



Research Networking Programmes

Science Meeting – Scientific Report

The scientific report (WORD or PDF file - maximum of seven A4 pages) should be submitted online within two months of the event. It will be published on the ESF website.

Proposal Title: Livestock Genomic Resources in a Changing World

Application Reference N°: Science Meeting 5482



Livestock Genomic Resources in a Changing World

June 17th-19th, 2014
Cardiff University
School of Biosciences



1) Summary (up to one page)

Livestock conservation practice is changing rapidly in light of policy developments, climate change and diversifying market demands. The last decade has seen a step change in technology and analytical approaches available to define, manage and conserve Farm Animal Genetic Resources (FAnGR). However, these rapid changes pose challenges for FAnGR conservation in terms of technological continuity, analytical capacity and integrative methodologies needed to fully exploit the new, multidimensional data. The final conference of the ESF Genomic Resources program aimed to address these interdisciplinary problems in an attempt not only to provide a legacy from which an accurate description of the state-of-the-art in FAnGR conservation can be made available, but also to set the agenda for future research and policy development directions leading up to the end of the present decade. By this time, according to the Convention on Biodiversity's Aichi Target 13, signatories should ensure that *"..the genetic diversity of ... farmed and domesticated animals and of wild relatives... is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity."* This challenging target demands a fuller and more efficient utilization of the tsunami of genomic and environmental data that have been produced during the last decade and, importantly, the development of optimized ways to integrate these data with the social sciences and policy analysis to enable more flexible, evidence-based models to underpin future actions aimed at better conserving FAnGR in a rapidly changing world. This background motivated the conference described here, which was 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.

The conference spanned a 2½ day period and was the final workshop organised on behalf of the Genomic-Resources program. Forty-seven scientists attended, representing 15 countries, 14 of whom were previous recipients of Genomic-Resources training bursaries. Thirty-two oral presentations and seven posters were contributed: some accepted contributions could not be presented because the authors could not gain entry visas for the UK. The meeting was divided into four half-day Symposia and one workshop. The first Symposium was oriented to producing a horizon-spanning document on important questions for the conservation of genomic resources for the coming decade and was thus deliberately broad and integrative. The second focused on prioritisation of livestock populations for conservation, examining progress during the last decade and what likely gains will be made in the future. The third symposium focused on minority and 'genomically-neglected' livestock breeds and species and examined the state of the art in these regionally important resources. The final symposium focused on addressing the challenges of the genomics data 'tsunami' and on how to abstract biologically significant data from vast genomic datasets. On the final morning, a workshop was convened to further develop the horizon-scanning exercise signposted on the first day, with working groups examining important questions in the areas of livestock conservation and prioritisation, bioinformatics challenges, molecular tools and statistical analysis of molecular data. A list of important questions was produced by each group, which are currently being synthesised with the aim to submit a paper for the *Frontiers in Genetics* special issue on Genomics Resources by the end of September 2014.

2) Description of the scientific content of and discussions at the event (up to four pages)

The first morning of the event was devoted to a diverse range of papers aimed at spanning the field of livestock genomic resources, offering perspectives on the current state-of-the-art and providing the raw material for discussion on the final day and for the publication that will result. The meeting had an **integrative activity** at its core, taking the form of a horizon-scanning exercise to identify the most important new questions that need to be answered in conserving farm animal genomic resources for the next decade, involving geneticists, social scientists, geospatial modelers and policy developers. The first session of the meeting was therefore devoted to establishing this exercise with a series of agenda-setting talks, but continued for the three days (via a board with post-it notes and informal discussion sessions at the end of each day) and culminated in a plenary session at the end of the meeting (see below). A publication is currently being produced similar to those produced for wild biodiversity conservation by WJ Sutherland and colleagues (these are produced on an almost annual basis) and was a joint task for all delegates of the meeting, who will all be authors on the paper. This first activity was designed to elicit an 'esprit de corps' for the meeting, giving it a unique flavour.

The Symposium was therefore entitled: **Horizon Scanning important questions and challenges for livestock genomics resources for the next decade**. Four invited speakers presented presentations on subjects ranging from pure 'omics (pig variomics; **Dr Hendrik-Jan Megens**, Wageningen University), through 'omics consortium-building and the anatomy of a large-scale collaborative project (Italian goats; **Professor Paolo Ajmone-Marsan**, Catholic University of the Sacred Heart, Piacenza), the use of geospatial architecture to understand 'omics and conservation in livestock (**Dr Stephane Joost**, EPFL, Lausanne) and the role of local breeds and consumer choice in animal product markets across the EU (**Professor Jutta Roosen**, Technical University of Munich). These diverse talks aimed to cover most of the research domain of the Genomic-Resources program and set the scene nicely for the rest of the meeting. After this Symposium there was a free session devoted to contributed papers, covering areas such as inbreeding, decision-making tools for monitoring genomic resources, and captive breeding (see program).

The second Symposium, entitled **Beyond Weitzmann: prioritizing genomic resources using genomic data**, focused on using a mixture of case studies and theoretical discussion on the use of genetic and genomic data to assist prioritization efforts for conserving livestock breeds and populations. Following the most recent review of these approaches by Boettcher et al (2010), Hall et al (2011) pointed out that for cattle at least, conserving populations and /or breeds based neutral genetic data alone risks eliminating important selected variants and there is almost has been almost no recent discussion on other indicators of viability that could be used that are not genetic or demographic. The aim of this symposium, therefore, is to first ask whether there are better ways to use genome data that comprise both neutral and adaptive genetic variants, to assist this prioritisation process and if so, how might this best be achieved and integrated with other measures of livestock viability? For instance, what balance needs to be struck between these two types of diversity, how conditional might a weighting scheme be, based on the perceived economic or cultural importance of the selected traits, the strength of selection signature and landscape correlates? These issues need to be clarified going forward to 2020. We were fortunate enough to be able to have **Dr Irene Hoffmann** of the UN's Food and Agriculture Organisation (Rome), where she is Head of the Animal Genetic Resources branch, to provide a necessary global perspective on animal genetic resources conservation and prioritisation as our keynote lecture in this Symposium. Secondly, we had **Professor Stephen Hall** (University of Lincoln), one of the key recent authors in this area, to talk about the integration of selected traits into

conservation prioritization and finally **Dr Catarina Ginja**, of the University of Lisbon, gave a talk on the best recent example of the application of genetic approaches to regional livestock prioritisation, focusing on Iberian cattle and their creole descendents.

The Symposium was followed by a free session with contributed talks from a number of ESF bursary recipients and others on topics as diverse as the use of principle components analysis and genetic structure approaches to manage Swiss horse breeds to a description of the first major population genomics study of a non-model wild mammal – the giant panda, and what challenges such analysis poses to livestock studies. Immediately after this session there was a poster session, giving ample time given for further discussion around the posters and around production of ideas for the Horizon scanning exercise. Discussion was lively and lengthy and went on until dinner, which was served close to the conference centre.

The third Symposium, entitled **Genetic Resources in Minority Livestock Breeds and Species**, dealt with genomic resources for minority domestic animal species and their wild relatives. Much data exist for major livestock species and its public fraction has been well disseminated and catalogued through meetings dedicated to livestock genomics and online databases. However, genomic resources for minority domestic species such as those which inhabit tropical ecosystems and wild relatives such as alpaca, rabbit, water buffalo and even turkey, are few because genomic efforts for some of these species has been limited, and they lack the wide integration through common resources that major livestock species have available. This symposium brought together specialists on minority domestic animals in order to help i) census the genomic and other relevant conservation data already available and in production, ii) define common issues limiting the uptake of conservation programs across species, and iii) translate or refine approaches implemented in common livestock.

The Symposium was kicked off by **Professor Olivier Hanotte** (University of Nottingham), who discussed management strategies needed for maintaining genomic diversity in sub-Saharan African cattle breeds. This talk was followed by **Dr Hans Lenstra** (Utrecht University), who talked about genomic resources in south-east Asian wild and domestic cattle, their evolutionary origins, current status and hybridization threats. This talk was followed by **Professor Mike Bruford** (Cardiff University), who discussed genomic conservation in domestic South American camelids and their wild relatives (alpaca, llama, vicuna and guanaco). This was delivered within the context of extensive hybridization between the two domestic forms and its impact on fleece/wool quality. Next **Dr Francois Pompanon** (Joseph Fourier University, Grenoble) discussed the recent results of the EU FP7's 'Nextgen' project, which among others has examined genomic diversity and resource implications in wild presumed ancestral populations of sheep (mouflon) and goat (bezoar) in Iran. Finally, the use and status of minority breed products in the slow food movement in Italy was discussed, and its implications for genomic resource conservation, by **Dr Mara Miele** (Cardiff University).

The Symposium was followed by a contributed session spanning subjects such as genomic resources for Ugandan goats, aquaculture and population genomics of Mediterranean mussels and genome sequencing of Old World camelids.

The fourth and final Symposium, entitled “**The data tsunami – how to avoid throwing the baby out with the bathwater!**”, was centred on techniques and methodologies needed to take better advantage of full new livestock datasets in genomics and conservation. Technological advances in genomic data harvesting in the past decade, the necessity to generate fast and cheap genetic screening methods and the increased use of GIScience

have produced many rich datasets which are challenging to fully exploit and which in many cases require specialized bioinformatics tools. The aims of this symposium were i) to bridge the gap between technological platforms and analytical tools in order to develop strategies for approaches that take full advantage of extant genomic and GIS datasets in livestock, ii) establish areas of interest for the development of analytical methods for genomic resources, and iii) identify pathways that allow integrating extant and future genomic resources beyond the limits of technological developments. The Symposium's first invited lecture was from **Dr Daniel Wegmann** (University of Fribourg, Switzerland) on how to accurately infer the evolutionary history of livestock populations using genomic data. This was followed by **Dr Ezequiel Nicolazzi** (Padano Technological Park, Italy) who discussed the merits, challenges and prospects for integrating large, genomic datasets, particularly the various SNP data that have been produced during the last five years in cattle, sheep, goats and pigs. Finally, **Dr Pablo Orozco-terWengel** (Cardiff University) examined the currently and likely future approaches to detect the signatures of natural, artificial and other forms of selection in the genomic data of livestock species. A final free session followed this Symposium and covered areas as diverse as the conservation genomics of the Nordic brown bee, landscape genomics of Moroccan sheep and goats and the development of resequencing analysis pipelines. Once again a lively poster session followed, with further discussion on the most important questions for the Horizon-Scanning exercise. At the end of this session the post-it notes were taken in by the host team and **Michael Bruford** synthesised the questions posed for presentation during the following day's workshop.

It was clear from the Horizon-Scanning post-it note questions that the issues being discussed fell into four broad categories: Data management, Methodological Challenges, Analytical Challenges and a broad category covering Conservation, Management and Prioritization. It was therefore decided to split into four working groups that would focus on each of these issues separately, and then discuss them in session at the end of the morning. Although some generic and important issues emerged such as the need for phenotyping methods to keep pace with genotyping methods (so-called "next-generation phenotyping"), most issues could be separated into these general categories. The groups were duly formed and facilitated by **Dr Stephane Joost** (Data Management), **Dr Catarina Ginja** (Method Challenges – molecular approaches), **Dr Pablo Orozco-terWengel** (Analytical challenges – bioinformatics) and **Dr Irene Hoffmann** (Conservation, Management and Prioritization). Documents were produced by each group and the headline conclusions were communicated in Plenary for feedback at the end of the morning's session. A summary of the recommendations is below:

Data management: the main challenge was identified as being to *establish links* between the major databases, which have largely been set up independently. The livestock genomics community needs either to build on an existing platform (eg the ARK system operated at Roslin) or establish a new, bespoke online resource, able to federate resources and act as an educational central point. Raw data should be made publicly available, and incentives should be in place to ensure data contributors update their datasets regularly. A next generation phenotyping database should be set up, including GIS and anonymized farm-level data, animal photographs and meta-data. A major challenge was deemed to be the ownership and hosting of such a resource. Use of citizen science should be encouraged as should use of smart-phone apps and technologies for sample data storage (eg 'do-forms').

Methodological challenges: major areas requiring concerted effort included deep ("high resolution") phenotyping, because phenotype data is now lagging behind genotype data in terms of resolution and detail; Genome and Epigenome Wide Association Studies were thought to require better and more standardised methodologies in livestock; the role of the

environment on the epigenome and transcriptome needs more thorough investigation, the genetic diversity on the Y-chromosome remains understudied and ancient DNA genomics, while technically demanding, could yield major new insights, especially into the domestication process.

Analytical challenges: major issues identified by this group included the identification of genomic regions that livestock conservationists deem irreplaceable by evolution alone in the coming decades. This could include genomic elements that confer climate-habitat flexibility, disease resistance and/or tolerance to sustainable intensification practices. A second important question concerns the role of haplotype diversity as opposed to SNP diversity and its importance in selection and admixture studies. An important and very current challenge concerned to the best way to integrate past (microsatellite) datasets with current (SNP-based or genome sequence) data. Identification of the most appropriate (least biased, most informative) summary statistics for genome diversity was highlighted as was the importance of using genome data to provide new insights into inbreeding and inbreeding depression. Finally, a common method needs to be developed to produce an unbiased estimate for the geographic concentration of breeds.

Conservation, management and prioritization: issues requiring major efforts in the near future included a need to ask the question why is genomic prioritization (available for 15 years plus) *not* being taken up by FAO countries. A census is needed on prioritization approaches in different regions / countries – there is widely divergent practice. Molecular data are not even being used to assist germplasm storage decisions in many cases. At the same time genetic/genomic data are having profound impacts on the way diversity is managed (eg scrapie testing) and commercially (eg Jersey cattle / off-island admixture). Conservation designations are thus meaningless *in extremis*. Genetics should not be considered in the absence of understanding the ecosystem and production environment – currently the link is not being made. FAO's criteria are being followed in a few countries, but mainly where funding is the 'carrot' and there is no 'stick'... It was agreed that prioritization among breeds is almost irrelevant (a breed is a breed if enough people say it is, and will be conserved if enough people want it), but WITHIN breeds molecular data can be very important – perhaps this is the best emphasis. Molecular data can be used for cryobank management, defining the breeding unit, detecting genetic structure geographically, with respect to phenotype and breed history.

3) Assessment of the results and impact of the event on the future directions of the field (up to two pages)

The relatively intimate and small nature of the meeting was a happy consequence of the time of year the meeting had to be held (in June, during undergraduate exam season) and the relatively short notice that the conference was advertised. Strenuous efforts were made to advertise the meeting widely and to especially encourage previous recipients of Genomics-Resources travel bursaries to attend the meeting, but the timescale was short and several people who committed to come were not able to attend ultimately due to visa problems. Nevertheless the general feedback from all attendees of the meeting was that it has been highly enjoyable, informative, informal and overall extremely useful. All students and early career researchers who were asked felt that they had good access to more well-established attendees, especially the invited speakers and were able to learn a lot.

The balance and overall orientation of the meeting was very much towards the genomics end of the spectrum within the range of the ESF program but the inclusion of two socio-economists as invited speakers, whose presentations provoked a lot of discussion, as well as animal scientists, wildlife biologists, policy-makers and bioinformaticians gave the meeting a truly interdisciplinary flavour.

The geographic distribution of participants was wide and would have been wider if there had been enough time to resolve some of the UK visa issues. Participants came from as far as Uganda, Croatia and Norway with a number of attendees being based in European institutions while carrying out postgraduate study, although originating from Third Countries (eg Thailand and Pakistan). Thus we hope and anticipate that the reach of the meeting will be global in nature.

Perhaps the most significant outcome and feature of the meeting with regards to the impact of the event on the future direction of the field is the Horizon-Scanning exercise carried out during the meeting. This process had a positive impact on the meeting during the time it was held, since it provided a focus for discussion outside of the poster sessions and the prospect of a publication served as an incentive to persuade buy-in from all concerned. Horizon-Scanning papers can be extremely influential if well-timed. For example, Sutherland et al (2009; One Hundred Questions of Importance for the Conservation of Global Biological Diversity) has already attracted 151 citations and Pretty et al (2010; The top 100 questions for the future of global agriculture) has attracted 60 citations. The latter article contained almost no reference to genetics and genetic/genomic resources. Therefore if the article foreseen for this exercise – which we anticipate will be published in the *Frontiers in Genetics* issue on Genomics-Resources – follows the above trend, it may become one of the most cited articles to come from the program.

The field of conservation genomics and genomic resources in agriculture is undergoing a rapid evolution and for example has already given rise to a number of important related publications from the ESF ConGen (Conservation Genomics) program. We hope and anticipate that the outcomes from this meeting and in particular the *Frontiers* Horizon-Scanning article, will have a similar transformative effect. The publication that will arise from this exercise is likely to be published within 2014 or shortly thereafter, so it will hopefully not only be an up-to-date reflection of the current important questions in the field but will retain its currency due to the fact that new research avenues will be able to refer to it as a source that has identified the potential importance of a research program, lending credibility to publications that cite it. Given the current emphasis on this research area within Europe, in the context of changing consumer preferences, climate-smart agriculture, ecosystem services and traceability (Horizon 2020 food security themes for 2014 and 2015), it is hoped that our Conference can have a lasting impact on the field at a crucial juncture in its development.

4) Annex 4a: Programme of the meeting

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

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

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

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?

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

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

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

** did not attend

Annex 4b: Full list of speakers and participants

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