



ISAG CONFERENCE 2010, Edinburgh, Scotland

ISAG-FAO Advisory Group on Animal Genetic Diversity

Time: July 26, 2010, 13:30

Name of workshop convenor: Dr. J.A. Lenstra, Utrecht University, The Netherlands

Approximate number of attendees: >100

Length of workshop: 4 hours

Report on any business conducted:

The **Workshop of the ISAG-FAO Advisory Group on Animal Genetic Diversity** was held during the XXXII ISAG Congress in Edinburgh on the afternoon of Monday, 26 July, 13.30-17.30. The workshop was chaired by Dr. Johannes A. Lenstra (Utrecht, the Netherlands). The program included 10 invited presentations and an announcement by Dr. H. Oddy of the Ruminant Genome Biology Consortium. The meeting was attended by ca. 100 participants.

On Wednesday July 28 at 17.00 The ISAG-FAO Advisory Group on Animal Genetic diversity convened for a **business meeting**.

The following members were present:

- Hans Lenstra (Utrecht, chair, cattle representative)
- Paul Boettcher (FAO, Roma, secretary)
- Paolo Ajmone-Marsan (Piacenza, sheep and goat representative)
- Han Jianlin, (Beijing, yak, camelid representative)
- Steffen Wiegand (Mariensee, chicken representative)
- Yves Plante (Saskatchewan, standing in for Gus Cothran as horse representative)
- Martien Groenen, Richard Crooijmans (Wageningen, standing in for Denis Milan as pig representative)

The following members were unable to attend:

- Gus Cothran (College Station, Texas)
- Denis Milan (Toulouse)
- Satish Kumar (water buffalo representative)

The following items were discussed:

1. The meeting was opened and introductions were made .
2. **Ongoing international projects.** A considerable part of the research on genetic diversity is done in international projects or collaborations.
 - **GlobalDiv** (www.globaldiv.eu) promotes molecular diversity at the Global Level via Workshops, Summer Schools and reviews.
 - A new ESF-**Genetic Resources** project (www.esf.org/activities/) with a similar mission.
 - The **NEXTGEN** project (nextgen.epfl.ch) will sequence whole genomes of cattle, sheep, goats and the wild ancestors Asiatic mouflon and bezoar goat in order to study diversity in relation to disease resistance and landscape genomics with case studies in Morocco and Uganda
 - The **QUANTOMICS** project (www.quantomics.eu/page.ph) will carry out genome-level studies of European Livestock
 - The **Porcine HapMap Project** (www.intl-pag.org/18/abstracts/W86_PAGXVIII_609.html) carries out 60K SNP analysis of 2500 animals and whole-genome sequencing of 150 animals
 - The **International Sheep Genomic Consortium** (www.sheephapmap.org) has carried out 50K SNP typing of 74 breeds, which now initiates several follow-up studies with the same SNP panel.
 - **CONBIAND** (biovis.jimdo.com) of Latin American and Iberian cattle and sheep
 - **3SR** project which will develop and test genomic tools to evaluate sustainability traits (mastitis, disease resistance, reproduction) in sheep and goats.

In addition, two national projects target comprehensive studies

- **Turkhaygen** studies the livestock genetic resources of Turkey
- In Germany, as part of **SYNBREED** project funded by German Ministry of Education and Research, genetic diversity of cattle and chickens will be studied using HD SNP chips and DNA sequencing.

3. As one of its activities of the Committee, new FAO **Recommendations for molecular characterization of animal genetic diversity** has been drafted, which will replace the Guidelines from 1993. This has already been circulated among the members of the Committee and the participants of the GlobalDiv project. It will be sent also to the attendees of this meeting who are not official members of the committee.
4. **State-of-the art.** The accomplishments of molecular research on livestock diversity has been summarized in a recent review commissioned by GlobalDiv (Groeneveld et al., 2010, [Genetic diversity in farm animals--a review](#). Anim Genet. 41 Suppl 1:6-31). The species representatives presented the perspectives for the different species:
 - **Cattle** genetic diversity (Hans Lenstra) has grown into a most active field of research with many data on variation in mtDNA, microsatellite and Y-chromosomal DNA. Most studies of a local scope have used the FAO-recommended microsatellites, which allows a metaanalysis of combined datasets. New results have been obtained by a systematic 50K SNP study, but

- using many Holstein-derived SNPs probably introduced an ascertainment bias. A new 770 K SNP panel has been designed on the basis of variation in a representative panel of breeds. This offers new possibilities, but there is not yet an organized effort for a systematic study of breed diversity. The many whole-genome sequencing efforts allow a new approach to diversity and breed conservation, for instance by revealing adaptive diversity.
- For **sheep** and **goat** (Paolo Ajmone Marsan) the Econogene datasets cover mainly European and SW Asian breeds, but these will be combined by metanalysis with other data: Nordic sheep and goats; Asian sheep; Swiss goats). For sheep the 50 K SNP panel typed in 74 breeds added essentially new and more accurate phylogenetic information. SNP panels for goat are being developed, supported by recent Chinese (re)sequencing projects. Goat appear to have among the livestock species the strongest phylogeographic structure.
 - The diversity of **pig** (Martien Groenen, Richard Crooijmans) has at least as well been characterized as done for cattle with the ongoing, large-scale 60K SNP project and resequencing work.
 - As with cattle, microsatellites are still useful for studying **chicken** genetic diversity with a growing role for SNP and whole-genome sequence analysis. During ISAG conference a first not official microsatellite comparison test had taken place in which members decided to catalog chicken populations genotyped in different laboratories using the FAO suggested panel of micorsatellites (Steffen Weigend). Furthermore, joint analysis of available microsatellite data in chickens has been planned for fall 2010. An international effort to develop a public available HD SNP chip (500K) in chickens is underway which will also be usable for future biodiversity studies as it is, for example, foreseen within the framework of the German project SYNBREED.
 - **Water buffalo, yak** and **camelids** (Han Jianlin, Hans Lenstra) are catching up with mtDNA and microsatellite and even Y-chromosomal DNA datasets.
 - The world **horse** population has no outspoken phylogenetic structure, which perhaps explains why so far there have been few large-scale comprehensive studies of the equine molecular diversity. Commercial availability of a 50K SNP dataset is even problematic, although a coordinated effort to obtain representative data would certainly yield most valuable data (Yves Plante).
 - Microsatellite markers as well as 384-SNP panels have now also been optimized for **Peking duck** and wild relatives (Han Jianlin, Richard Crooijmans).
5. **Data standardization.** During previous meetings we have discussed a central storage of reference samples. Since these are mainly for microsatellite typing, there are now only occasionally requests for such samples. Scoring of SNP alleles is nearly always unambiguous, although a common format of the data sets is needed in order to be able to combine data sets. Paul Boettcher agreed to be listed as the primary contact in the FAO Guidelines for inquiries on reference samples and would then contact appropriate members of the Advisory Group.

6. **Accessibility** of samples for international collaboration. The Committee noted with some concern that legal restrictions on the access to genetic resources impedes access to samples of several Asian countries, which is essential for obtaining a global view of the diversity pattern. It is hoped that agreements can be worked out that fully protect the interests of the countries of origin but allow relatively free exchange of samples for fundamental research. It is advisable to carry out genetic diversity studies of breeds in collaboration with scientists from their country of origin.
7. Genotype data **repository**. There is no central repository for genotyping data comparable to the Genbank for sequence data. Dr. Massoud Malek (IAEA, Vienna) is compiling published microsatellite data (www.globalgenomic.com). In practice, published microsatellite, SNP and sequence data are available on request. However, the rapid accumulation of data makes it difficult to survey what is available.
8. No other points were put forward and the meeting was closed