

Livestock Genomic Resources in a Changing World Conference

June 17th-19th

Cardiff University

School of Biosciences



Program and Abstracts



Livestock Genomic Resources in a Changing World

Livestock conservation practice is changing rapidly in light of policy developments, climate change and diversifying market demands. Understanding this dynamic motivates this conference, which is focused on four themes:

- 1) Redefining the role of genome data in livestock conservation and prioritisation
- 2) Identifying improved and more integrative analysis methods for livestock genomic, environmental and socio-economic data
- 3) Censusing genomic resources for minority livestock species and breeds – where are we and what do we need?
- 4) Horizon-scanning for the twenty most important problems we need to overcome for effective livestock genomic resource conservation during the next decade.

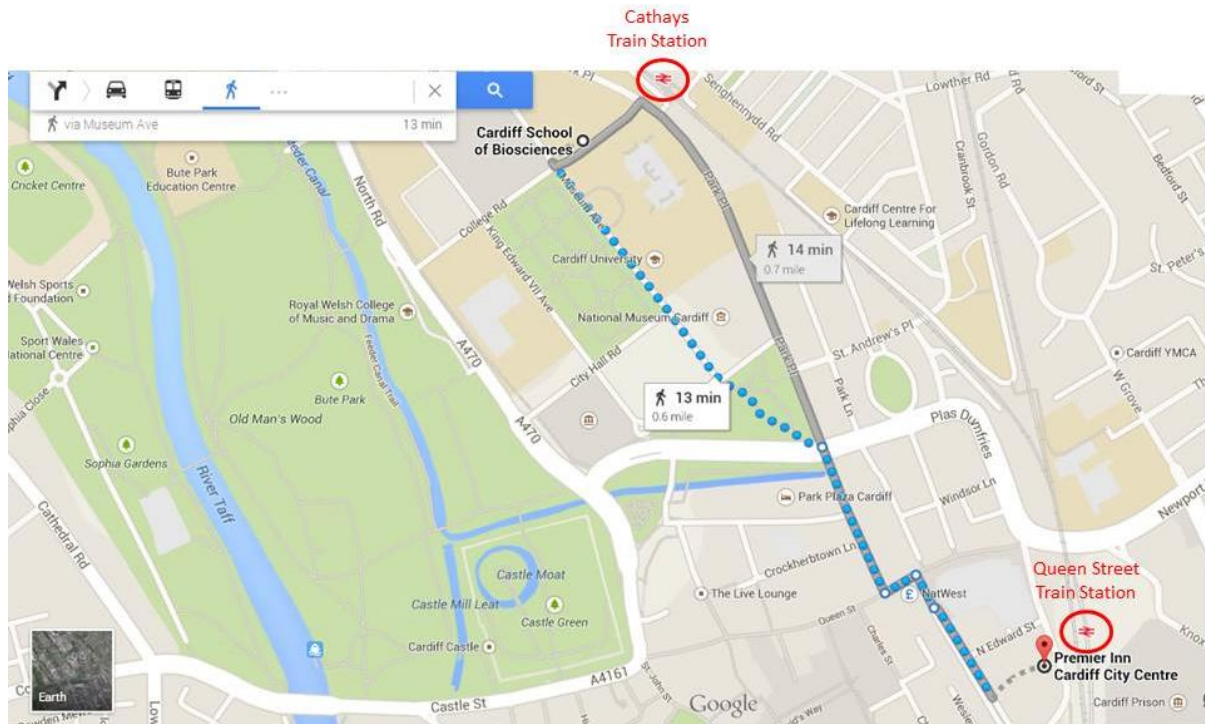
Livestock Genomic Resources in a Changing World Conference

VENUE

The Cardiff School of Biosciences hosts the Livestock Genomic Resources in a Changing World Conference.

The Cardiff School of Biosciences is known for the work of its former (and founding) director, Professor Sir Martin Evans FRS, which was recognized by the award of the Nobel Prize in Physiology or Medicine 2007 (together with Mario Capecchi and Oliver Smithies) "for their discoveries of principles for introducing specific gene modifications in mice by the use of embryonic stem cells".

Under its current director, Medical Research Council Professor Ole Petersen CBE FRS, Cardiff School of Biosciences is one of the largest bioscience departments in the UK with over 100 academic staff, ~150 research staff, more than 160 postgraduates and ~2000 undergraduate students. Research spans the full range of the Life Sciences from whole (eco) systems to molecular biology. In the 2013 Annual World University Ranking compiled by Shanghai Jiao Tong University (<http://www.shanghairanking.com/FieldLIFE2013.html>), Life Sciences at Cardiff University is in the top 100 worldwide and in the top 10 in the UK.



LOCAL ORGANISING COMMITTEE

SCHOOL OF BIOSCIENCES, CARDIFF UNIVERSITY

Michael W Bruford

Pablo Orozco-terWengel

Mafalda Costa

CONFERENCE VENUE

Cardiff University – School of Biosciences hosts the Livestock Genomic Resources in a Changing World Conference

Sir Martin Evans Building, Museum Avenue
Cardiff CF10 3AX

CONFERENCE WEBSITE

<http://livestockgenomics.wordpress.com/>

OTHER INFO

The **registration desk** will be open from 08:30 to 17:00 in the main lobby of the Sir Martin Evans building on the 17th and 18th of June, and from 08:30 to 12:00 on the 19th of June.

The main conference room is located in the Sir Martin Evans building next to the porters' desk (Physiology A Lecture Theatre (C/0.07)).

In order to allow testing the oral presentations, authors should bring them to the conference room between 8:30 and 9:00 of the presentation day.

Participants presenting **posters** are asked to set them at the main lobby of the Sir Martin Evans building as early as possible. **Fixing materials** will be available at the registration desk. During the poster sessions authors are requested to stand by their posters.

Participants that wish to **access the Internet** can use the university wireless connection. Please ask more information at the registration desk.

In case of **emergency** please contact the **registration desk**.

Livestock Genomic Resources in a Changing World Conference

MEALS

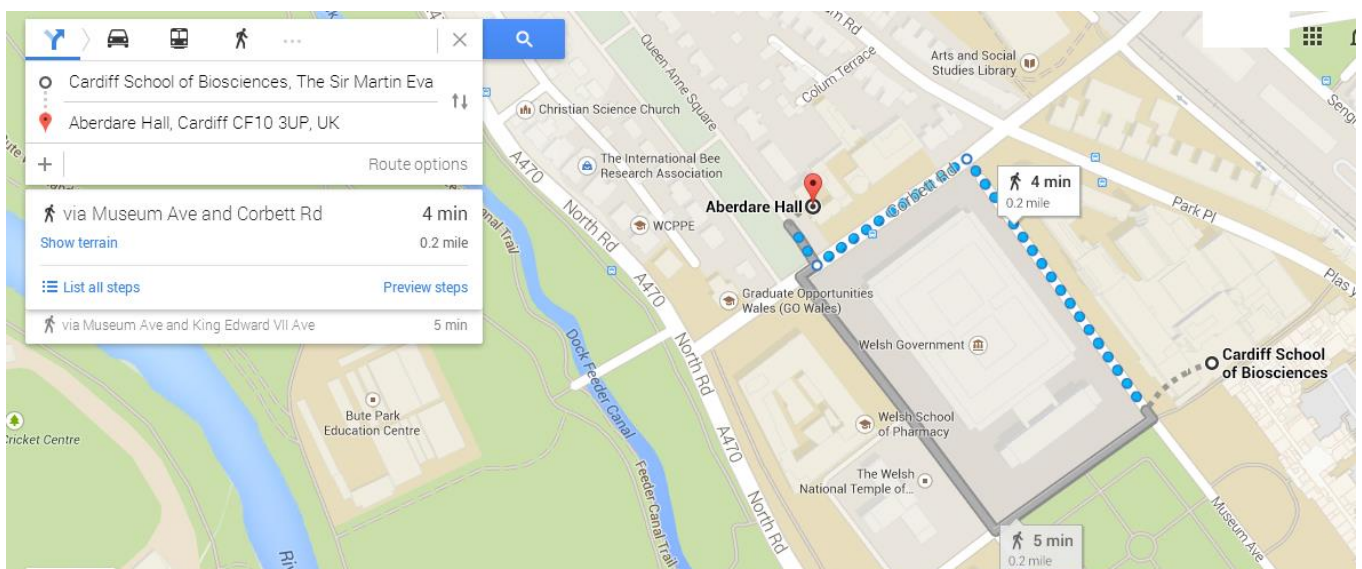
Coffee/Tea breaks and Lunches

Coffee/Tea breaks and **Lunches** will be served in the coffee shop of the Sir Martin Evans building.



Dinners

Dinners will be served at the Aberdare Hall (Corbett Road, Cathays Park, Cardiff, CF10 3UP) located 4 minutes by foot from the School of Biosciences.



JUNE 17TH (TUESDAY)

8:30 – 9:20 WELCOME COFFEE/TEA, REGISTRATION

Symposium on Horizon Scanning important questions and challenges for livestock genomics resources for the next decade

09:20 MICHAEL BRUFORD

Welcome to the conference and introduction to the session

09:30 HENDRICK-JAN MEGENS

*Pig variomics: understanding the when, where, and why of variation in the genome of *Sus scrofa**

10:00 PAOLO AJMONE-MARSAN

The coalition between Italian goats and Italian researchers: the Italian goat Consortium

10.30 COFFEE/TEA BREAK

11:00 STEPHANE JOOST

Biogeoinformatics of livestock genomic resources

11:30 JUTTA ROOSEN

Local breeds in global markets – exploiting consumer preferences for local and regional specialties

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FREE SESSION (4 X 15 MINUTE TALKS)

12:00 MAJA FERENČAKOVIĆ

Modeling genome wise dissection of inbreeding depression for bull fertility traits

12:15 NATALIA SEVANE

Genomic tools for detecting individuals with greater ability to face pathogens and other external aggressions

12:30 SOLANGE DURUZ

Data integration, GIS and multi-criteria decision making for the monitoring of livestock genomic resources

12:45 PHILIPPE HELSEN

From livestock to conservation breeding and back again

13:00 – 14:00 LUNCH

Symposium on “Beyond Weitzmann: prioritizing genomic resources using genomic data

14:00 IRENE HOFFMANN

A global view on prioritizing genomic resources

14:30 STEPHEN HALL

Prioritization of livestock genetic resources in relation to neutral and selected genetic variation

15:00 CATARINA GINJA

The challenge of defining conservation priorities for livestock breeds: the example of cattle

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15:30 – 16:00 COFFEE/TEA BREAK

FREE SESSION (6 X 15 MINUTE TALKS)

16:00 ANAMARIJA SMETKO

Trypanosomosis: Conservation of tolerance in African cattle

16:15 ELLISON MUSIMUKO

*Unveiling hidden treasures in Zambian indigenous cattle (*Bos indicus*) using 32 microsatellite markers*

16:30 MARKUS NEUDITSCHKO

PCA-Informative individuals for Structure Identification within Populations

16:45 HILAL BTISSAM

Genetic characterization of “Beni Arouss” goat in Morocco using microsatellite markers

17:00 DANIEL FISCHER

Identification of Signatures of Selection in Dairy Cattle from Next-Generation Sequencing Data

17:15 XIANGJIANG ZHAN

Reconstruction of a continuous demographic history of giant pandas based on genome data

17:30 – 19:30 Poster Session and Integration Activity

19:30 DINNER – ABERDARE HALL

JUNE 18TH (WEDNESDAY)

Symposium on genomic resources in minority livestock species

09:00 OLIVIER HANOTTE

Genome diversity of livestock: What does it mean for African cattle?

09:30 HANS LENSTRA

Cattle: more than taurine and zebu

10:00 MIKE BRUFORD

Genomic Resources in South American Camelids: Opportunities and Challenges

10:30 – 11:00 COFFEE/TEA BREAK

11:00 FRANÇOIS POMPANON

Estimating the potential of wild relatives and indigenous breeds to act as genomic resources: the case of sheep and goats

11:30 MARA MIELE

Slow Food presidia on rare /typical breeds in Italy: valuing or constructing the unique?

Livestock Genomic Resources in a Changing World Conference

PROGRAM

FREE SESSION (4 X 15 MINUTE TALKS)

12:00 ANAMARIA ŠTAMBUK

*Next-generation population genomics of native and aquacultured Mediterranean mussel, *Mytilus galloprovincialis**

12:15 CHARLES MASEMBE

A landscape genomics approach towards improving production and conservation of the Ugandan domestic goat (GOATGEN)

12:30 LAURA IACOLINA

Effects of isolation and human-mediated introgression in shaping the genomic distinctiveness of an insular large mammal

12:45 ROBERT FITAK

Complete genome re-sequencing reveals patterns of domestication in Old World camelids

13:00 – 14:00 LUNCH

Symposium on The data tsunami – how to avoid throwing the baby out with the bathwater!

14:00 DANIEL WEGMANN

Inferring Evolutionary Histories from Genetic Data

14:30 EZEQUIEL NICOLAZZI

Development of Approaches to Compare and Integrate Technologies

15:00 PABLO OROZCO-TERWENGEL

Signatures of Selection in Large Datasets

Livestock Genomic Resources in a Changing World Conference

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15:30 – 16:00 COFFEE/TEA BREAK

FREE SESSION (5 X 15 MINUTE TALKS)

16:00 FILIPPO BISCARINI

Can runs of homozygosity be used as an alternative or a complement to GWAS?

16:15 KEVIN LEEMPOEL

Subsampling as an economic consequence of using whole genome sequence data in landscape genomics: how to maximize environmental information from a reduced number of locations?

16:30 SYLVIE STUCKI

Riding the whole-genome data tsunami: a landscape genomic study of local adaptation in Moroccan sheep and goats

16:45 IAN STREETER

A high quality resequencing analysis pipeline for the NextGen project livestock data

17:00 LINN FENNA GROENEVELD

Conservation of the Nordic Brown bee

17:15 – 19:30 Poster Session and Integration Activity

19:30 DINNER – ABERDARE HALL

Livestock Genomic Resources in a Changing World Conference

PROGRAM

JUNE 19TH (THURSDAY)

9:00 Working Groups defined by Integration Activity (5 key questions per group).

10:30 – 11:00 COFFEE/TEA BREAK

11:00 Plenary Session and discussion on horizon scanning results. Publication tasks.

13:00 – 14:00 LUNCH

ABSTRACTS - ORAL PRESENTATIONS

(Ordered alphabetically by surname)

CAN RUNS OF HOMOZYGOSITY BE USED AS AN ALTERNATIVE OR A COMPLEMENT TO GWAS?

F Biscarini, S Biffani, E Nicolazzi and A Stella
Email: filippo.biscarini@tecnoparco.org

Runs of homozygosity (ROH) are contiguous stretches of homozygous genotypes which likely reflect transmission from common ancestors and can be used to track the inheritance of haplotypes of interest. ROH may potentially underlie recessive traits, and could therefore be used to detect phenotype-genotype associations in observational studies, such as case/control or cohort studies, and in experimental trials. In this perspective, ROH may provide an alternative or a complement to single-SNP genome-wide association studies (GWAS). GWAS methods typically analyse one locus at a time, are prone to spurious associations and, but for clear signals, are not always of straightforward interpretation. ROH may help overcome some of the limitations of standard GWAS studies. However, several statistical issues need still to be addressed: constructing a significance test, the issue of multiple comparisons, correcting for systematic effects and population stratification, accounting for selection bias due to the culling of animals for health or productive reasons. In this work, ROH were extracted from 50 K SNPs genotypes and used to detect genomic regions associated with susceptibility to diseases in 468 Holstein-Friesian cows. Infectious, metabolic, reproductive, locomotive diseases and mastitis were considered. ROH associated with infectious and locomotive diseases and mastitis were found on BTA 12. ROH associated with infectious, metabolic and reproductive diseases, and mastitis were observed on chromosomes 3, 5, 7, 13 and 18. Previous studies reported QTLs for milk production traits on these regions, thus substantiating the known negative relationship between selection for milk production and health in dairy cattle.

GENOMIC RESOURCES IN SOUTH AMERICAN CAMELIDS: OPPORTUNITIES AND CHALLENGES

MW Bruford

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South American Camelids (SAC) are of great importance to the Andean economy yet a coordinated approach to managing their genomic resources is lacking, which is negatively affecting their potential. I will review the current state of knowledge of SAC genetics and genomics, highlighting especially issues around the relationships between wild and domestic species, current breeding practices and fibre production. I will discuss SACs as a potential model for 'genome democratisation', highlighting how genome biology can solve production issues for the llama and alpaca and the role of their wild ancestors, the guanaco and vicuna, in their future development. A road map will be proposed for the characterisation and improvement of indigenous populations, a prerequisite for the future development of livestock rearing in one of the poorest highland regions in the world.

DATA INTEGRATION, GIS AND MULTI-CRITERIA DECISION MAKING FOR THE MONITORING OF LIVESTOCK GENOMIC RESOURCES

S Duruz, C Flury and S Joost
Email: solange.duruz@epfl.ch

In 2007, FAO initiated the Global plan of action for Farm Animal Genetic Resources (FAnGR) to reduce further loss of genetic diversity in farm animals. One of the key issues mentioned is to identify endangered breeds to support conservation prioritization programs. In this context, the Swiss Federal Office for Agriculture attributed a mandate to explore the feasibility of the implementation of a monitoring concept. The report mentioned the relevance of including the geographic location of the populations monitored. Accordingly, we used open source software (PostgreSQL, PostGIS, OpenLayers, Geoserver), to develop a WebGIS platform prototype (GenMon) designed to assess pedigree information, geographical concentration, socio-economic and environmental information. GenMon includes PopRep developed by the Institute of Farm Animal Genetics (FLI, Germany) to run the pedigree analysis and to provide parameters such as inbreeding coefficient, effective population size. Additionally introgression will be considered. Current developments will soon make it possible to process these indices based on genetic information as well. In parallel, the combined socio-economic/environmental index assesses the attractiveness and the risk of potential future agricultural practice abandonment in the regions where populations are bred. Finally, a multi-criteria decision support tool aggregates criteria using the MACBETH method, which is based on a weighted average using satisfaction thresholds. The system permits to upload basic information for each animal (parents, birth date, sex, location, introgression) and to choose relevant weighting parameters and thresholds. Based on these inputs, the system completes a pedigree analysis, and computes a final ranking of breeds based on an integrated prioritization score to be visualized on a map.

MODELING GENOME WISE DISSECTION OF INBREEDING DEPRESSION FOR BULL FERTILITY TRAITS

M Ferenčaković, I Curik and J Sölkner
Email: mferencakovic@agr.hr

In spite of inbreeding depression importance, its genetic basis is still unclear. To dissect genetic architecture of inbreeding depression, we provided a genetic model that enables estimation of inbreeding depression at the single SNP level using information of allele frequencies (p and q), dominance effect estimates (d) and mean SNP autozygosity in the population (f_{SNP}). Our models were tested on the fertility traits measured on 162 Brown Swiss bulls from Artificial Insemination station Birkenberg (Tyrol, Austria), genotyped with the Bovine SNP50 Beadchip (v1.). After editing, data consisted of 8756 recorded ejaculates with information for volume of ejaculate (VE ml), concentration of ejaculate (CE $10^9/\text{ml}$) and percent of viable spermatozoa (VS %) and 28792 SNPs. Runs of Homozygosity (ROH) were used to estimate individual inbreeding coefficients ($F_{\text{ROH}>4 \text{ Mb}}$) as well as to determine mean autozygosity of each SNP in the population (f_{SNP}). Results obtained indicated polygenic pattern of inbreeding depression as the highest contributions of single SNP were 0.06% (VE), 0.04% (CE) and 0.05% (VS) of the overall genome-wise $2pqdf_{\text{SNP}}$ score ($|\sum 2pqdf_{\text{SNP}}|$). The percentage of all SNPs with showing over- or under-dominance (absolute dominance over additive effects ratio $|d/a|>1$) was 56.1%, 55.7% and 59% for VE, CE and VS, respectively. However, this percentage was reduced to 22.5% (416/1852) for VE, 16.0% (216/1349) for CE and 27.7% (660/2382) for VS when only SNPs with significant ($P<0.05$) additive effects were considered. All three traits exhibited inbreeding depression defined by negative $\sum 2pqdf_{\text{SNP}}$ value, calculated over all SNPs.

IDENTIFICATION OF SIGNATURES OF SELECTION IN DAIRY CATTLE FROM NEXT-GENERATION SEQUENCING DATA

D Fischer, F Panitz, A Bagnato, E Santus, J Vilkki and MA Dolezal
Email: daniel.fischer@mtt.fi

We present a genome scan for signatures of selection based on autosome-wide SNPs called from Illumina paired-end next-generation whole genome re-sequencing data in 20 Brown Swiss (BSW) and 17 Finnish Ayrshire (FAY) dairy cattle bulls. This data is available to us from the FP7 funded project QUANTOMICS (contract n. 222664-2). SNPs had been called with SAMtools (Li et al., (2009)) as part of run 3 of the 1000 Bulls consortium (<http://www.1000bullgenomes.com/>) in a multi sample setting. Beagle v3 (Browning and Browning (2011)) was run to reduce false positive calls and to phase the data. We performed within population screens using classical population genetic parameters like π (Nei et al. 1979) and Tajima's D (Tajima (1989)) using VCFtools (Danecek et al. (2011)). We further calculated composite likelihood ratios (CLR) proposed by Nielsen et al. (2005) implemented in the parallelized version by SweeD (REF). Due to lack of sound theory on how to estimate optimal window sizes, we empirically determined 1kb windows to yield best signal to noise ratios. We furthermore contrasted BSW and FAY calculating the fixation index F_{st} between the two populations. This way selective sweeps could be identified in regions that host genes that were clearly expected to have reduced genetic variation. Selection signature scans based on the somewhat complementary integrated haplotype score (iHS) suggested by Voight et al. (2006) implemented in SelScan (Szpiech and Hernandez, (2014)) are still ongoing.

COMPLETE GENOME RE-SEQUENCING REVEALS PATTERNS OF DOMESTICATION IN OLD WORLD CAMELIDS

R Fitak, E Mohandesan and P Burger
Email: Rfitak9@gmail.com

In the Old World, two varieties of domesticated camel are recognized: the two-humped Bactrian camel (*Camelus bactrianus*) and the single-humped dromedary (*C. dromedarius*). Archeozoological and genetic studies have suggested that domestication of camels occurred between 5000 and 6000 years ago in the Bactrian and approximately 3000 years ago in the dromedary. Throughout their range camels are bred for a multitude of purposes including meat and milk production, transportation, wool, and sport. Additionally, several camel products, like camel milk, have proven beneficial for human health. Contrary to many other domestic mammals, however, camels do not manifest many of the canonical traits associated with domestication relative to their wild counterparts (e.g. retention of juvenile characteristics, continual reproduction, short maturation period). Therefore, we propose that an investigation of artificial selection in the camel genomes will yield comparably different results from that of other domesticated species. To date, genome sequencing of the Bactrian camel and its extant wild relative, *C. ferus*, has suggested that olfaction may have played an important role during Bactrian camel domestication. However, no dromedary genome exists, and certain inferences regarding artificial selection cannot be made from a single individual's genome. In our study, we sequenced 25 camel genomes to medium coverage (~15X), including individuals from all three species. We also sequenced at high coverage (~60X) and assembled *de novo* the dromedary genome. In addition to a description of the dromedary genome, this presentation discusses our preliminary investigation of how artificial selection and demography have shaped the camel genomes. We also present a genome-wide set of single nucleotide variants for Old World camels and review the potential for high-throughput genotyping and implementation of marker-assisted breeding programs to improve economically relevant traits.

THE CHALLENGE OF DEFINING CONSERVATION PRIORITIES FOR LIVESTOCK BREEDS: THE EXAMPLE OF CATTLE

C Ginja and The BIOBOVIS Consortium
Email: cjginja@fc.ul.pt

It is essential to determine the conservation value of livestock breeds to define priorities and to manage genetic diversity. Several methods based on the establishment of conservation priorities have been developed to maintain high levels of neutral genetic variation. Assuming that both within- and between-breed contributions to genetic diversity should be taken into account, various weights applied to each component have been proposed. Here the results of a comprehensive analysis of conservation priorities of Iberoamerican cattle are discussed. Microsatellite data on over 80 worldwide bovine breeds, collected in the framework of the BIOBOVIS Consortium, were used to investigate the contribution of geographical breed-groups to the genetic diversity of cattle. Contributions to global diversity were investigated using alternative methods, namely molecular kinships, the Weitzman algorithm, and combined approaches. Conservation priorities differed significantly according to the weight given to within- and between-breed genetic diversity. Nonetheless, these analyses provided a detailed perspective on how genetic variation is distributed among peripheral and more variable breeds, as well as between breed-groups from different biogeographic areas which can represent specific evolutionary processes (e.g., adaptation). Such information can help refine decision-making when undertaking conservation programs. The risk status of each breed is defined on the basis of demographic and cultural factors, and when establishing conservation priorities, it is necessary to account for other features. Creole and local isolated breeds retain high genetic diversity. The development of sustainable breeding programs for these breeds, and the added value resulting from their products should be considered to ensure their long-term survival. More recently, whole-genome approaches allow identification of genomic regions under selection, and can provide more reliable estimates of the conservation value of breeds. But, selection for adaptive alleles can result in further losses of genetic variation, thus the usefulness of whole-genome SNPs to define conservation priorities lacks careful evaluation.

CONSERVATION OF THE NORDIC BROWN BEE

LF Groeneveld, L Ruottinen, P Berg, J Kantanen, T Kristensen and A Præbel
Email: linn.groeneveld@nordgen.org

Apis mellifera mellifera, the Nordic brown bee, was the first honeybee subspecies to colonize the Northern European region and honey has been collected and consumed in this region for about 8000 years. The Nordic brown bee displays excellent characteristics, such as high winter hardiness, strong drive to collect pollen, high longevity of the worker bees and the queen, and flight strength even in cold weather. However, from a beekeeping perspective, some colonies have undesirable characteristics, such as showing a high swarming tendency, being runny on the comb, and being relatively aggressive and defensive. During the 20th century, *A. m. mellifera* thus has been introgressed or replaced by Southern European or synthetic subspecies, to the degree that it is currently endangered. Conservation of genetic diversity is imperative for maintaining the future adaptive potential of species and populations in general, and for obtaining products with potentially unique characteristics. In 2012, NordGen Farm Animals established an ad-hoc working group to clarify the current status of the Nordic brown bee in the Nordic and Baltic countries, as well as to summarize the current *in situ* and *ex situ* conservation of *A. m. mellifera* and to provide suggestions for future research activities and initiatives. One of the main results of this working group was that the Nordic brown bee suffers from a bad reputation within the beekeeping community. It is not clear which of the perceived negative characteristics are actually found across all *A. m. mellifera* populations and which of these unfavourable traits can be remedied by *A. m. mellifera*-specific management. Moreover, many populations have low effective population sizes, which may lead to inbreeding depression. Additionally, due to their sex determination mechanism, small populations of these haplodiploid bees are at a higher risk of extinction than comparable diploid populations. Genomic information from *A. m. mellifera* populations could help to a) detect populations with declining effective population sizes in need of introduction of new genetic material b) identify pure *A. m. mellifera* colonies for breeding purposes c) detect differential gene expression between healthy and parasitised colonies, which may be useful to predict the 'health' of a population d) identify the genetic basis of important production traits and e) identify selective sweeps and adaptation of different *A. m. mellifera* populations to various environments.

PRIORITIZATION OF LIVESTOCK GENETIC RESOURCES IN RELATION TO NEUTRAL AND SELECTED GENETIC VARIATION

SJG Hall

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Considerable effort has gone into calculation of genetic distances among livestock breeds but there is little or no evidence of this work having been used by policy makers for prioritization of breeds for conservation (Boettcher et al. 2010), though it has been widely used for creation of breed inventories. However, through elucidating breed histories these studies have contributed very significantly to an appreciation of the cultural significance of breeds. Genetic distances among cattle breeds, calculated from microsatellites and SNPs, are not necessarily correlated with phenotypic distances among them (Hall et al. 2012), so prioritization on the basis of genetic distances will not necessarily maximize retention of useful genetic variation. In practice, eligibility for inclusion of breeds in priority lists and their relative positions within these lists are usually determined by such factors as cultural significance, advocacy by interested parties, geographical concentration and numerical status. Nevertheless, genetic distances based on neutral variation are a measure of evolutionary history and should play a part in conservation decisions. One approach is to calculate an index of conservation significance by combining, for each candidate breed, the scores achieved on a set of indices (Ruane 2000) but a concern might be the dependence on "expert opinion" for the scoring process. A concept of "ecological exchangeability" coupled with a graphical method of deciding on resource allocation is proposed.

GENOME DIVERSITY OF LIVESTOCK: WHAT DOES IT MEAN FOR AFRICAN CATTLE?

O Hanotte and H Bahbahani
Email: Olivier.Hanotte@nottingham.ac.uk

African cattle are characterized by a unique display of phenotypic diversity; the result of centuries of human preferences and natural selection. Morphologically, they are classified as taurine, zebu and crossbreed, the latter being sometimes referred to as sanga. At the genetic level autosomal and Y chromosomes microsatellites and mtDNA studies have revealed a mosaic of pure taurine, taurine recently introgressed with zebu, and zebu anciently introgressed with taurine. Genome wide diversity analysis is now offering new insights on African cattle diversity. Through genome wide characterization of an East African Shorthorn Zebu population from western Kenya, this talk will illustrate the challenges of unravelling and understanding the genome 'make-up' of an African tropical cattle population. We will report diversity and signature of selection results from BovineSNP50, BovineHD BeadChips and high genome coverage re-sequencing data. We will then consider the implication of our findings for the conservation and utilisation of these unique indigenous livestock resources in the context of the 21st century challenges faced by the livestock production sector on African continent.

FROM LIVESTOCK TO CONSERVATION BREEDING AND BACK AGAIN

P Helsen

Email: Philippe.helsen@kmda.org

Although livestock and wildlife breeding seem to serve different goals, recently encouraging efforts have been made to narrow the gap between both. From the historical adoption of technical and/or analytical tools, collaborations nowadays seem to move towards a common interest in problems associated in conserving diversity in small populations, preventing them from extinction in the near future. Sharing characteristics with both livestock breeding (e.g. studbook based management) - and wildlife conservation (e.g. focus on non-domesticated species), ex-situ conservation in zoos seems to take a pivotal position in the conservation landscape. Notwithstanding the general success of some international breeding programs in retaining genetic diversity, zoo populations might turn out to be interesting showcases of how gradual loss of diversity, inbreeding –and outbreeding depression among others, interfere with the long-term viability. Are there things to be learned from research on these captive breeding programs? The rise of massive parallel sequencing on the other hand allowed more comprehensive studies on the genetic consequences of breeding species outside their natural range. Conservation genetics slowly shifted towards conservation genomics, redirecting the focus from neutral towards more adaptive/functional processes in what used to be non-model species. A central theme is whether and how populations adapt to new environments. Interestingly, genomics also infiltrates in our rational on how to preserve genetic diversity, reopening the debate on optimal breeding strategies. This talk focuses on our research on the nature and dynamics of genetic diversity in captive breeding, highlighting potential links to livestock breeding.

GENETIC CHARACTERIZATION OF "BENI AROUSS" GOAT IN MOROCCO USING MICROSATELLITE MARKERS

B Hilal, S El Otmani, M Ibnelbachyr, B Benjelloun, M Ben Bati, M Chentouf and I Boujenane
Email: hilalbtissam@gmail.com

Northern goat farmers prefer import foreign breeds or crossing local goats with imported, because these breeds are characterized by high performance. Unfortunately, these crossings are uncontrolled which may cause genetic erosion and extinction of local goat population. These local breeds are characterized by a good adaptation to harsh climatic conditions, and resistance to local pests and diseases. Therefore, the development of characterization, preservation and improvement program of local goats is necessary. "Beni Arouss" goat is an important local goat breed in the north of Morocco. This breed has to be preserved and characterized. In this context, this study aims to characterize the genetic diversity of "Beni Arouss" population in the objective to contribute to its preservation. To achieve this objective, the experiment was conducted on 60 genomics DNA samples of unrelated goat using 16 microsatellites markers selected from the list suggested by the FAO and ISAG for biodiversity studies. All of the 16 microsatellites were well amplified. In results, fourteen of the 16 markers used in this analysis had four or more alleles per locus. The observed number of alleles detected per locus ranged from 2-14 with an over mean of 8.13 ± 3.05 . The average of observed heterozygosity (H_o) and expected heterozygosity (H_e) values were respectively 0.59 and 0.93. Overall mean of H_o was lower than H_e . Within the population inbreeding estimate ($F_{is} = 0.36$). This positive value of loci showed a significant heterozygote deficiency in the "Beni Arouss" population. This heterozygote deficiency can be explained by some factors such as inbreeding, drift, selection, differentiation. In conclusion, there is a substantial genetic variation across the studied loci in "Beni Arouss" goat and the microsatellites markers were useful for the genetic characterization of this population.

A GLOBAL VIEW ON PRIORITIZING GENOMIC RESOURCES

I Hoffmann, P Boettcher and R Baumung
Email: Irene.Hoffmann@fao.org

Our present animal genetic resources (AnGR) diversity is the result of a combination of forces (e.g. domestication, migration and genetic isolation, environmental adaptation and selective breeding, introgression and admixture of subpopulations). The Global Plan of Action for AnGR is the international framework for the management of these resources. With 8% of breeds extinct and 22% at risk, conservation and priority setting for conservation are becoming important, although it is recognized that conservation of all at-risk breeds is impossible and may also not be scientifically justified. The presentation will describe how emerging molecular genetic methods help to unravel breed history and contribute to current decision making. It concludes that genomics can be a powerful tool in the management of AnGR, especially as abundance and precision of data will increase. However, prioritization for conservation relies on genomic and non-genomic methods and criteria. The gap in capacity in developing countries needs to be closed with continued and increased international collaboration and capacity building.

EFFECTS OF ISOLATION AND HUMAN-MEDIATED INTROGRESSION IN SHAPING THE GENOMIC DISTINCTIVENESS OF AN INSULAR LARGE MAMMAL

L. Iacolina, M Scandura, DJ Goedbloed, P Alexandri, RPMA Crooijmans, G Larson, A Archibald, M Apollonio, LB Schook, MAM Groenen and H-J Megens
Email: liacolina@uniss.it

The evolution of island populations in natural systems is driven by local adaptation and genetic drift. However humans can affect evolutionary pathways in several ways, especially in managed species. The wild boar (*Sus scrofa*) is an iconic game species and is highly managed throughout its distribution range, including islands where it was introduced in prehistoric times. We examined the current genomic diversity of the Sardinian wild boar population analysing the variation at 49,803 SNPs in 99 wild boars collected throughout the island and comparing them with 196 mainland wild specimens and 105 domestic pigs belonging to 11 breeds. The analysis of SNP data by Bayesian clustering approaches and Allele Frequency Spectrum Assessment revealed that the Sardinian wild boar population is highly differentiated from the other European populations ($F_{ST} = 0.126 - 0.138$), and from domestic pigs, including local free-ranging stocks ($F_{ST} = 0.169$). Signatures of introgression were investigated by different methods and detected in 6% of the Sardinian sample. The removal of these introgressed individuals changed only slightly the distinctiveness of the Sardinian population and its overall levels of genomic variation, part of which showed possible signs of local adaptation. The patterns of diversity emerging from our analyses suggest a long history of isolation and demographic stability of the population, followed by more recent admixture. This study confirms the usefulness of genome-wide genotyping in recognizing native versus exotic sources of genetic variation in wild populations and opens new perspectives towards the understanding of microevolutionary processes in managed species.

BIOGEOINFORMATICS OF LIVESTOCK GENOMIC RESOURCES

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In 2008, FAO and WAAP published a report on production environment descriptors for animal genetic resources. One of the main conclusions was that it was necessary to quickly systematize the recording of breeds' geographical coordinates worldwide in order to enable links to any kind of information available in other geo-referenced databases. Today we must recognize that this recommendation has hardly been applied and that even important projects on genomic resources did not take care of characterizing sampled animals with their precise location. Indeed, livestock conservation tasks require complementary data on population and evolutionary genetics, on animal husbandry practices, but also data characterizing the socio-economic and environmental conditions of the regions where animals are bred. Only the integration of these different information levels is likely to facilitate and optimize the processes used to establish priorities in the conservation of livestock genetic resources. In addition, in conjunction with molecular data the use of geographical coordinates enables the implementation of livestock landscape genomics to seek regions of the genome influencing the ability of animals to cope with environmental variations. This approach can be used to identify key traits involved in parasite resistance, to conserve the adaptive potential of local breeds, and even to increase adaptability in industrial breeds. In both cases computer science and biogeoinformatics have a more important role than ever. New knowledge will be extracted from the present data tsunami—constituted by the advent of high throughput molecular data, new sources of high resolution environmental data, new sources of socio-economic data, etc.—only if innovative, transdisciplinary and efficient computing tools are developed. But for biogeoinformatics can keep its promises, an important challenge for the livestock genomics resources community for the next decade remains to enforce the recording of geographical coordinates of any sampled animals as a standard rule.

SUBSAMPLING AS AN ECONOMIC CONSEQUENCE OF USING WHOLE GENOME SEQUENCE DATA IN LANDSCAPE GENOMICS: HOW TO MAXIMIZE ENVIRONMENTAL INFORMATION FROM A REDUCED NUMBER OF LOCATIONS?

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The recent availability of whole genome sequence (WGS) data implies to reconsider sampling strategies in landscape genomics for economic reasons. Indeed, while we had many individuals and few genetic markers ten years ago, we now face the contrary with high costs of WGS limiting the number of sequenced samples. In other words, molecular resolution is becoming excellent but it is achieved at the expense of spatial representativeness and statistic robustness. Therefore, when starting from a standard sampling, it is necessary to apply sub-sampling strategies in order to keep most of the environmental information. To study local adaptation of goats and sheep's breeds in Morocco, we used a sampling design based on a regular grid overlaid on the territory. In each cell of this grid, 3 individuals were sampled in 3 different farms. Then, the final subset destined to sequencing had to meet two criteria in order to ensure a regular cover of both environmental and physical spaces. The first was met by using stratified sampling techniques over a range of climatic variables, previously filtered using a PCA. The second was by minimising a clustering index in order to ensure spatial spread. The sub-sampling procedure using a hierarchical clustering resulted in two datasets of 162 goats selected over 1283, and 162 sheep over 1412 based on variables such as temperature, pluviometry and solar radiation. By maximising the environmental information collected, we were able to select individuals that are the most relevant to study adaptation.

CATTLE: MORE THAN TAURINE AND ZEBU

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Taurine (*Bos taurus*) and zebu (*Bos indicus*) are the most common cattle species with a combined head count of ca. 1.5 million animals. Taurine cattle are mostly found in the temperate regions. The characteristic appearance of zebu with a hump, dewlap, loose skin and shows the effective adaptation to hot and dry environments around the equator. Two Southeast-Asian domestic bovine species, Bali cattle (domestic banteng, *Bos javanicus*) and gayal (or mithan, *Bos frontalis*) are at least as well as the zebu adapted to tropical climates, but have a normal compact body conformation. With 4 million Bali cattle and 0.2 M gayals these are the minor domestic bovine species. We review the available evidence that these species, as well as the extinct kouprey (*Bos sauveli*) from Cambodja, have introgressed into zebu breeds from Indonesia, Southeast Asia and China. It is not yet clear if the banteng, gayal and zebu components are randomly distributed over the genome or if specific genes have been altered. The agricultural potential of Bali cattle and gayal to modulate the tropical adaptation of cattle has probably not been fully realized.

THE COALITION BETWEEN ITALIAN GOATS AND ITALIAN RESEARCHERS: THE ITALIAN GOAT CONSORTIUM

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The Italian Goat Consortium is formed by Italian researchers that, on top of seed funding provided by the Innovagen project financed by the Italian Ministry of Agriculture, contributed their time and a small amount of resources to characterise Italian goat breeds. Fifteen Italian goat breeds (Valdostana, Saanen, Orobica, Bionda dell'Adamello, Val Passiria, Grigia Ciociara, Teramana, Nicastrese, Aspromontana, Girgentana, Argentata dell'Etna, Sarda and Maltese sampled in Sardinia and Sicily) were genotyped using the Illumina SNP50 BeadChip medium density SNP array. Italian goats show a clear North South geographic pattern of diversity and a remarkable level of admixture, particularly along transhumance routes in Southern Italy. The diversity of neutral and adaptive genomes differs significantly and this has implication in marker based conservation strategies. The Italian Goat Consortium plan is to keep networking, expand collaborations by entering the Goat AdaptMap initiative and use in the near future improved SNP panels, less affected by ascertainment bias, and sequencing data to refine the genomic analysis of goats. Its main goal is to search for genes controlling the adaptation of this species to the very different environments of Alps and South Italy, hence making a lot out of a little.

A LANDSCAPE GENOMICS APPROACH TOWARDS IMPROVING PRODUCTION AND CONSERVATION OF THE UGANDAN DOMESTIC GOAT (GOATGEN)

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In Africa it is estimated that 70% of the rural poor keep goats and that some 200 million people rely on these animals for their livelihoods. Goats play an essential role in most agro-ecological production systems, showing how well they have adapted to the heterogeneous environments, surviving extreme conditions often under intense and diverse infection pressure. Indeed the goats are a source for meat, milk, pelts, have agricultural (e.g. fertilizer), economic, cultural and even religious roles since very early times in human civilization. Today, there are >1,000 goat breeds, and >830 million goats are kept around the world, of which Uganda contributes about 12.5 million. However, with the global trend of introducing high-yielding breeds, this diversity is threatened, and the rate of extinction seems to be on the rise. Twenty per cent of African livestock breeds are classified as at risk for extinction, and more than 50% are classified as of unknown status, indicating a huge knowledge gap. With this knowledge gap and the current rate of extinction, the risk is high that valuable goat are being lost, before their characteristics can be studied and their potential evaluated. The rapid developments in molecular genetics technology provide a matching counter to characterise the threatened genomic resources. This technology can be used in goat diversity assessment, production and conservation as is proposed in the GOATGEN project supported by the National Agricultural Research Organisation of Uganda.

PIG VARIOMICS: UNDERSTANDING THE WHEN, WHERE, AND WHY OF VARIATION IN THE GENOME OF *SUS SCROFA*

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Current developments in characterizing complex genomes cheaply and comprehensively, is redefining the study of origin (temporal and geographic) and selective advantages of variation. Since variation can now be studied at the sequence level, the geographic origin of haplotypes can be inferred on a genomic segment-by-segment basis. In addition, the selective advantage of haplotypes that have been introgressed from exotic populations can be determined. The pig is a good model to study such phenomena since the genomes of modern commercial pig breeds essentially are mosaics of two very distinct origins. These distinct origins, due to independent domestication on the Eastern and Western side of the Eurasian continent, have been merged in Europe in the past 250 years, and have given rise to modern commercial pig breeds. A comprehensive study, by which commercial pigs were compared to wild and various domesticated populations from Europe and East Asia, allowed for a genome-wide inference of geographic origin. Disentangling the Asian and European components, and performing demographic analyses on each of the geographic components separately, demonstrated that modern commercial pigs are indeed mosaics of highly distinct demographic origins. Association analyses for litter size and back fat further demonstrated the importance of the Asian component in shaping the modern phenotype. Our results suggest that selection increased the frequency of Asian-derived haplotypes in many regions in the genome. Introgression mapping is vital for understanding the distribution of variation in the genomes of many domesticated species. Furthermore, introgression mapping constitutes a powerful tool to dissect the genetic architecture of complex and economically important traits.

SLOW FOOD PRESIDIA ON RARE / TYPICAL BREEDS IN ITALY: VALUING OR CONSTRUCTING THE UNIQUE?

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In the last years the market for regional and typical food products has been characterised by many changes showing the rise of a new paradigm of consuming and offering. The goal of this presentation is to characterise the nature of these changes and the implications in terms of marketing strategies. The Slow Food experience in Italy is presented here as a best practice example of this process for its success in creating niche markets for typical products with highly sophisticated marketing techniques. This paper attempts to underline the characteristics of the product 'Evaluating' process and the techniques for 'Adding value' to the commercial goods generated by it.

UNVEILING HIDDEN TREASURES IN ZAMBIAN INDIGENOUS CATTLE (*BOS INDICUS*) USING 32 MICROSATELLITE MARKERS

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Selection has created a wide range of diverse breeds important for breeding and conservation programs. Yet, during the recent past, there has been concerns to losing this unique genetic diversity. Numerous studies have been conducted to assess genetic diversity in cattle, but this has not been undertaken in Zambia. Genetic diversity and population was assessed using genetic information from 32 microsatellite markers in 72 Zambian indigenous *Bos indicus* (Tonga, Tonga and Barotse) breeds. A total of 274 alleles (N_a) were detected and the Angoni and Barotse breeds exhibited a slightly excess average observed heterozygosity (1.0% and 0.9%) respectively, while the Tonga breed exhibited a slight deficit observed heterozygosity of 3.6%. The global heterozygosity deficit across all populations (F_{it}) was 4.2%, significantly different from zero ($p < 0.001$), because of observed inbreeding within breeds (F_{is}) was 1.0%. The breeds were only slightly genetic differentiation (F_{st}) was 3.2%, but still significantly different from zero ($p < 0.001$). Bayesian clustering shows that the three populations belonged to two genetic clusters ($K=2$) with some overlaps. High gene flow (11.3%) was evident between populations. Most of the results are in agreement with other studies; however, the results are quite preliminary and only indicative at best. Thus, analysis suffer from having a large dimension feature space compared to the sample size and should be viewed with caution. Nevertheless, the breeds have a large range of genetic diversity and offer valuable genetic resources with no apparent high level of inbreeding that is significant for genetic improvement and conservation programs in Zambia.

PCA-INFORMATIVE INDIVIDUALS FOR STRUCTURE IDENTIFICATION WITHIN POPULATIONS

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Existing methods can be successfully applied to ascertain key ancestors within populations. However, quantifying the role of each individual's contribution to population structure remains largely unresolved. Based on Principal Component Analysis (PCA), we present a novel approach to evaluate the genetic contribution of each individual within a population without use of ancestry information. Evaluating the method on three disparate datasets from sheep (1,430 individuals and 44,693 autosomal SNPs), horse (1,077 individuals and 38,124 autosomal SNPs) and cattle (59 individuals and 38,124 autosomal SNPs) populations, we demonstrate that this approach effectively evaluates the genetic contribution of each individual, simultaneously detecting high and less influential individuals within populations. Analyzing the sheep and horse dataset we successfully allocated most influential individuals within the populations, whilst in cattle we applied the method to investigate differences in ancestry and sample origin. Furthermore, we show that combined with a redundancy removal approach, PCA informative individuals can be successfully used to select a reference population that facilitates most accurate genotype imputation. Compared to common applied analyses, our approach, although unsupervised, achieved similar results. Application of this method to the analysis of population structures opens new perspectives in the characterization and sustainment of populations in general, particular in areas such as selective animal breeding and conservation genetics, where assessing the contribution of individuals to population structure is crucial for research and management applications.

DEVELOPMENT OF APPROACHES TO COMPARE AND INTEGRATE TECHNOLOGIES

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In the last few years, the availability of genomic data in livestock species has grown exponentially. Nowadays, researchers are asked to deal with large genomic datasets coming from many sources and produced with different technologies on a daily basis, and will soon be (if are not already) called to evaluate, integrate and compare these technologies. This poses several complex technical and practical problems, often underestimated, that need to be completely understood, and solved, before accessing the data, such as: i) the use of different genotype formats (e.g. row, vcf or vcf-like, matrix, plink, Affymetrix, etc) and allele-strand coding systems (e.g. Forward/Reverse, Top/Bottom, A/B) used by the genotyping platforms; ii) the lack of a standard for the exchange of genotypic and genotype-related data; iii) the presence of different reference genome assemblies in public databases; iv) the fragmentation of the sources of information and the difficulty to have access to them in short time. Recently, we developed a couple of tools (SNPchimp v.2 and AffyPipe) to address many of these problems. Real-case scenarios have shown the utility of such tools in handling genomic data efficiently. Further efforts are currently being undertaken to extend these services to even more species, data types and to build a centralized network of information able to connect commercial genotyping companies and final users.

SIGNATURES OF SELECTION IN LARGE DATASETS

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Collecting large genetic datasets (i.e. in terms of the number of organisms sampled and the extent of their genome studied) is becoming easier and cheaper with time. Consequently, small and medium laboratories are becoming able to collect data for millions of single nucleotide polymorphism (SNPs) using arrays that broadly cover the majority of their genome at regular intervals, and, alternatively, whole genome data at various coverage levels. This data is largely suitable for carrying out analyses of population demographic history, and depending on the nature of the data, it is also possible to identify signatures of natural and artificial selection in the data. One of the most interesting questions in biology is how species/populations adapt to the environment they live in and what is the balance between natural and artificial selection for this process in livestock. This talk will give an overview of approaches to detect the signature of selection in large scale data with an example on their application to the data collected by the NextGen consortium.

ESTIMATING THE POTENTIAL OF WILD RELATIVES AND INDIGENOUS BREEDS TO ACT AS GENOMIC RESOURCES: THE CASE OF SHEEP AND GOATS

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The short-term need for improving the economic value of livestock has promoted industrial breeds while the value of maintaining traditional and wild genetic resources still remains difficult to assess. Nevertheless locally adapted populations would constitute a primordial reservoir of genomic variation. In this context, the NEXTGEN project (EU-FP7) proposed a comparative analysis of whole genome data to optimise genetic management of farm animal diversity. Whole Genomes Sequences (WGS) at 10x coverage were produced for about 200 sheep (*Ovis aries*) and 200 goats (*Capra hircus*) mainly from traditional breeds, and with representatives of their wild ancestors (the Bezoar *Capra aegagrus* and the Asiatic mouflon *Ovis orientalis*). Based on these data, I will first address the key question of the genotyping strategy to choose for describing the diversity of indigenous breeds or wild populations. I will present how the choice of SNPs (including exome and SNP panels composing commercial DNA-chips) affects the bias and precision of estimates of genetic diversity and the ability to detect signatures of selection. Then I will show that a panel of randomly chosen SNPs can be designed as a surrogate of whole genome data to accurately approximate genomic diversity and whole genome processes in both indigenous and industrial breeds. Second, I will present preliminary analyses on neutral diversity to estimate the potential of wild populations and traditional breeds to act as Farm Animal Genetic Resources. Finally, I will discuss the way to take into account both neutral and adaptive variability to define conservation priorities.

LOCAL BREEDS IN GLOBAL MARKETS – EXPLOITING CONSUMER PREFERENCES FOR LOCAL AND REGIONAL SPECIALTIES

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In globalized markets, consumers recognize the importance of food product authenticity and their relation to food products. This desire is expressed in a demand in “natural” products, “authentic products”, “storytelling” and regional relationships. This presentation will review some of the relevant concepts from consumer research and food marketing that can help to understand how the preference for local food and regional specialties can be understood and leveraged in the marketing of products from local breeds. Exploring some of consumers' motivations related to production technology such as food technology neophobia and consumer preference such as consumer ethnocentrism the presentation will explore the literature on consumer willingness to pay for local breeds and implications for marketing arrangements.

GENOMIC TOOLS FOR DETECTING INDIVIDUALS WITH GREATER ABILITY TO FACE PATHOGENS AND OTHER EXTERNAL AGGRESSIONS

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The stress generated by the adaptation of animals to the changing conditions of their ecosystem prompted by the global climate change, along with the progressive restriction on the use of drugs in animal production systems, has given rise research in alternative methods to prevent diseases on farms. A strategy to improve general immunity may be to select individuals with the best immune function. In this study, non-infectious challenges with phytohemagglutinin (PHA) and sheep red blood cells allowed the classification of red-legged partridges (*Alectoris rufa*) according to their overall innate and acquired immune responses (IR). Skin from the area of injection of PHA and spleen, both from animals showing extreme high and low IR, were selected to investigate the transcriptional profiles underlying the different ability to cope with pathogens and external aggressions. RNA-seq yielded 97 million raw reads from eight sequencing libraries and about 84% of the processed reads were mapped to the reference chicken genome. Differential expression analysis identified 1488 up- and 108 down-regulated loci in individuals with high IR versus low IR. Gene ontology enrichment analysis of high IR annotated genes revealed that cellular proliferation and, T and B cell signaling pathways were the most highly enriched processes. Alternative splicing of 24 loci and differences in promoter switching of other 24 loci were also found between high and low IR. These preliminary findings indicate that the immune system's ability to respond to environmental aggressions extensively involved transcriptional and post-transcriptional regulations, and expand our understanding on the molecular mechanisms of the avian immunity system.

TRYPANOSOMOSIS: CONSERVATION OF TOLERANCE IN AFRICAN CATTLE

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Trypanosomosis is a serious health problem for cattle in tsetse challenged areas of Africa. A study done on 214 animals, 90 Baoule, 90 Zebu and 34 composite animals and 155 SNP in candidate regions responsible for trypanotolerance and 25 microsatellites across the genome gave result of average Baoule admixture across genomes of the Baoule-Zebu composites of 0.31, and in trypanosomosis candidate regions, 0.37 ($P=0.15$). Fixation index F_{ST} measured overall genome or with SNPs from candidate regions indicates strong differentiation between breeds. Nine of 23 regions had $F_{ST} \geq 0.20$ calculated from haplotypes or individual SNPs. Levels of admixture were significantly different from background admixture as revealed by microsatellite data for 6 of these 9 regions. All except one of these regions showed an excess of Baoule ancestry. The comparison of ancestries for specific regions shows promise for identifying regions under natural and artificial selection. Power of the analysis will be boosted with high density SNP information of 90 animals (30 Zebu, 30 Baoule and 30 crosses). Furthermore in case that in the candidate regions we don't find Baoule ancestry excess, information of age of admixture for these crosses can give us valuable information about time needed for adaptation. Intention of the research is to better understand complex inheritance of trypanotolerance. Information about best levels of breed composition will be useful for future breeding activities, aiming at trypanotolerant animals with higher productive capacity.

**NEXT-GENERATION POPULATION GENOMICS OF NATIVE AND AQUACULTURED
MEDITERRANEAN MUSSEL, MYTILUS GALLOPROVINCIALIS**

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During the last decade, European aquaculture production of *Mytilus* sp. mussels has steadily grown, becoming one of the most important maricultures. Knowledge concerning native and cultivated mussel populations' genomics can provide insight into adaptation of mussels to numerous environmental variables and fitness-genotype interactions, which could help increase mussel production yield. Aquaculture regimes alter environmental variables creating new selective pressures acting upon exposed populations, which can lead to yet unknown genomic responses. Moreover, due to high connectivity of marine ecosystems and long-lived pelagic larvae, gene flow between natural and cultivated mussel populations can be high, making their genomic backgrounds inseparably entangled. Thus, population genomic studies of adaptation and gene flow in mussels are needed to guarantee long-term sustainable management of natural and farmed populations. In this regard, reduced costs of next-generation sequencing (NGS) have made genotyping by sequencing (GBS) a tool of choice to investigate genome-wide patterns in non-model species. We applied and optimized GBS to the genome of 283 *Mytilus galloprovincialis* individuals from 14 populations thereby adding a new species in the livestock genomics arena. Preliminary analyses based on over 100,000 single nucleotide polymorphisms (SNPs) revealed genomic structuring of native populations but this structuring was not concordant with isolation by distance. These intriguing results suggest adaptive processes could be shaping the genomic patterns of mussel populations. Further genomic analyses and transplant experiments aimed to define specific interactions between mussels' fitness, phenotype, genotype and environment are under way.

A HIGH QUALITY RESEQUENCING ANALYSIS PIPELINE FOR THE NEXTGEN PROJECT LIVESTOCK DATA

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NextGen is an international collaborative project using whole genome sequencing data to investigate livestock species. Its principal aim is to optimize present and future breeding options of farm animals that maximize genetic progress while preserving biodiversity. NextGen produced sequencing data and variation data on a prodigious scale for a livestock genomics project. Challenges arose in developing a pipeline for processing the NextGen data, because of the varying quality of livestock reference genomes and reference data sets of known variation (compared to model organism reference data). A standard pipeline for processing resequencing data involves aligning short reads to a reference genome, calling variants and genotypes from the aligned reads, and then filtering out potential false positive calls. Filtering procedures can be complex and involve statistical modelling (e.g. VQSR). NextGen used this standard pipeline as a base model, but with adaptations to produce results of the highest possible quality without requiring high quality reference resources.

RIDING THE WHOLE-GENOME DATA TSUNAMI: A LANDSCAPE GENOMIC STUDY OF LOCAL ADAPTATION IN MOROCCAN SHEEP AND GOATS

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In Morocco, like in other developing countries, small ruminants play an important role in the livelihood of a large proportion of farmers and landless shepherds. Conserving traditional breeds is essential in these countries since they are able to prosper in challenging habitats and their rich genomic resources allow them to adapt to new conditions. Therefore the key genetic features of local adaptation must be identified, notably with landscape genomic approaches, in order to support and encourage sustainable breeding of low-input livestock. To this end, the NEXTGEN project led an extended sampling campaign of local small ruminants to study local adaptation in Morocco. Over 2000 sheep and goats were sampled in small farms and flocks spread over the whole country. For each species, 164 samples were selected in order to reliably represent the environmental conditions while having an even spatial distribution. A landscape genomic approach was applied to detect selection signatures among 28 million SNPs in sheep and 19 million SNPs in goats. In summary, the habitat of each sample is characterised with environmental variables and significant genotype/environment associations point out the loci potentially under selection. Data were processed with SamBada, a specific landscape genomic software program. Preliminary results show that the method is able to process whole-genome sequence data. However the relatively low number of samples compared with the number of SNPs implies the existence of false positives among the most significant results. Measuring the spatial dependence between samples, as featured in SamBada, may facilitate their detection and interpretation. Thus combining whole-genome analysis with spatial statistics may lead to an integrated biogeoinformatic approach to study local adaptation.

INFERRING EVOLUTIONARY HISTORIES FROM GENETIC DATA

D Wegmann

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Genomic resources are becoming available at an unprecedented scale, mostly as a result of efforts to discover the genetic bases of morphological traits. However, such resources also offer the exciting opportunity to study the evolutionary histories of a wide array of species and to answer questions such as where and when a species was domesticated and to infer the genes that were targeted by selection during domestication. The goal of my talk will be to illustrate some of the more recent inference techniques applicable to genomic data sets and complex models. Specifically, I will focus on two numerical approaches: a composite likelihood approach and Approximate Bayesian Computation (ABC), an approximate technique to side-step analytical likelihood evaluations by means of simulations. I will then illustrate the potential of these methods through applications to the estimation of mutation rates from human data and the characterization of the divergence between two related rose finch species.

RECONSTRUCTION OF A CONTINUOUS DEMOGRAPHIC HISTORY OF GIANT PANDAS BASED ON GENOME DATA

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The evolutionary history of the panda lineage dates back 7~8 million years ago, and ultimately leads to only one extant species, the giant panda (*Ailuropoda melanoleuca*). The pandas have thrived for millions of years, but now face a high risk of extinction. Although global climate change and anthropogenic disturbances are recognized to shape animal population demography, their contribution to panda population dynamics remains largely unknown. We sequenced the whole genomes of 34 pandas and used this data set together with the previously deep-sequenced reference panda genome to reconstruct a continuous demographic history of pandas from their origin to the present. We identify two population expansions, two bottlenecks and two divergences. Evidence indicated that, whereas global changes in climate were the primary drivers of population fluctuation for millions of years, human activities likely underlie recent population divergence and serious decline. For the current six populations, we identified three genetic populations. The panda populations with distinct genetic compositions need specific conservation measures; however, there is one key element in common: the need to eliminate negative anthropogenic activities which pandas have suffered for 3,000 years.

ABSTRACTS – POSTER PRESENTATIONS

(Ordered alphabetically by surname)

CHARACTERIZATION OF INDIGENOUS POPULATIONS OF MOROCCAN GOATS (*CAPRA HIRCUS*) USING WGS DATA

F Alberto, B Benjelloun, I Streeter, F Boyer, E Coissac, MB Bati, M Ibbelbachyr, M Chentouf, A Bechchari, A Alberti, S Engelen, A Stella, A Chikhi, L Clarke, P Taberlet and F Pompanon

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Since their domestication more than 10.000 years ago, goats have been managed for different purposes leading to a large variety of locally adapted populations in response to different human and environmental pressures. These local populations are threatened of extinction due to their substitution by industrial breeds and climate changes, while they have a high potential to act as farm animal genomic resources. It is thus crucial to characterize local populations in terms of both neutral and adaptive genetic resources. Identifying adaptive alleles related to contrasted environmental conditions would be highly valuable, and keeping a reservoir of neutral diversity could help facing new environmental conditions. The recent progress of sequencing technologies making the Whole Genome diversity accessible has opened new perspectives for the characterization of indigenous breeds/populations. In this study, we characterized the genome (Whole Genome Sequences at 10X coverage) of 161 indigenous goats (*Capra hircus*) widely spread over Morocco. Among them, 68 belonged to 3 distinct phenotypic groups corresponding to local populations, while the others presented intermediate phenotypes. We characterized the neutral variations to evaluate the level of genetic diversity present in Morocco and to characterize the genetic structure of populations. Additionally, we used genome scan approaches to identify potential regions differentially selected among these local populations.

ALENTEJANO PIG: ONE IMPORTANT PIECE OF THE PUZZLE TO UNCOVER THE GENETIC BASIS OF LIPOGENESIS

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In contrast to commercial pig breeds, Iberian pigs (of which Alentejano is a branch raised in southern Portugal) are characterized by producing high-quality meat, and consequently pork products, which are highly valued by consumers. This is largely due to the inherent ability of Iberian pigs to deposit intra-muscular and subcutaneous fat, especially when they are finished on pasture and acorn, producing carcasses with a high proportion of oleic fatty acid (>53%), which is of high nutritional value for the human diet. This inherent ability must have a genetic background, which is not well understood, and is highly dependent on several environmental factors, the major one being the availability of acorns in the finishing diet. In ruminants, changes in fatty acid profiles in response to different finishing diets differ among cattle genetic groups and genetic polymorphisms have been described in loci regulating enzymes involved in lipid metabolism. However, to our knowledge, the information available for pigs is more limited, and no specific mutations have been associated with fatty acid profiles, even though previous research using a QTL approach indicates that genetic variability, especially in some regions of chromosome 4, may be related with lipid metabolism. In our presentation we will present the experimental design and expected outcome of our study that aims to uncover the genetic basis of differences in meat quality and ability to produce intra-muscular fat between Alentejano and commercial pigs based in genome- wide approaches and measuring a wide range of performance traits and biochemical parameters.

AN ANALYSIS PIPELINE TO DETECT SIGNATURES OF SELECTION USING CROSS POPULATION EXTENDED HAPLOTYPE HOMOZYGOSITY (XP-EHH)

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Numerous methods have been developed to identify selection signature caused by recent adaptation. These methods have been extensively applied to livestock SNP-Chip data to identify genomic regions related with traits of interest. These methods can be divided in three classes: frequency based, population-differentiation based and linkage disequilibrium based. Several methods that rely on the latter have been implemented so far: EHH, iHS and XP-EHH. The latter index has been used broadly, alone or in association with other indices to identify signatures of selection between pairs of populations. The statistical significance of this test is usually obtained calculating genome-wide normalised Z-scores and by defining an *ad hoc* significance threshold value of 2. This might lead to arbitrary exclusion of low signals due to the genome-wide score distribution but might be meaningful region-wise. To understand if the occurrence of a “selection” signal is merely due to chance or potentially represents true positive results we produced 10,000 permutations of the two populations tested and compared the distribution at each SNP position with the results obtained analysing the original ones. The method was applied to Sardinian sheep (*Ovis aries*) 50k SNP-Chip data. The results obtained showed that the permutation approach tends to confirm the most significant signals obtained by Z-score normalization, but is also able to pick up SNPs close to a region under selection not identified by the previous method.

GENOMIC DIVERSITY AND POPULATION STRUCTURE ANALYSIS OF UGANDAN CATTLE BY MEANS OF MEDIUM AND HIGH DENSITY SNP PANELS

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To identify possible associations between genotypes and resistance to endemic livestock diseases, an extensive sampling of local Ugandan cattle was carried out over the whole country: a total of 915 animals, representative of the Ankole breed group (crossbred between *Bos indicus* and *Bos taurus*), Zebu and Ankole-Zebu crosses, were sampled and genotyped with the Medium (Illumina BovineSNP50 BeadChip, about 54K SNPs; sample size = 815 animals) and High-Density (BovineHD Genotyping BeadChip, about 800K SNPs; sample size = 102 animals) SNP chips. The 54K data were compared to SNP data from 22 breeds representative of African and European *B. taurus* and *B. indicus* characterized in the course of the Bovine HapMap project, while 800K data for Ugandan cattle were analysed separately as an independent test. The software Admixture (Alexander et al., 2009. *Genome Res.*, 19: 1655-1664) was used to investigate the population structure through a Bayesian clustering procedure. The population structure of Ugandan cattle was consistent across the 54K and 800K datasets resolutions and highlighted the presence of two major genomic components, generally corresponding to Ankole and Zebu breed groups. These clusters were also geographically structured, with indicine genomes being prevalent in N-E and taurine genomes in S-W Uganda. Two sub-clusters within the indicine component were revealed, suggesting a contribution from distinct ancestral zebu populations introduced from Asia in different historical times. A few Ugandan cattle genotypes also clustered into some minor genomic components, whose origin could not be traced back to any of the HapMap reference breeds.

PATTERNS OF GENOMIC INBREEDING IN WORLDWIDE SHEEP POPULATIONS

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Inbreeding is a fundamental parameter in conservation genetics of any small population as its increase results in the reduction of effective population size, increase in frequency of deleterious alleles and the concomitant inbreeding depression of fitness and fertility. We have inferred levels of inbreeding in 77 sheep populations (2938 individuals) from different continents, using individual runs of homozygosity (ROH) estimates of 4, 8 and 16 Mb in 47502 autosomal SNPs and expressed as the coefficients FROH>4Mb, FROH>8Mb and FROH>16Mb. Inbreeding level estimates ranged from 0.005 (Rasa Aragonesa) to 0.309 (MacArthur Merino) for FROH>4Mb (average 0.07), from 0.002 (Rasa Aragonesa) to 0.202 (MacArthur Merino) for FROH>8Mb (average 0.047) and from 0.001 (Rasa Aragonesa) to 0.090 (Wiltshire) for FROH>16Mb (average 0.025). Pearson correlations among inbreeding levels ranged from 0.877 (FROH>4Mb : FROH>16Mb) to 0.974 (FROH>4Mb : FROH>8Mb). Negative Pearson correlations between allele richness/observed heterozygosity were -0.746/-0.823 for FROH>4Mb, but lower for longer ROHs (-0.533/-0.688 for FROH>16Mb). The results presented provide the first global insight on the genomic inbreeding levels in various sheep populations.

CONSERVATION OF SAHIWAL CATTLE IN PAKISTAN -THREATS, CHALLENGES AND PROSPECTS

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Diverse wealth of livestock genetic resources are playing lead role in economy and prosperity of the Pakistan. Country inhabits large number of unique livestock breeds well adapted to diverse agro-climatic conditions. Sahiwal is the main dairy cattle breed of Pakistan with a population of more than two millions. It is well known internationally for its heat and tick resistance abilities which makes it ideal dairy animal under tropical environments. Due to potential of its functional abilities and cultural importance it is often called as “Red Gold of Pakistan”. Unfortunately, different external pressures are threatening the breed. Chief threats include competition from exotic breeds like Holsteins either following breed replacement or crossbreeding. Poor performance recording in private herds, where most of the population is present, undervaluing the potential of breed and impacting breed improvement program. There is an increasing trend of inbreeding levels in institutional herds and deterioration in phenotypic and genetic ability in most of the economical traits is alarming. Inception of “Research Centre for Conservation of Sahiwal Cattle (RCCSC)” has stimulated the public awareness about breed’s potential by conducting national milk and beauty competitions. Registration of breeding cows and provision of free artificial insemination facility by this centre is also contributing towards propagation of the breed. Establishment of “Red Gold Club” is another good step to involve farmers through Sahiwal Cattle Breeder’s Society. This paper reviews status and prospects of conservation efforts for Sahiwal breed in Pakistan while analyzing various threats and challenges.

IDENTIFICATION AND CHARACTERIZATION OF ANAEROBIC GUT FUNGI USING MOLECULAR METHODOLOGIES BASED ON ITS1

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The purpose of this study was to investigate the phylogenetic diversity of anaerobic fungi in the digestive tract of ruminants such as cattle, sheep and buffalo native province of Mazandaran and Lorestan (Iran), using a molecular method of polymerase chain reaction. Subjects including ITS1 sequences from anaerobic fungi in the digestive portion of the large intestine of sheep, cattle and buffalo were extracted. Sequences used in this study was Internal Transcribed Spacer Region-1 (ITS1) used as a phylogenetic marker, 10 sequences in the phylogenetic study were between 378 to 477 nucleotides in length, In this study, the most frequent species found *Anaeromyces Sp* and the minimum frequency of the *Orpinomyces Sp*. Distinguish between groups of anaerobic fungi in digestive tract using conventional techniques is difficult, costly and time-consuming. In this study methods based on molecular and genetic material was used for this purpose, In order to compare the reproducibility between different types of relationships that anaerobic fungi were collected from different geographical locations, to be conducted. Due to the effects of feeding on rumen biochemical conditions, samples were taken from the distal portion of the gastrointestinal tract. Most Gut ruminant microorganisms can not be cultured or may not reproduce, *in vitro* thus sampling was used directly from the gastrointestinal tract.

GENETIC POLYMORPHISMS OF CAPRINE STEAROYL-COA DESATURASE (SCD) GENE AND IT'S RELATIONSHIP WITH CHOLESTEROL LEVEL IN SOUTHERN THAILAND

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The present study attempts to study the effect of genetic polymorphisms of stearoyl-coA desaturase (SCD) gene on cholesterol level in meat goat at a commercial goat farm in Thailand. Genetic variability in caprine SCD, analyzing 290 animals belonging to several types of Boer, Thai native, Anglo-nubian and Saanen breed fractions were detected by single strand conformation polymorphism and DNA sequencing. Four single nucleotide polymorphisms were identified in exon 3 (601A→G; Ref. AF422168), exon 5 (878C→T; AF422170), exon 6 (690A→G, 718C→G and 802A→C; Ref. AF422171) and 3'untranslated region (UTR) (TGT deletion). Conformational patterns of SCD gene were classified into 2 genotypes in exon 3, exon 5 and 3'UTR and 3 genotypes in exon 6. Five haplotypes were constructed but only the lowest frequency of a haplotype C was not included in the dataset. The haplotypes of SCD gene were also significantly correlated with plasma cholesterol level ($P < 0.01$) by χ^2 test. The results suggested a possible use of the SCD locus in gene assisted selection programs for healthy improvement in this meat goat population.

CRB-ANIM: A NETWORK OF BIOLOGICAL RESSOURCES CENTERS FOR GENOMIC AND REPRODUCTIVE MATERIALS OF DOMESTIC ANIMALS

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Biobanks play a key role for present day animal genomics. They are needed for the development of breeding programmes, for the *ex situ* preservation of biodiversity, and for the restauration of extinct or depopulated breeds. Moreover, they are a basic tool for the understanding of the relationships between genotype and phenotype. In the aftermath of the Convention on Biological Diversity signed in Rio de Janeiro in 1992, several Biological Resources Centers (BRCs) focusing on domestic animals were developed in France. They belong to two main categories, namely (a) cryobanks, for reproductive materials and (b) repositories specialized on the storage of tissues and genomic samples. Within this context, the French government is supporting an ambitious program called 'CRB-Anim', (2012-2019) to set up a network of BRCs dedicated to reproductive and genomic material of domestic animals, either farmed or pets. At present, the network stores about 530,000 biological samples (i.e. semen, embryos, tissues, nucleic acids) for 22 different species. Several public institutions, one research foundation, technical institutes and private partners have started to share their know-how, to develop common practices, to better characterize and document their materials. Regarding genomic BRCs, one of the most important issues is to maintain the integrity of the specimens to the highest possible standards, in order to ensure the validity of the data generated by the downstream analysis. Several quality control (QC) metrics are being now implemented. It is planned to set up a web portal for users to submit their requests for samples or services.

Livestock Genomic Resources in a Changing World Conference

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