years in both breeds: the increase was 12% (from 1.28 to 1.46) in Horro and 8% (from 1.48 to 1.61) in Bonga. This increase combined with the increased bodyweight has made a substantial impact on the incomes of the farmers. Our results show that CBBPs are technically feasible and result in measurable genetic gains in performance traits.

Key Words: sheep and related species, animal breeding, genetic improvement

155 Identification of two major genes affecting prolificacy in the French Noire du Velay sheep. L. Chantepie^{*}, L. Bodin, F. Woloszyn, J. Sarry, and S. Fabre, *GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet Tolosan, France*.

Classical selection methods of prolificacy in sheep assume a full polygenic inheritance, each gene having an infinitesimal effect. However, in the last decades, many mutations having a major effect on prolificacy were discovered in four major fecundity genes namely *BMP15 (FecX)*, *BMP1B (FecB)*, *GDF9 (FecG)* and *B4GALNT2 (FecL)*. When present, these mutations should be taken into account to obtain relevant prolificacy breeding values for the selection process. Based on litter size records (LS), we suspected the segregation of such major gene in the French Noire du Velay (NdV) sheep population. The first approach was to genotype selected highly prolific ewes for the already known mutations at the four major loci. We