

Poster 5001

Title: Evaluation of feed efficiency in beef cattle under low and high energy feedlot diets

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Abstract:

Residual feed intake (RFI) measures the difference between an animal's actual and expected feed intakes (EFI) based on the maintenance of body weight and its growth. Little is known about the effects of different diets on animals' RFI measures. Our objective was to evaluate the effect of diet energy density on animal RFI ranking. One hundred and seventy six randomly chosen steers, 5-7.5 mo of age were used for the feeding trials at the Kinsella ranch, University of Alberta. The steers were crosses between Angus, Charolais or Alberta hybrid bulls and hybrid dams. The diets were offered sequentially (*ad-libitum*) with low energy diet in Period 1(P1) then high energy diet in Period 2 (P2). Individual feed intakes were collected using the Growsafe® feeding system. Body weights were measured biweekly. Average daily gain (ADG) and EFI were estimated using a linear regression analysis for each period. RFI for each animal was calculated separately in each period. Means of RFI were 0.00 ± 0.03 and 0.00 ± 0.06 respectively for P1 and P2. Pearson and Spearman-rank correlations between P1 and P2 RFI indices were 43% and 41% respectively. One hundred and four steers (59.1%) changed in their RFI rankings. This re-ranking of RFI may be an indication of genotype by environment interaction.

Poster 5002

Title: Population Studies for Arabian Horses by 15 Microsatellite loci

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Abstract :

Prior to the introduction of any DNA marker as a tool for human paternity test and personal identification, a

population genetic database should be established. A similar database should also be made for establishing equine paternity. There are several commercial available kits for equine DNA genotyping but population genetic studies are limited. This paper describes allele frequencies together with some statistical parameters of parentage interest for 15 STRs (VHL20, HTG4, AHT4, HMS7, HTG6, AHT5, HMS6, ASB23, ASB2, HTG10, HTG7, HMS3, HMS2, ASB17, HMS1) included in the *Equine StockMarks* and the *Equine Panel1.1* systems in a sample of 283 unrelated Arabian horses. Genetic parameters were calculated using *Cervus (v.3.0)* and *PowerStats (v.1.2)* software. No significant deviations from the Hardy – Weinberg Equilibrium (HWE) were detected, with the exception of the HMS3 locus. The polymorphic information content (PIC) varied from 0.35 to 0.75 and the power of discrimination (PD) from 59.5% to 91.8%. The combined power of exclusion (CPE) for 8 out of 9 loci (without HMS3) recommended by the International Society for Animal Genetics (ISAG) was 98.34% and the CPE for 14 markers was 99.84%. Analyzed parameters demonstrate that the abovementioned STR markers are suitable for paternity investigation in the Arabian horse population, but with some limits to estimating a paternity as certainty.

Poster 5003

Title: Developmental validation of a single-tube amplification of the 17 loci for parentage of horse with StockMarks for Horses

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Abstract

The PCR technology provides a sensitive method for parentage verification and individual identification of horses. For the 17 microsatellites designated (VHL20, HTG4, AHT4, HMS7, HTG6, AHT5, HMS6, ASB23, ASB2, HTG10, HTG7, HMS3, HMS2, ABS17, LEX3, HMS1, CA425) , amplification of the STR loci was realized by multiplex PCR using StockMarks for Horse Paternity PCR Typing Kit (AppliedBiosystems). Characterized by defined critical control points, the assay was conducted within a quality assurance system compliant with ISO/IEC 17025:2005 guidelines.

Taking into account that we are employing an "in house"- developed method the necessary validation

process was carried out with horse DNA samples extracted from blood. The key parameters of method validation include specificity, LOD (limit of detection), robustness, repeatability, reproducibility, selectivity and the reproducibility of DNA extraction. In conclusion microsatellites can give sufficient and reliable information for paternity testing and in horse breeding this technology has the potential to be of great use in monitoring levels of genetic variation.

Poster 5004

Title: Developmental Validation of a Sensitive and Discriminating Panel of Novel Canine STR Markers for Forensic Testing

Presenting Author: Elizabeth Wictum, Forensic Unit, Veterinary Genetics Laboratory, University of California, Davis, California, USA

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Abstract :

The molecular analysis of forensic evidence has revolutionized the criminal justice system. Its strength has been used to both incriminate the guilty and free the innocent. While analysis of human biological material has been extensively vetted in courtrooms worldwide, forensic analysis of animal DNA is still gaining acceptance. As the oldest domesticated species, dogs (*Canis lupus familiaris*) inhabit 39% of households in America and, after humans, are the species of greatest forensic interest. Numerous genetic markers have been employed to individualize canids for parentage verification, breed identification, phylogeny, and diversity assessment; however, forensic analysis requires the application of more stringent marker selection criteria. To address the lack of a standardized canid forensic panel that meets those criteria, tools were developed to mine the 7x dog genome sequence data. Fifteen unlinked highly discriminating tetranucleotide-repeat markers were identified and assembled with a sex-determination marker into a multiplex capable of generating a full profile with less than 0.1 ng of nuclear DNA. This panel has the potential to be not only a valuable tool for the emerging field of veterinary forensic science but also demonstrates utility for parentage verification in highly inbred dog populations and for phylogenetic analyses of unique canid populations.

Poster 5005

Title: Structure and breed assignment of river buffalo populations using microsatellite markers (preliminary results)

Presenting Author: DANIELA IAMARTINO, LGS – Laboratorio Genetica e Servizi, Via Bergamo 292, 26100 Cremona Italy.

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Abstract :

Given the increasing importance of food traceability for safety and quality and with aim to safeguard of the made in Italy products, we have investigated on possible genetic differences among river buffalo populations coming from different geographical areas: Italy, North-Africa, East Europe, China and Brazil. Fourteen microsatellite loci, amplified with a protocol of one multiplex-PCR, were used to assess genetic diversity within and across the populations. We analysed a total of 318 animals: 60 from Italy, 60 from North Africa, 58 from Romania, 67 from Bulgaria, 8 from China and two groups from Brazil, respectively of 32 and 33 animals. The mean number of alleles was 5.7 and the expected heterozygosity ranged from 0.526 (Jaffarabadi, Brazil) to 0.720 (Murrah, Bulgaria). Although there was abundant genetic variation, genetic differentiation between populations was low ($F_{st}=0.075\pm 0.01$). Individuals were clustered applying a parametric genetic mixture analysis implemented in the Structure 2.2 software. The number of genetic clusters K was tested using the admixture model, a burning period of 100.000 followed by 100.000 MCMC repeats. Even if the demarcation within East Europe groups is lower than the others, the method resolved 7 clusters, being able to correctly identify buffalo populations.

Poster 5006

Title: Admixture analysis of European and Chinese pig breeds

Presenting Author: Christoph Knorr, Institute of Veterinary Medicine, University of Göttingen, Burckhardtweg 2, 37077 Göttingen, Germany

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Abstract :

We present population genetic analysis of microsatellite variation based on 17 microsatellite markers in 15 different pig breeds from Europe (Angeln Saddleback, Bunte Bentheimer, German Edelschwein, German Landrace, Göttingen Minipig, Hampshire, Pietrain, European Wild boar and Swabian-Haellian swine) and Asia (Jiangquhai, Luchuan, Minzhu, Rongchang, Yujiang, and Tibetan). The European group included the native European wild boar and the breed Göttingen minipig; in total 336 pigs were investigated. Chinese breeds showed a higher average mean number of alleles per locus (4.7) than the European population (3.9). Unique alleles were present in 6 breeds. To analyse admixture between these populations following approaches were used: the systematic selection of population associated alleles for European and Asian breeds and examination of their frequency; examination of genetic distances between breeds; and a model-based Bayesian admixture analysis. The results show an influence of Asian breeds in European populations, more in commercial dam lines than in sire lines. Within the European breeds, the Göttingen minipig, a crossbred of Asian and European breeds, showed strongest influence of Asian admixture. Tibetan pigs were the most admixed and allelic diverse Chinese sample. For two Asian breeds (Tibetan and Minzhu), geographical outliers in the sample, signature of European admixture was found.

Poster 5007

Title: Polymorphisms in *DRB3* binding pockets affect immune response to a FMDV peptide in cattle

Presenting Author: Rebecca Baxter, The Roslin Institute and R(D)SVS, University of Edinburgh

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Abstract :

Immune responsiveness is a complex trait involving many genes, but Major Histocompatibility Complex (MHC) genes are consistently implicated as having a significant impact. However their relative importance in out-bred species such as cattle is less apparent. In this study we have investigated the effect of bovine MHC class II (*BoLA*) - *DRB3* polymorphism on the response to a Foot-and-Mouth disease virus (FMDV) peptide in a genotypically diverse Charolais- Holstein F2 cross population. The majority of functionally relevant polymorphisms alter the conformation of 'pockets' within the peptide binding cleft. The pockets

act as anchors for pathogen peptides and thus these polymorphisms determine the binding affinity of peptides to MHC molecules. We are evaluating how the polymorphisms in the pockets affect the binding of the FMDV peptide and the consequent response of both B and T cells. We found that the specific polymorphisms in pocket 4 significantly affect anti FMDV IgG1 and IgG2 responses. To enable us to fully comprehend the interactions between the differences in the *DRB3* pockets within the DR molecule and the FMDV peptide we are currently using a modelling based approach.

Poster 5008

Title: Structural equation modeling to find the relationship between different genetic loci and different phenotypes influencing body composition

Presenting Author: Gudrun A. Brockmann, Humboldt-Universität zu Berlin, Institut für Nutztierwissenschaften, Invalidenstraße 42, 10115 Berlin, Germany

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Abstract :

We used the method of structural equation modeling to find the relationship between different genetic loci and different phenotypes influencing body composition in mice. We use an intercross population between the mouse lines NMRI8 (selected for high body weight) and DBA/2 (control) in which QTLs for body weight, adiposity, and muscle weights were mapped. The traits were measured at 6 weeks, when animals became fertile and have finished the fastest growth phase. Using the technique of structural model analysis, we considered body weight as lean mass and fat mass and were able to distinguish genetic loci that affect adiposity from those that affect lean mass. The results show that the NMRI8 alleles of the selection line on chromosomes 7 and 14 have pleiotropic positive effects on both muscle and fat tissue mass, while a locus on chromosome 13 contributed to the selection response only by increased fat deposition. The fat mass was also affected by a complex pattern of interaction between loci on chromosomes 6 and 14. The sex of individuals affected the fat mass either directly or indirectly via the muscle as a mediator. The analysis sheds new light on the action of genes controlling body weight as composite trait of fat and muscle tissues.

Poster 5009

Title: Plasmid-Mediated Muscle-Targeted Gene Nutrition: The Porcine GHRH myogenic expression plasmid for enhancing body weight in rat

Presenting Author: Qingyong Meng, College of Biological Science, China Agricultural University, No. 2 Yuanmingyuan west Road, Beijing 100094, China

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Abstract :

Plasmid-mediated myogenic expression was used to enhancing animal growth as gene nutrition. It was a promising, simple, and inexpensive approach in this field. In this report, a myogenic expression plasmid, ppG-H6, containing the porcine GHRH cDNA under the control of a alpha-actin promoter was constructed. Based on the expression of this plasmid transfer in C2C12 cells, ppG-H6 showed the ability of driving GHRH expression in muscle cell. A single 300ug dose of this plasmid was injected intramuscularly into rat. Follow-up evaluation demonstrated increased body weight and GH level by the plasmid. After injection with ppG-H6, these rats showed a more than seven-fold increase in serum GH and the increased body weight as $234.99 \pm 5.73\text{g}$ vs $203.19 \pm 13.11\text{g}$ of control group ppG-CK. These results suggest plasmid-mediated GHRH ectopic and myogenic expression are methods for increasing the body weight of an animal.

Poster 5010

Title: EVALUATION OF MARKERS FOR SPECIES IDENTIFICATION IN VETERINARY FORENSIC GENETICS.

Presenting Author: Riina Maria Vittoria – CEA, Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta – Turin, Italy.

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Abstract :

Identifying the species of origin of biological traces is important in veterinary forensic caseworks. A morphological approach is not always sufficient or feasible and the analysis of genetic markers can be useful.

We analyzed mitochondrial genetic markers to evaluate their suitability for species identification and discrimination. We also describe their practical application in a case report.

Samples from domestic and wild animal species were analyzed sequencing cytochrome *b* (*cytb*) and cytochrome oxidase I (*COI*) genes. Obtained sequences were compared with those deposited in public databases.

For the case report we also carried out an alignment for a direct comparison between the sample and the sequences of the most suspected involved species. The genetic distance was calculated and a phylogenetic tree was constructed. The bootstrap test confidence was used to determine the statistical significance of the species assignment.

Obtained results showed that *cytb* is an effective marker for species identification and is a promising tool for forensic genetic purposes. *COI* showed a lower discriminatory power regarding phylogenetically close species.

The developed analysis protocol appeared a good approach for veterinary forensic investigations, where, different than in human forensics, numerous animal species need to be discriminated and no standardized methods are available.

Poster 5011

Title: Patterns of genetic diversity near genes under selection in cattle

Presenting Author: Pam Wiener, The Roslin Institute, University of Edinburgh, Roslin, EH25 9PS United Kingdom

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Abstract :

Because of their well-documented histories, domestic species provide an important resource for understanding the patterns of variation left by selection. Such information is useful for interpreting patterns in other species as well as for identifying as yet undiscovered genes in domestic species. This study characterizes diversity patterns across genes under selection in cattle, with associated phenotypes related to both domestic use (muscle conformation) and physical appearance (coat color). The analysis includes

two marker types (microsatellites and SNPs) and applies various statistical approaches, from which comparisons of statistical power and inferences can be made. While results of these analyses demonstrate that selection can be detected using comparisons of breeds bred for different phenotypes, some limitations in the methodologies and markers are also highlighted. This work has important implications for assessing the methodologies available for detecting past selection and for understanding the process of domestication.

Poster 5012

Title: Microsatellite mutation rates in the eastern tiger salamander (*Ambystoma tigrinum tigrinum*)

Presenting Author: Zafer Bulut, Selcuk University Faculty of Veterinary Medicine Department of Biochemistry Campus/Konya/TURKEY

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Abstract :

Microsatellites are commonly used for mapping and population genetics because of their high heterozygosities and allelic variability (i.e., polymorphism). Microsatellite markers are generally more polymorphic than other types of molecular markers (e.g., allozymes or SNPs) because the insertions/deletions that give rise to microsatellite variability are relatively common compared to nucleotide substitutions. Nevertheless, empirical evidence on microsatellite mutation rates (MMRs) is lacking in most vertebrate groups despite the importance of such estimates to key population genetic parameters such as the effective population size. Here, we present empirical data on MMRs in eastern tiger salamanders (*Ambystoma tigrinum tigrinum*). We conducted dozens of captive breeding trials, then genotyped over 1000 offspring (i.e., >2000 meioses) at a suite of microsatellite loci in an effort to determine a) genetic parentage and b) MMRs. Our results provide the first estimates of MMRs in urodeles (newts and salamanders), and they illustrate that MMRs can vary by more than an order of magnitude across loci within a given species.

Poster 5013

Title: Data validation and algorithmic design for chromosome grouping of SNPs from a 7K genome-wide porcine chip

Presenting Author: Vivi Raundahl Gregersen, Dept. of Genetics and Biotechnology, University of Aarhus, Blichers allé 20, P.O. box 50, DK-8830 Tjele, Denmark

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Abstract :

High-throughput marker systems increases the data output drastically, hence the need for rapid validation methods. An Illumina Infinium® SNP BeadChip was produced for mapping and QTL purposes. Initially, a data set of about 1,000 animals divided in ten sire families was used together with 100 replicate samples to generate a configuration template for the clustering of the SNPs. The dataset was divided into unsuccessful, not segregating and segregating SNPs and deviation from Hardy-Weinberg Equilibrium was calculated. Secondly, additional 350 animal samples of different breeds were included in the sample set and processed. About 10,000 animals were genotyped by both the original and new configuration templates and discrepancies were further investigated. The resulting set of 4,366 segregating SNPs was grouped into the 18 porcine autosome groups using two-point linkage calculated by the Crimap 4.2 package. Prior knowledge of location for 400 SNPs was used as a backbone. Ten SNP sets overlapping each other by 500 SNPs was used for the initial group placement (LODS>50). New linkage sets was produced of the remaining SNPs combined with each of the autosome groups. This procedure was performed until the LODS could be relaxed to seven. A total of 4,181 SNPs could be uniquely divided into the 18 groups. The remaining 185 SNPs were either singletons or linked together in small groups.

Poster 5014

Title: The Mitochondrial DNA (mtDNA) Haplogroup Compositions of Three Native Turkish Sheep Breeds and Their Implications on the Conservation Studies

Presenting Author: Eren Yüncü, Middle East Technical University Department of Biological Sciences Lab:147

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Abstract :

Sheep domestication is believed to have occurred at least by three separate events in different domestication centres. Archaeological studies suggest

that Turkey might be harbouring the earliest one. Since, there were no wild sheep in Europe before domestication, European domestic sheep might be mainly extends of this centre. However, native Turkish sheep might still be harbouring variability which is absent in extend breeds. Their high genetic variability can be a signature for maintained diversity since domestication. Therefore, they must be conserved. Furthermore, Turkey is close to other assumed domestication centres. Hence Turkish breeds might also be admixture of products of these domestication centres. The evolutionary history of breeds may help to resolve different causes of high diversity in Turkish breeds.

The aim of the study is to determine composition of sheep mtDNA haplogroups indicating three domestication events, among native breeds, as a part of a national project TURKHAYGEN-I. Three native Turkish breeds (Karayaka, Akkaraman, Gökçeada) are studied for mtDNA control and ND4 region by RFLP and SSCP methods, respectively. Results are employed to enlarge existing data to reveal evolutionary history of the Turkish sheep breeds. Results will also be used to prioritize Turkish domestic sheep breeds in conservation studies.

Poster 5015

Title: The *Bos taurus* Genome Database: an integrated database for Bovine Genome research

Presenting Author: Dajeong Lim, National Institute of Animal Science, RDA, 564 Omockchun-dong Gwonseon-gu

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Abstract :

We constructed a database to study function genomics in the Bovine genome. The BGD integrated into UniGene, markers, QTLs, transcripts and SNP information and then provides a useful tool for studying genomics and biological mechanisms in the bovine. We experimentally determined 63,625 ESTs (Expressed Sequence Tags) from 3 full-length enriched cDNA libraries of Korean Native Cattle (KNC). QTL and marker were retrieved from the public databases. The EST data were clustered and assembled into unique sequences, contigs, and singletons. The BGD database provides functional annotation, identification of SNPs, genome mapping of coding sequences, and characterization of trait loci controlling. It also provides KNC specific information

compare other breeds of cattle. Especially, we are developing network model that is coexpressed genes for QTL region. This is accessible online and can answer queries using several search options, including clone IDs, marker, QTL and genes. The BGD supported advanced search interface, disease browser and comparative gene map of pig. Graphical map view and genome browser show ESTs and contigs from National Institute of Animal Science (NIAS). BGD is accessible at <http://bgd.nabc.go.kr>.

Poster 5016

Title: Genetic variability in Bolivian Llamas (*Lama glama*) using microsatellites: preliminary results

Authors: Julia Barreta¹, Volga Iñiguez¹, Roberto Chiri², Fernando Romero¹, Tito Rodríguez³, Beatriz Gutiérrez-Gil⁴ and Juan-Jose Arranz⁴

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Abstract :

Bolivia has the highest census of llamas in the world with approximately 2.400.000 animals. This species present an important degradation process; it is caused principally by the human press on the land. As a consequence, the study of this genetic resource is critical for the establishment of management and conservation plans that assures genetic conservation of llamas. In a preliminary study in coordination with the conservation plans of BANCAMEL, genetic variability at 10 microsatellite markers was examined in Bolivian Llamas. A total of 108 animals belonging to following ecotypes: Azanaque, Cruce Cultra, Kara, Ketena, Morejon, Orinoca, Rivera, Sajama, Totora, Tiutiri and Yawaroko were analyzed. Microsatellites were amplified in multiplex and alleles were identified using an ABI3130 sequencer and GeneMapper software. The number of alleles per loci, heterozygosity, and departures from Hardy Weinberg equilibrium were calculated for all microsatellite loci in the whole populations. All the populations show, in general, a good fit to HWE. The observed number of alleles per loci in the 108 animals varied between 6 for YWLL44 marker and 24 in YWLL29. The observed average heterozygosity in the populations ranges from 0.656 in Morejon ecotype to 0.759 in Titutiri llamas.

Poster 5017

Title: QTL detection for milk protein composition of bovine milk

Presenting Author: G.C.B Schopen, Animal Breeding and Genomics Centre, Wageningen University, Wageningen, P.O. Box 338, 6700AH, The Netherlands

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Abstract :

The objective of this study was to map QTLs for milk protein composition in Dutch Holstein-Friesians. From 1912 first parity cows, one morning milk sample was collected and analyzed for the major milk proteins using capillary zone electrophoresis. The 1912 phenotypes were corrected for systematic environmental effects. The heritabilities, i.e. the proportion of phenotypic variation due to genetics, were moderate to high for the major milk proteins. DNA was isolated from blood samples from 849 cows and semen samples from their 7 sires. A whole genome scan using 1536 single nucleotide polymorphisms was performed. The QTL analysis consists of a multimarker regression approach for interval mapping in half-sib families. In this study, we covered 2831 cM of the cattle genome. Several genome-wise significant ($P < 0.05$) QTLs were found for the major milk proteins distributed over eight chromosomal regions. Fine mapping of QTL regions to reduce confidence intervals of the detected QTLs, to facilitate new candidate genes that affect milk protein composition, is in progress.

Poster 5018

Title: Phylogenetic and population structure of Thai indigenous pigs and Thai wild boars assessed by mitochondrial DNA sequence polymorphism

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Abstract :

The study of mitochondrial DNA (mtDNA) D-loop sequence were carried out using 72 Thai indigenous pigs and 11 Thai wild boars collected at twelve locations in five provinces in Northern Thailand. To infer phylogenetic relationships between Thai pigs, other Asian pigs, and European pigs, published D-loop sequences from GenBank were used for comparison with our data. Moreover, molecular diversity and population demographic statistics were calculated to determine the genetic structure of Thai pig populations. The genetic distances between groups further indicate that Thai pigs are closely related with other Asian pigs (mean distance \pm SD; 0.0074 ± 0.0016), but are very different from European pigs (0.0205 ± 0.0039). In total, 24 different mtDNA haplotypes of Thai pigs have been described. Finally, 19 haplotypes specific for Thai indigenous pigs, and four haplotypes specific for Thai wild boars belonged to the Asian group and only one haplotype - although specific for Thai indigenous pigs - fits into the European group. This study proposes firstly that the indigenous Thai pigs are closely related with Thai wild boars and may eventually go back to the common Asian ancestor. Secondly, Thai and Asian pigs are distinctly different from European pigs.

Poster 5019

Title: Genetic diversity of Churra Tensina breed sheep, and relationship with other Churra group breeds using microsatellites.

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Abstract :

Churra Tensina sheep is an endangered local course-wooled hardy breed belonging to Churra group which is raised for lamb production, although it has been milked for years. Thirty microsatellites proposed by FAO and ISAG for biodiversity studies have been used to characterize Churra Tensina, Churra, Churra Lebrijana and Latxa sheep breeds. All microsatellite loci analysed were found to be polymorphic, showing an observed heterozygosity ranged from 0.6599 to 0.7084 for Churra lebrijana and Latxa, respectively. All populations showed significant deviations from Hardy-Weinberg proportions. The fixation indices showed statistically significant differentiation between breeds ($F_{st}=0.119$), low inbreeding related to the whole population ($F_{it}=0.146$) and within population

($F_{is}=0.031$). Results from GeneClass assignment test revealed that 100% animals were assigned to the population they were collected from. Structure programme inferred 4 clusters for the best estimated of the log probability of the Churra Tensina population, indicating that Churra Tensina was structured in 4 sub-populations. Reynolds distance results showed the higher and lower distance between Churra Tensina and Churra Lebrijana, and Churra Tensina and Latxa pairs, respectively. In conclusion, Churra Tensina sheep breed showed good diversity values despite its low effective population size.

Poster 5020

Title: Conservation genetics of the endangered “Altamura” sheep breed from Southern Italy

Presenting Author: Elena Ciani, General and Environmental Physiology Department, University of Bari, Via Amendola 165/a 70126 Bari, Italy

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Abstract :

Altamura is an originally triple-purpose sheep breed from Southern Italy that has experienced a drastic population size contraction. A total of 89 animals, sampled from two different farms in the province of Bari (Apulia), were genotyped at 19 microsatellite loci belonging to the ISAG-FAO panel. Samples were chosen according to genealogical records in order to minimize relatedness among animals. A high level of linkage disequilibrium was observed in the total sample, also among non syntenic locus pairs, suggesting the presence of population substructuring. A genetic partitioning at the farm level was supported by the F_{ST} value between the two farms (0.056 ; $P < 0.0001$) and by two different population assignment tests. In particular, using a Bayesian approach, different ancestralities within a single farm were highlighted, corresponding to different farm origins. Within-group linkage disequilibrium greatly decreased when clustering the animals based on the different ancestralities. These results confirm the power of STR loci to detect fine-scale genetic structure and highlight a noticeable differentiation among the ancestralities, probably arisen from reproductive isolation and/or different selection strategies across farms. This should be seriously taken into consideration, due to critical implications for the breed conservation.

Poster 5021

Title: Dynamic annotation of DNA sequences in agricultural species.

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Abstract :

Several millions of DNA sequences exist in public databases deriving from ESTs projects and various other contributions. Moreover, parallel sequencing nowadays permits to achieve a throughput of hundreds of thousands of cDNA sequences in a single experiment. Annotation of these sequences is required to perform several tasks, like microarray generation, species comparison for expressed genomes, metabolic pathway assessment in orthologous species etc.

We developed a public domain portal where large databases of sequences can be automatically annotated starting from those of model species related to the one of interest. The portal has been developed for agricultural species and particularly for animals and plants -.

users can request annotation of sequences available in specific NCBI databases or supply a set of his/her own set of data.

The procedures are based on a redundancy filter for very similar sequences and a BLAST on annotated databases which can be selected by the user, who can also set the parameters to fine tune the search process. The search is performed sequentially on a list of databases ranked according to their suitability to retrieve the best information for the species of interest. Here we present some examples concerning cattle and sheep.

Poster 5022

Title: GENETIC AND PHENOTYPIC RELATIONSHIPS BETWEEN BLOOD GAS PARAMETERS AND ASCITES-RELATED TRAITS IN BROILERS

Presenting Author: Ane Marie Closter, Wageningen University, Animal Breeding and Genomics Centre, Marijkweg 40, 6709 PG Wageningen, The Netherlands

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5. Henk Bovenhuis

Abstract :

Ascites is a metabolic disorder in broilers associated with rapid growth and high demand for O₂. The tendency of broilers to develop ascites is heritable. Successful selection against ascites susceptibility requires good and easy-to-measure indicator traits. In juvenile chicken, blood gas parameters have been suggested as indicator traits. The aim of the present study was to estimate heritability and genetic correlations between blood gas parameters (measured during week 4), body weight and heart ratio (post-mortem indicator for ascites).

For this purpose total blood gas traits were available on nearly 3000 broilers from generation 7 and 8 of an advanced intercross line from 2 dam lines. The birds were challenged under cold conditions. Heritability for heart ratio was 0.43, for pH 0.15, and 0.19 for HCO₃⁻. Heritabilities for *pv*CO₂ (0.02), *pv*O₂ (0.03) and *s*O₂ (0.07) were low. Genetic correlation between heart ratio and HCO₃ was 0.31 (±0.15), -0.62 (±0.21) between heart ratio and *pv*O₂, and -0.04 (± 0.45) between heart ratio and *pv*CO₂. Heritability for blood gas parameters and the genetic correlations with heart ratio estimated in the current data do not support the suggestion that at that age blood gas parameters are useful traits in selection against ascites susceptibility. Supported by Hendrix Genetics B.V. (The Netherlands) and by grant 401-138-8000 from STW (The Netherlands).

Poster 5023

Title: Centromeric/pericentromeric junction within the MHC locus on chromosome 7 in pig

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Abstract :

In swine, the centromere of chromosome 7 (SSC7) splits the Major Histocompatibility Complex (MHC) into two regions, the class III (p arm) and class II (q

arm) regions. Although swine MHC is completely annotated, its centromeric junction remains uncharacterized. Screening our pig BAC library with primers specific of the centromeric genetic marker SW472 identified three BACs containing 3.6Kb-long tandem repeats. Fluorescence in situ hybridization showed that the 3.6Kb repeat and BACs are specific of the SSC7 centromere. Screening with the 3.6Kb probe isolated additional BACs localized at the SSC7 pericentromeric/centromeric junction, eight of which were sequenced with a threefold coverage. Pig VEGA annotation and sequence comparison with BAC ends from the swine genome physical map revealed that one BAC mapped to a locus 21Kb from the BTNL4 gene on SSC7 q arm. Some BACs contained SINE elements characteristic of euchromatin and one BAC end was similar to the mc2 centromeric sequence, previously described as specific of metacentric pig chromosomes. Therefore, we have identified BACs spanning the pericentromeric/centromeric junction within MHC on the q arm of SSC7. These results represent the first step in the sequence analysis and further expression studies of the junction between euchromatin and heterochromatin regions in pig.

Poster 5024

Title: MHC HAPLOTYPES AND RETROVIRUS-CAUSED DISEASES IN SHEEP: OVINE PULMONARY ADENOMATOSIS AND MAEDI-VISNA

Presenting Author: AMAIA LARRUSKAIN, Genetics, Physical Anthropology and Animal Physiology Department. Faculty of Science and Technology. University of the Basque Country

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Abstract :

The Major Histocompatibility Complex (MHC) is a region of highly polymorphic genes involved in the immune response. As it has previously demonstrated association with susceptibility/resistance to diseases with viral aetiology, an association analysis was carried out to identify haplotypes of the ovine-MHC associated with the development of Ovine Pulmonary Adenocarcinoma (OPA) and Maedi-Visna (MV), two chronic contagious diseases affecting sheep, caused respectively, by Jaagsiekte Retrovirus (JSRV) and Maedi-Visna Virus (MVV).

Two microsatellite markers located in the Class-I and Class-II regions were genotyped in 167 individuals of Latxa breed, and haplotypes reconstructed using the

program PHASE v2.1.1 in absence of familiar data. The analyzed microsatellites are highly polymorphic in this breed compared with other breeds. In consequence, the haplotype variability is remarkably high (73 haplotypes), requiring specially designed statistical tests able to deal with this variability. Moreover, sample structuration by flock was included in the analysis. The statistical tests were performed by SASv9.0 and Rv2.7.0. Several haplotypes were found to be significantly associated with susceptibility/resistance to both OPA and MV, although the results are sensitive to the inclusion of flock-effect in the analysis. It can be concluded that the parameters used in this work can improve the haplotype-based association studies in domestic animal species.

Poster 5025

Title: In vitro Conservation and Preliminary Molecular Characterization of Some Turkish Native Domestic Animal Genetic Resources-I (TURKHAYGEN-I)

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Abstract :

Dramatic changes of environmental conditions including global warming and environmental pollution have irreversibly affected the world's flora and fauna. As in other countries, several endemic domestic animals have been totally lost or under danger in Turkey. This matter has been discussed on various platforms in Turkey and was declared as a priority and various action plans have been prepared. In order to solve this problem, the Turkish Ministry of Agriculture and Rural Affairs (TKB) has taken precautions by application of conservation programs for some animal genetic resources. By the contribution of the TKB, Turkish National Science and Research Foundation (TUBITAK) and 10 universities, a consortium was founded to take other efficient

measures. The main objective of TURKHAYGEN-I is the application of in vitro conservation programs by foundation of two cryo-banks in which duplicated samples will be preserved. The project covers endemic sheep (13), cattle (6), goat (5), horse (5) breeds and Anatolian water buffalo. A total of 1500 animals have been collected from different parts of Turkey and the herds are placed in research farms of the participating institutions where somatic cells, embryos, DNA, and semen samples are collected. All preserved animals are also characterized at DNA level using microsatellite and mtDNA markers.

Poster 5026

Title: Animal QTLdb: A tool set to warehouse and compare cattle, pigs, chicken and sheep QTL within and between species.

Presenting Author: Zhi-Liang Hu, Department of Animal Science, Iowa State University, 2255 Kildee Hall, Ames, IA 50011

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Abstract :

The Animal QTL database (QTLdb; URL: <http://www.animalgenome.org/QTLdb/>) was developed to aid with identifying causal mutations responsible for economically important traits by allowing comparative viewing of all published porcine QTL data. The capability of AnimalQTLdb has since been expanded by: (1) modifying the database so that QTL from multiple species can be warehoused and comparisons made within and across species; and (2) extending QTL map alignments to a greater range of structural genomic features, such as radiation hybrid markers, microsatellites, finger printed contig BAC clones, SNPs, and microarray elements. AnimalQTLdb now contains QTL data for cattle,

swine, chicken and sheep; serves as both a data warehouse and search tool; and a powerful QTL oriented, map based data mining tool through easy-to-use and user-friendly web interfaces. Animal Trait Ontology (ATO) was introduced to improve consistency of trait nomenclature and organise traits for database management. Current initiatives include extending the utility of AnimalQTLdb by integrating mouse, rat and human QTL information and by working with livestock, rat and mouse communities to extend the ATO to facilitate cross-species trait comparisons. As new types of data (e.g. copy number variation and metabolomics) become available these will be incorporated into AnimalQTLdb to further enhance data mining.

Poster 5027

Title: Molecular estimation of effective population size – a new perspective for the assessment of risk status for livestock breeds?

Presenting Author: M. Tapio, International Livestock Research Institute ILRI, PO Box 30709, Nairobi 00100, Kenya

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Abstract :

For livestock breeds of the developing world demographic information is often lacking and effective population size cannot be estimated accurately. With dense marker information the application of LD-based methods for the estimation of effective population sizes might offer new perspectives to overcome this problem. In an international project genome-wide SNP data from two African cattle breeds (Sheko and N'Dama) and one Swiss breed (Eringer) will be evaluated. So far, information for 17 Sheko individuals and 22 N'Dama individuals, respectively genotyped within the bovine HapMap-project were available. Thereof three chromosomes with frequent indications of selection and three "neutral" chromosomes were selected. Effective population size was estimated based on r^2 . Levels of LD and development of estimated effective population size over generations were compared between chromosomes. A decreasing population trend was found for both breeds, however with large standard deviations. The practical results were compared with simulated results. The goal of the overall study is the evaluation of marker based estimation of effective population size for the

management of livestock populations in developing countries.

Poster 5028

Title: ANEXdb: An Intuitive Animal Microarray Expression and Functional Annotation Database

Presenting Author: Oliver Couture, Iowa State University, Ames, IA, USA

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Abstract :

The Animal Expression Database (www.ANEXdb.org) allows users to upload microarray experiments with Affymetrix® GeneChip®-based expression data using a user-friendly web interface. The database can accommodate any species or any chip based on the Affymetrix® platform. Data can be stored as private information within the database, and the database streamlines public submission to GEO using an automatic SOFT formatter. In addition to storing expression data, the database is connected to an annotation database, annotDB, which currently contains an in-house alignment of 1,691,062 porcine sequences assembled into 98,452 consensus sequences and 192,736 singletons. Through BLAST, these sequences will not only be connected to the Affymetrix® porcine GeneChip®, but to other species using NCBI's RefSeq database. This BLAST analysis allows additional information from NCBI Gene, KEGG, Pfam, GO, and Ensemble to be tied to the sequences for further annotation. The design of annotDB is species-independent, and can accommodate any type of sequence. The annotation and expression databases are modular in design, and can be independently updated. EBI's Bio-Mart will be used as an interface for querying both expression and annotation simultaneously. Currently data for over 400 Porcine GeneChip® hybridizations are being uploaded to ANEXdb.

Poster 5029

Title: Single nucleotide polymorphisms of the *KITLG* and *KIT* genes in pigs

Presenting Author: Naohiko OKUMURA, Second Research Division, STAFF-Institute, 446-1 Ippaizuka, Kamiyokoba, Tsukuba, Ibaraki 305-0854, Japan.

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Abstract :

Here we report the variability in genes encoding KIT tyrosine kinase receptor and its ligand KITLG by determining single nucleotide polymorphisms (SNPs) in 384 individuals constituted by 16 pig groups of 11 breeds, two synthetic-line cross pigs, two cross breeds, and Japanese wild boar. SNPs and indels within the coding sequence regions of *KITLG* and *KIT* and their 5'-flanking regions were detected by aligning sequences from 8 pigs; subsequently, the SNPs were genotyped using MALDI TOF-MS (SEQUENOM MassARRAY system). Principal component analysis using allele frequencies in the SNP loci showed a distant relationship between Asian and Euro-American pig groups, except for Berkshire and Tokyo X breeds. These breeds were located within the mid-portion of the distribution in the first principal component. The Hampshire breed was distant from the other pig groups on the axis of the second principal component. Haplotype estimation revealed each unique haplotype of *KIT* gene being in the white and Hampshire breeds because of the causative gene for their coloration. On the other hand, the haplotypes of *KITLG* and *KIT* detected in the Berkshire breed were prevalent in Asian pig groups; this tendency is different from that observed in other Euro-American pig breeds.

Poster 5030

Title: Genetic analyses of Ghanaian chicken ecotypes: diversity and relationships with other breeds

Presenting Author: Boniface Baboreka KAYANG, Wildlife Research Center of Kyoto University, c/o JASSO, Tanaka-Sekiden-cho, Sakyo, Kyoto 606-8203, JAPAN

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Abstract :

This study investigated the genetic diversity of local chicken populations in three different agro-ecological zones of Ghana and examined their extent of genetic differentiation and phylogenetic relationships with other breeds. A total of 494 birds randomly sampled from one Red Jungle Fowl and nine domestic fowl populations, comprising the Ghanaian ecotypes (Interior Savannah, Forest and Coastal Savannah), Japanese native breeds (Nagoya, Mikawa and Gifujidori), White Leghorn, Rhode Island Red and Fayoumi, were genotyped across 21 microsatellite loci from the recommended FAO panel. Out of a total of 178 alleles observed, 27 were unique to the Ghanaian populations. The average number (\pm SD) of alleles/locus and the observed heterozygosity were, respectively, higher in the Ghanaian populations (7.76 ± 3.39 and 0.591 ± 0.110) compared to the rest (6.24 ± 2.79 and 0.374 ± 0.100). Genetic differentiation (F_{ST}), heterozygote deficiency (F_{IS}), Nei's genetic distance and cluster analysis (STRUCTURE) indicated that the three Ghanaian ecotypes were distinct from the other populations but were closely related to one another and showed high diversity but lacked sub-structuring. The results suggest that the Ghanaian populations are derived from a mixture of egg- and meat-type breeds and comparison of phenotype and genotype will provide information for selection.

Poster 5031

Title: Probabilistic Expert Systems (PES) as a tool for parentage testing in horses with lack of parental genotypes.

Presenting Author: Paolo De Iuliis, UNIRELAB s.r.l., Laboratorio di Genetica Forense Veterinaria, Via Campobello 7/c, 00040 - Pomezia (RM) Italy

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4. Marina Dobosz

Abstract:

Accurate determination of relatedness is of great importance in horse breeding industry. Currently the majority of horse breed registries adopted DNA technology in order to verify pedigree records and to solve queries of parentage. When genetic data of one of the individuals in comparison are missing, performance of a parentage test could be questionable. We present a new approach to analyze complex cases of identification inference. In a case of disputed maternity involving a thoroughbred foal, whose mare was dead, the relationship was initially excluded by genetic incompatibility between the foal and a bone that was supposed belonging to the mare. This result led us to bring forward two different hypothesis:

1. *the bone belongs to the mare and relationship is excluded;*
2. *the bone doesn't belong to the mare of the foal.*

Due to the impossibility to verify the identity of the bone, the relationship was then verified by statistical analysis of other genotypes in the family of the putative mare through Probabilistic Expert Systems. One of these systems (FINEX) was recently developed for forensic purposes and is particularly valuable for disputed paternity/maternity cases in humans. We will illustrate how this case has been successfully worked out by FINEX.

Poster 5032

Title: Genetic diversity of the mtDNA in five Italian horse populations.

Presenting Author: Chiara Bocci, UNIRELAB s.r.l., Laboratorio di Genetica Forense Veterinaria, Via Campobello 7/c, 00040 - Pomezia (RM) Italy

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5. Paolo De Iuliis

Abstract:

Genetic variability of a 510bp fragment in the D-loop region of the mtDNA in five horse breeds bred in Italy was analysed. Two breeds are autochthonous: Maremmano (N=40) and Murgese (N=23). Other Italian populations were also included: Arabian (N=40), Thoroughbred (N=40) and Sicilian Oriental Thoroughbred (N=7). Murgese samples were selected at random, while selection for other breeds has been performed using pedigree information in order to maximise maternal diversity. Genomic DNA was extracted from blood on FTA[®] papers. PCR primers were designed according to Xu and Arnason (1994). Sequences obtained were aligned and compared with reference sequence from GenBank X79547. For a total of 150 individuals, 44 polymorphic sites representing 51 haplotypes were observed. Genetic distances were estimated by Slatkin's linearized Fst's (Schneider, Roessli, and Excoffier 2000) method using Arlequin package software 2.1 (Schneider et al. 2000). Our data were compared with 22 mtDNA sequences present in literature representing Italian horse breeds. An *Equus asinus* sequence was used as the outgroup. The aim of this study is to evaluate matrilineal relationships of these breeds in order to enlarge genetic information about horse populations bred in Italy and to confirm their multiple origin reported by other investigators.

Poster 5033

Title: Genome-wide analysis of pig alternative splicing with full-length enriched cDNA libraries.

Yong-Min Cho, Dajeong Lim, Kyung-Tai Lee, Mi-Jeong Byun, Yeonkyung Kang, Heebal Kim, Seok-ki Im
NIAS (National Institute of Animal Science, RDA), Seoul National Univ.

Abstract:

We produced 75,110 expressed sequence tags (ESTs) from a full-length enriched 6 cDNA libraries: porcine abdominal fat, porcine fat cell, porcine loin muscle, backfat, liver and pituitary gland. Alternative splicing is an important role of the functional complexity in mammalian genes, developmental stage and pathological state. Particularly, EST/mRNA alignment is important method for *in silico* detection of AS (Alternative Splicing) because ESTs and mRNAs are the most abundant resources and are regarded as a direct evidence of the expressed genes. Defining alternative splicing isoforms with EST fragment data faces the multiassembly problem. The multiassembly problem is the problem for reconstructing the most likely set of full-length isoform sequences from a mixture of EST fragment data. Our algorithm identifies novel alternative splicing events based on sequence similarity searches between each EST dataset and known gene set without multiassembly problem. We determined alternative splicing events using BLAST and validated AS events with SIM4 program. As a result, we found 717 sequences of case1 type (EST insertion) and 255 sequences of case2 type (EST deletion).

Poster 5034

Title: Evidence for cattle major histocompatibility complex (BoLA) class II DQA1 gene heterozygote advantage against clinical mastitis caused by *Streptococcus* and *Escherichia* species..

Presenting Author: Shin-nosuke Takeshima

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Abstract :

Mastitis, which is a mammary gland inflammatory response to bacterial infection, is a major problem in the dairy industry. We genotyped bovine major histocompatibility complex (BoLA)-DRB3 and BoLA-DQA1 in 120 cattle with clinical mastitis and

85 randomly selected Holstein cattle in Japan by polymerase chain reaction-sequence based typing (PCR-SBT). The mastitis cattle were divided into four groups according to the bacterial species causing the mastitis (Staphylococcus aureus, Streptococcus, Escherichia and coagulase-negative staphylococci). The BoLA-DRB3 and BoLA-DQA1 heterozygosity of each group was compared to that of the control cattle. The expected heterozygosities based on Hardy-Weinberg proportions and the observed heterozygosities for each locus were compared for each group. The Escherichia and Streptococcus mastitis groups showed significant differences between their expected and observed heterozygosities with regard to their BoLA-DQA1 genes. No differences were observed for any group with regard to the BoLA-DRB3 genes. We then found that two BoLA-DQA1 alleles promoted susceptibility to mastitis caused by Streptococcus, namely BoLA-DQA1*0101 and BoLA-DQA1*10012, and that the homozygous BoLA-DQA1*0101/0101 and BoLA-DQA1*10011/10011 genotypes promoted susceptibility to mastitis caused by Streptococcus and Escherichia, respectively. This is the first report in Japan showing that heterozygosity of the BoLA-DQA1 gene is associated with resistance to mastitis progression.

Poster 5035

Title: The “Osservatorio Italiano HCM Felina”: a Feline Inherited Diseases Network in Italy

Presenting Author: M. Longeri, Università degli Studi di Milano, Dipartimento di Scienze Animali, Sez. Zootecnica Veterinaria, Via Celoria, 10 - 20133 Milano (Italy)

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Abstract :

In Italy cat breeders are scattered in many associations and breed fan clubs. The availability of new genetic tools for inherited disease identification and the possibility of shipping buccal swabs directly from the cattery to diagnostic Labs, prevent a real control of veterinarians, geneticists and breed associations on diagnosis and selection of the diseases.

In 2008 to overcome the absence of a network the Italian Observatory on Feline Hypertrophic Cardiomyopathy (HCM) has been constituted. So far it associates the Italian Main Coon and other breed clubs, the Milan University (Spin-off Vetogene) and selected clinicians.

Main targets: 1) scientific monitoring on the cat inherited disease in Italy, mainly HCM, so far; 2) supporting to breeder in the selective choices; 3) constitution of a biological and data bank for further scientific studies; 4) improving link among cat breeders, selected veterinarians and scientific community, for the first time in Italy. A cat joining the Observatory is submitted to microchip implant, periodical clinical controls, DNA tests and blood storage. Data are anonymously available to Observatory associated.

Breed statistics, correlation between clinic and genetic results and some discussion on possible spin-off on feline genetic research are also proposed.

Poster 5036

Title: The trend of the inbreeding in the course of time in “Bracco Italiano” dog breed.

FRANCESCA CECCHI¹, ROBERTA CIAMPOLINI¹, BRUNO DE SANCTIS², FABIO CASETTI³, SILVANO PRESCIUTTINI¹

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Abstract :

We refer on a genealogical study on the “Bracco Italiano” dog breed, with the aim to study the investigate the trend of the inbreeding during a period of 38 years. The complete electronic record of the breed, including 20,499 animals born between 1970 and 2007, was downloaded from the ENCI database. Animals were divided in eight periods according to their year of birth. The following genetic parameters were calculated, using the program CFC: a) the level of inbreeding (F) of the total population; b) the individual inbreeding; c) the number and the percentage of inbreds and the average inbreeding coefficient in the inbreds animals for five-year periods.

The inbreeding coefficient was <0.05 in 8,103 dogs (39.53%) whereas it was >0.20 in 487 dogs (2.51%). The average inbreeding coefficient over all animals resulted 3.6% (from 0.4% in 1970-1975 to 5.5% in the last two years). The percentage of inbreds per year increased from 2.44% in 1976-1980 to 100% in the past two years. It is concluded that a regular monitoring of genetic variability of the population must be adopted, in order to avoid the danger of an

excessive increase of inbreeding in the future, which would result in significant inbreeding depression.

Poster 5037

Title: The prion protein gene (*Prnp*) polymorphisms in Slovenian sheep breeds

Presenting Author: Jelka Zabavnik Piano, Veterinary Faculty, University of Ljubljana, Gerbičeva 60, Ljubljana, Slovenia

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Abstract :

Scrapie is the transmissible spongiform encephalopathy (TSE) that occurs naturally in sheep. Three scrapie-linked polymorphisms in the prion protein gene (*Prnp*) located at the codons 136, 154 and 171 modulate the susceptibility to classical type of scrapie. In order to evaluate the *Prnp* polymorphisms in Slovenian sheep breeds and to evaluate the genetic susceptibility through the years sheep of four breeds (Bela Krajina Pramenka, Bovska sheep, Istrian Pramenka, Jezersko-Solcava) *Prnp* polymorphisms were analyzed from the year 2005. Polymorphisms at codons 136, 154 and 171 were determined by nucleotide sequencing of the *Prnp* and by allelic discrimination assay. Each year different sheep were randomly sampled for *Prnp* genotyping. The most frequent genotype in all Slovenian sheep breeds is ARQ/ARQ. Animals carrying this genotype are moderately susceptible to scrapie. The allelic variant VRQ, known to carry very high risk of scrapie is only poorly represented in the population of the examined Slovenian sheep breeds and is decreasing through the years. Slightly more abundant is the allelic variant ARR that is typical for sheep resistant to scrapie. This allelic variant is increasing through the years.

Poster 5038

Title: Viral-vector Mediated Transgenesis in the Göttingen Minipig Brain

Presenting Author: Claus Hedegaard, Dept. of Genetics and Biotechnology, Faculty of Agricultural Sciences, University of Aarhus, Blichers Allé, 8830 Tjele, Denmark.

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Abstract :

Transgenic large mammals for modelling human diseases are receiving increasing interest as potential elaboration of rodent models. Pigs offer splendid anatomic, physiologic, and genetic recapitulation of humans, avoiding ethical concerns with primates used for experiments. Particularly the architecture of the pig CNS provides an attractive basis for modelling neurological diseases. The considerable longevity expected for transgenic pigs to develop age-related neurodegenerative disorders has made us attempt to establish a proof of concept with surgery based, virus mediated gene transfer in Göttingen minipigs. Three anaesthetised minipigs were MRI-scanned for determination of coordinates for *substantia nigra* (SN). The animals then received six stereotaxic, unilateral deep brain injections with recombinant lentivirus harbouring the *EGFP* gene. After four weeks, the animals were euthanised, brains dissected, and relevant tissues recovered. Histology showed injection points targeting SN as visualised by Nissl staining while subsequent immunohistochemical staining with anti-*EGFP* demonstrated transgene expression and transport to striatum. PCR analysis confirmed presence of the *EGFP* gene in SN but not in striatum, reflecting the presence of the neuronal cell nuclei in SN, and axons extending to striatum. The obtained results indicate the present technique to be an efficient means of transducing discrete, selective tissues of the Göttingen minipig brain.

Poster 5039

Title: Profile of the Circulating DNA in Healthy Cattle

Presenting Author: Julia Beck, Chronix Biomedical GmbH, Goetheallee 8, 37073 Goettingen, Germany

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Abstract :

Circulating nucleic acids (CNAs) have been shown to have diagnostic utility in human diseases. The aim of this study was to sequence and organize DNA obtained from serum of apparently healthy cattle providing an extensive catalog of the circulating DNA profile.

Serum DNA from 79 cattle was extracted, amplified, sequenced using high-throughput pyrosequencing (454/Roche) and categorized by: 1) origin (bovine versus exogenous), 2) functionality (repeats, coding or non-coding sequences), and 3) chromosomal localization.

7.81E+05 sequences were obtained consisting of 1.27E+08 nucleotides, of which 78% was attributed to known database sequences. Of the known sequences 95% were genomic and 5% were of bacterial or viral origin. Of the genomic sequences, 48% originated from repeats and 34% from annotated genes, which is within the expected range. Interestingly, coding sequences (CDSs) were significantly underrepresented in the circulating DNA pool. Whereas, sequences matching to repetitive elements were found in amounts as expected from the genome.

The under-representation of CDSs argues strongly against a solely apoptotic/necrotic origin of CNAs. The normal bovine circulating DNA profile described here and the technique of high-throughput sequencing together with a detailed analysis of the origin of the circulating DNA may open a diagnostic horizon.

Poster 5040

Title: Genetic diversity among goat populations in Turkey

Genetic Diversity Among Goat Populations in Turkey

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Abstract

Microsatellites are one of the favored markers used in population genetics studies because of their high heterozygosity and versatility. In this study, 11 microsatellites loci were used as molecular markers to determine the intra and inter genetic diversities of eight different goat breeds including Kil, Angora, Kilis, Yayladag, Shami, Honamli, Saanen, and Alpine. The genetic differentiation between breeds was considerable as a result of the statistically significant ($P < 0.001$) pair wise F_{ST} values of each pair of breeds. Exceptionally, F_{ST} values calculated for Honamli and Kil breeds were statistically non-significant ($P > 0.05$). Heterozygosity values were ranged between 0.62 and 0.73. According to the Structure and assignment test, individuals of Angora and Yayladag goat were assigned to the breed they belong to, while other breeds were assigned to two more different groups. Because, this study for the first time presented genetic

data for the Yayladag goat, structure analysis and assigned test results were interesting for the Yayladag goat. Additional and different molecular markers are needed for future analyses.

Poster 5041

Title: Metanalysis of microsatellite data allows a molecular classification of European cattle

Presenting Author: J.A.Lenstra, Faculty of Veterinary Medicine, Utrecht University, Yalelaan 2, 3584 CM, Utrecht, Netherlands

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1. European Cattle Genetic Diversity Consortium

Abstract :

Several European research groups have studied the molecular diversity of cattle by microsatellite genotyping. A combined dataset now contains genotypes of >10,000 animals from 186 European, African and Asian taurindicine breeds, 98 of which have been analyzed with all 30 FAO-recommended microsatellites. Combination of data from different sources and different marker panels was validated by metaanalysis of 39 breeds sampled and genotyped by different laboratories. Model-based clustering and distance analysis resulted in a molecular classification of European cattle that correlates better with geographical origin than with breeding objectives: (1) Northern-European breed clusters: Lowland Pied, Baltic-Highland Red, North-West Intermediate, British, Nordic, Nordic-Ayrshire and Russian cattle; (2) Central-European clusters: Southern French, Central Brown and Western-Central breeds, the last cluster containing Central Spotted, Western-Alpine and German Yellow subclusters; (3) Mediterranean clusters: Balkan, Podolian and Iberian breeds, the last cluster containing Cantabrian, Andalusian, Morena and Lidia as distinct subgroups. SNP analysis of 1079 Y-chromosomes revealed two haplotypes Y1 and Y2. Y1 is predominant in most Northern-European breeds but is also carried by several Northern-Spanish bulls. The geographical distribution of breed clusters and paternal lineages is proposed to reflect successive migrations as well as relatively recent expansions of successful breeds.

Poster 5042

Title: Presence of Southeast Asian and Indian subcontinent maternal lineages in a genetically unstructured Zimbabwean chicken population

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Abstract :

Genetic diversity and population structure of village chickens of five agro-ecological zones in Zimbabwe was investigated using twenty-nine autosomal microsatellites and 455bp of the mitochondrial DNA D-Loop region. A comparison to a set of reference populations from Malawi, Sudan, Northwest Europe and six purebred lines was made. The maternal origin of the Zimbabwean chickens was investigated by comparing mtDNA haplotypes to those of the presumed centers of domestication. Both microsatellites and mtDNA analyses did not support that Zimbabwean chicken eco-types are substructured according to agro-ecological zones. Based on microsatellites, the five chicken eco-types of Zimbabwe clustered together. Marker estimated kinship values indicated that the level of genetic variation was high and very similar within and between eco-types. Zimbabwean chickens were distinguishable from the reference populations, particularly purebred lines. Analysis of mtDNA indicated that two distinct maternal lineages exist in the five Zimbabwean eco-types. For one of these lineages, chickens from Zimbabwe and Malawi shared major haplotypes with populations that have a Southeast Asian background. The second maternal lineage, probably from the Indian subcontinent, was common to the five Zimbabwean ecotypes, Sudanese and European chickens as well as purebred broiler and layer lines.

Poster 5043

Title: DNA testing of urine identifies horses that have undergone post-race drug testing.

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Abstract :

This investigation followed a question regarding the identity of a specific horse that tested positive to an illegal substance on a post-race urine sample. The urine sample from the horse was submitted to the Veterinary Genetics Laboratory at Onderstepoort (VGL) for DNA testing by the National Horseracing Authority (NHA) of South Africa Drug Testing

Laboratory. The resulting genotype was compared to the genotypes of South African Thoroughbred horses. It was matched, without exclusion, to 12 STR loci and Amelogenin. This included the 9 loci recommended by ISAG. The NHA requested that a standard sampling and transport methodology be set up as guideline to facilitate the DNA testing of urine samples in future in cases in which the test results are challenged. The NHA provided a total of 13 samples from various racecourses in the country. The samples were analyzed using the Genra Puregene Cell and Tissue Kit (Qiagen) with the addition of Hydrochloric acid as an initial step to remove calcium carbonate present in horse urine. PCR was performed using 12 STR loci in two plexes and Amelogenin. Results were analyzed and recommendations prepared for future sample collection, handling and analysis.

Poster 5044

Title: "Molecular characterization of epistatic interactions in a M16i X Myostatin mouse cross

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Abstract:

Animals that lack functional Myostatin are known for their extreme muscle growth and lack of adipose accumulation. To identify QTL that have differential effects in the presence and absence of functional Myostatin, M16i mice, which was derived from a line which was selected for weight gain before six weeks of age, were reciprocally crossed with Myostatin-null mice to generate F1s, which were mated to generate F2s. A total of 1072 F2 generation progeny that were homozygous Myostatin wild-type or Myostatin-null were genotyped for 186 SNP distributed across the genome. Initial statistical analysis of body weight indicated that the main effects of Myostatin genotype and reciprocal cross were significant across all ages. The main effect of sex was significant at 1, 4, 5, 6 weeks of age. Single nucleotides that were statistically associated with body weight ($P < 10^{-10}$) were clustered on several chromosomes. Significant ($P < 0.05$) two-way interactions were detected between Myostatin and cross, sex and Myostatin, Myostatin and SNP. Significant Myostatin by SNP interactions may indicate epistatic interactions. Segregation distortion was observed on chromosome 1 and was independent of Myostatin genotype. In contrast, the segregation distortion observed on chromosome X was only present in homozygous Myostatin wild-type mice. These preliminary results indicate that this population will be a valuable resource to better understand

epistatic interactions. Funded by a grant from USDA-NRI 2006-35205-16696.

Poster 5045

Title: Bayesian analysis of 15,110 single nucleotide polymorphisms in the bovine genome

Presenting Author: Jennifer J. Michal, Department of Animal Sciences, Washington State University, Pullman, WA 99164-6351 USA

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Abstract :

In order to further understand molecular mechanisms of mutation and genome evolution, single nucleotide polymorphisms (SNPs) neighborhood patterns in cattle were determined using Bayesian analysis on 15,110 SNPs, each with flanking sequences of 500 bp. Approximately 70% of SNPs were transitions. Transversion SNPs occurred most frequently (38.6%) when the A+T content equaled two at their immediate adjacent sites. In addition, C↔T and A↔G transitions and A↔C and G↔T transversions had reverse complementary neighborhood patterns. This study revealed several previously unreported SNP neighborhood patterns. First, cattle and humans share an overall SNP pattern, which is indicative of a common mutation system. Second, true neighborhood patterns for A↔T and C↔G are unclear since the sense and antisense sequences flanking these mutations are not recognizable. Third, the neighborhood ratio between A+T and G+C was very different, being lowest for C↔G, followed by C↔T/A↔G, A↔C/G↔T, and highest for A↔T. Fourth, transitions were significantly increased when two immediate adjacent sites provided structures for CpG. Lastly, methylation induced deamination reactions were responsible for approximately 20% of all transitions due to the unequal occurrence between A↔G and C↔T in five paired neighboring structures. The conversion occurred at both CpG and non-CpG sites.

Poster 5046

Title: Mangalarga marchador horse: genetic diversity and population structure

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Abstract :

In order to ascertain genetic diversity and structure for Mangalarga Marchador breed, 115 unrelated animals, born from October/2004 and May/2005, were sampled from three regions of Minas Gerais State, Brazil (South, Southeast and Northeast) and tested for 10 microsatellite *loci*. Under Hardy-Weinberg assumptions, seven markers were at equilibrium (LEX014, LEX017, LEX019,SGCV23, TKY321, VHL20, and VIASH39) while two (ABS3 and LEX031) presented significant homozygotes excess. Total number of alleles identified was 75, with a mean number of alleles of 8.22. Mean heterozygosity was 0.637 and mean PIC (*Polymorphism Information Content*) was 0.662. Most informative markers (PIC>0.7) were ABS3, LEX019, SGCV23, TKY321, and VHL20. F_{ST} values (0.06) indicates a mild geographical structure. A Bayesian based cluster analysis under a three cluster model was used to estimate populatiuon structure: 93.9% of the 115 animals were correctly assigned to the subpopulations from where they were sampled out. Comparitions of pairwise inbreeding coefficients resulted in 11% of the pairs sharing more than 20% of the alleles, thus suggesting that these animals are closely related. These results suggst that the population is genetically structured. Gene flow occurs between South and Southeast and South and Noprtheast regions, but less frequently between Southeast and Northeast regions.

Poster 5047

Title: Establishment of a small ruminant genetic database

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Abstract:

Sheep and goats are among the most important livestock species globally, especially in developing countries. The infrastructure for animal breeding and research in these countries is generally limited,

however. For this reason, the IAEA supports projects to increase the technical capacity of animal scientists and research institutes in its developing Member States. Genetic evaluations are unavailable in many of these countries and would be expensive to implement, so selection based upon molecular information, established through studies in developed countries, may be an economical approach to improve productivity. Although much of this information is published, access is often limited, due to lack of resources at research libraries. We have therefore created a web-accessible RT-db (Real Time database) for QTL in small ruminants. The database makes available the results regarding genomic locations of QTL from all known studies in these species (currently 314 QTL from 43 publications). Built by using PHP, MySQL and Ajax, the RT-db allows users to graphically positions of QTL, filtered according to a number of criteria, such as trait name, chromosome number, and statistical significance. By using this information, scientists will be able to design studies to confirm QTL in their populations or include them in selection programs.