ISAG FAO Genetic Diversity

STANDING COMMITTEES / WORKSHOPS  Information will be posted online

Organised by a standing committee: yes

Date and meeting time: July 17, 2012, 14.00

Chair, name and contact email: J.A.Lenstra@uu.nl

Agenda / programme attached Yes

Number of participants at meeting: ca. 50

Summary of the meeting including votes, decisions taken and plans for future conferences

See attached report

Committee members

Chair  Dr. J.A.Lenstra (also cattle representative  term of service From 2008
E mail address: J.A.Lenstra@uu

Other members  term of service (all from 2008)
Dr. P. Ajmone Marsan (sheep and goat representative)
Dr. P.Boettcher (FAO, secretary)
Dr. G. Cothran (horse representative)
Dr. O. Hanotte (camelids and yak representative)
Dr. H. Jianlin (camelids and yak representative)
Dr. S. Kumar (water buffalo representative)
Dr. D. Milan (pig representative)
Dr. S. Weigend (chicken representative)
WORKSHOP REPORT

Name of workshop: ISAG-FAO Advisory Group on Animal Genetic Diversity (July 17, 2012, 14.0)

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

Approximate number of attendees: >50

Length of workshop: 4 hours

The Workshop of the ISAG-FAO Advisory Group on Animal Genetic Diversity was held during the XXXIII ISAG Congress in Cairns on the afternoon of Tuesday, 17 July, 14.0-17.30. The workshop was chaired by Dr. Johannes A. Lenstra (Utrecht, the Netherlands). The meeting was attended by ca. 50 participants. The following lectures were presented:

P. Boettcher  New opportunities and new objectives for the ISAG-FAO Advisory Group on Animal Genetic Diversity
W Barendse  The use of single nucleotide polymorphism array data to analyse the genetic structure of a cattle herd
W.M.S.P. Weerasinghe  Genetic Structure and Diversity of Australian Sheep Breeds
L. Liaubet  Genetic and phenotypic fine characterizations of French porcine reference populations
S. Zhao  Phylogeny and Assessment of Conservation Priority for Asian Native Chicken Genetic Resources
Rytis Juras  Genetic analysis of feral horse population from Brittany Triangle, British Columbia
J.A. Lenstra  Compilation and analysis of high-density SNP and genomic sequence data for investigation of livestock diversity
I.A.S. Randhawa  A composite test to detect positive selection in cattle and sheep
J. Gongora  Evolution and diversity of MHC class I and class II genes in suids and peccaries

Business meeting

During a short and informal business meeting immediately following the workshop, it was agreed that this workshop fulfils a useful purpose and deserves to be continued.

Because of the distances from Europe, only four members of the Advisory Group (Hans Lenstra, Utrecht, chair, cattle representative, Paul Boettcher, FAO, Rome, secretary, Dennis Milan, Toulouse, pig representative, and Han Jianlin, Beijing, yak, camelid representative) attended of the conference. Therefore we did not, as in 2010 in Edinburgh, discuss in a separate meeting the scientific trends, state-of-the art and ongoing internationally coordinated projects. This is being compensated by regular contacts between the Advisory Group members by email and during European project meetings. In addition, the presentation of the Chairman (see an outline below) summarizes the progress and perspectives of molecular diversity studies.

Despite the relative lack of activity by the Advisory Group at the Cairns meeting, the need for its existence has never been greater. As pointed out in the presentation by FAO, the rapid advancement in genomic technologies has created many new opportunities for study and application. Discussion among members of the Advisory Group (and the ISAG community in general) is needed to help map out possible plans for FAO to guide its member countries in the adoption and use these new tools.
Compilation and analysis of high-density SNP and genomic sequence data for investigation of livestock diversity

J.A. Lenstra, Faculty of Veterinary Medicine, Utrecht University
Paolo Ajmone-Marsan, Catholic University of the Sacred Heart, Piacenza
Paul Boettcher, FAO-AGAG, Rome

1. Studying breed diversity: state-of-the-art

Genetic diversity in farm animals – a review

L. F. Groeneveld¹, J. A. Lenstra¹, H. Eding², M. A. Toro³, B. Scherf⁴, D. Pilling⁵, R. Negrini⁶,⁷, E. K. Finlay⁸, H. Jianlin⁹, E. Groeneveld*, S. Weigend* and The GLOBALDIV Consortium

Genetic markers

1. MtDNA reveals ancestral species and domestication sites
2. MtDNA haplotypes differentiate on continental level

The Multifaceted Origin of Taurine Cattle Reflected by the Mitochondrial Genome

Alessandro Achilli¹,², Silvia Bonfiglio¹,², Anna Olivieri¹, Arianna Malusà¹, Maria Pala¹, Baharak Hooshiar Kashani¹, Ugo A. Perego¹,², Paolo Ajmone-Marsan⁶, Luigi Liotta¹, Ornella Semino¹, Hans-Jürgen Bandelt⁶, Luca Ferretti⁶, Antonio Torroni²

3. Y-chromosomal haplotypes (if available): phylogeographic differentiation of paternal lineages

Dual Origins of Dairy Cattle Farming – Evidence from a Comprehensive Survey of European Y-Chromosomal Variation

Ceiridwen J. Edwards¹,², Catarina Ginjá³,⁴, Juha Kantanen⁵, Lucía Pérez-Pardal⁶, Anne Tresset⁷, Frauke Stock⁷, European Cattle Genetic Diversity Consortium⁷, Luis T. Gama⁸, M. Cecilia T. Penedo⁸, Daniel G. Bradley⁷, Johannes A. Lenstra⁸, Isaäc J. Nijman⁸
4. Autosomal microsatellite/SNP allele frequencies:
   » Heterozygosity indicates diversity per breed
   » Golden trio reveals complementary aspects of breed relationships
     - Coordination analysis > geographic clines > migration
     - Model-based clustering > breed composition
     - Phylogenetic trees, networks > clusters > common descent

Rules and exceptions
Rule 1. Diversity decreases with distance from domestication site
   Exceptions: Sheep, horse: admixture in many breeds
   Pigs: secondary domestication in Europe
   Cattle: introgression of European aurochs?
Rule 2. Clustering of authentic landraces follow geography

Drawbacks of microsatellites
1. Quality of microsatellite datasets variable
2. FAO recommendations of standardized microsatellite marker panels too often not followed up
   sheep, goat horse: few common markers  » several local diversity studies a waste of effort!
   cattle: meta-analysis of datasets with common markers feasible
3. Microsatellites: no information on adaptive variation
4. No practical estimation of conservation values on the basis of neutral allele frequencies problematic
Estimation of conservation values

- Weitzmann approach (genetic distances)
  - confounded by inbreeding;
  - computations too heavy for real-life datasets

- Eding approach (minimizing kinships)
  - indicates breeds with high diversity
  - accuracy of kinship calculations; some bias towards inbred breeds
  - not for SNPs

- FAO guidelines: qualitative considerations
  - High-diversity breeds near domestication site
  - Breeds with exotic influence
  - Breeds with separate history
  - Breeds with unique phenotypes

Objectives, criteria and methods for using molecular genetic data in priority setting for conservation of animal genetic resources

2. Impact of genomic technologies

- High-density SNPs: golden-trio analysis much more accurate
  - Coordination analysis (PCA) of individuals now meaningful

- Sensitive detection of admixture on the basis of shared haplotypes
  - If an allele is a note, a haplotype is a melody

- Future software
  - partitioning the genome: authentic - introgressed?
  - reconstruction of authentic breed?

- Genomic localization of adaptive variation via differentiation of pools with different phenotypes

- SNPs distortion of diversity parameters by ascertainment bias:
  - populations where SNPs were found look most diverse
  - However, this has little effect on patterns of breed clustering

- Genomic sequencing
  - Unbiased diversity measures
- Survey of DNA variants (SNV/CNV, coding/non-coding, etc.)
  » adaptive variation
- Shared haplotypes » introgression
- History of genome and population
- etc.

3. Compilation of data
- Comprehensive studies of breed diversity require international coordination
- Existing datasets (SNPs, NG sequencing)
  - for whole-genome association studies
  - for breeding value estimations
  - for local diversity studies
- Combination of data more feasible than with microsatellites
- Collaborating by making data available: win-win!
  Survey and collect available datasets
  cattle (50K, 770K, genomic sequences?)
  sheep (50K)
  . . .
- Role of international organizations?

4. Handling the data
- Generation of genomic data outpaces data analysis
- New algorithms being developed
  - phasing
  - hidden Kinship
  - population history
  - selection
  - etc.
- Useful SNP programs available: PLINK, PEAS, TreeMix
- Huge datasets need special software
  - (Again) different formats without conversion tools
  - e.g., no easy calculation of classical genetic distances between breeds for PLINK data
- Many people now develop in-house R-scripts
  - standardization?
  - bugs?
  » New and easy program packages
  » Stick to existing formats!

Summary
1. Studying breed diversity: state-of-the-art: many accomplishments
2. Impact of genomic technologies: exciting perspectives
3. Compilation of data: new opportunities, new consortia,
4. Handling the data: next-generation technology needs next-generation tools