

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 membersterm 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, Bejing, 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. Groeneveld*, J. A. Lenstra⁺, H. Eding[‡], M. A. Toro[§], B. Scherf¹, D. Pilling¹, R. Negrini**,
- E. K. Finlay⁺⁺, H. Jianlin⁺⁺, 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

OPEN access Freely available online

PLos one

The Multifaceted Origin of Taurine Cattle Reflected by the Mitochondrial Genome

Alessandro Achilli^{1,2®}, Silvia Bonfiglio^{1®}, Anna Olivieri¹, Arianna Malusà¹, Maria Pala¹, Baharak Hooshiar Kashani¹, Ugo A. Perego^{1,3}, Paolo Ajmone-Marsan⁴, Luigi Liotta⁵, Ornella Semino¹, Hans-Jürgen Bandelt⁶, Luca Ferretti¹*, Antonio Torroni¹*

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

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

Ceiridwen J. Edwards^{1,2}, Catarina Ginja^{3,4}, Juha Kantanen⁵, Lucía Pérez-Pardal⁶, Anne Tresset⁷, Frauke Stock¹, European Cattle Genetic Diversity Consortium¹, Luis T. Gama⁴, M. Cecilia T. Penedo³, Daniel G. Bradley¹, Johannes A. Lenstra⁸*, Isaäc J. Nijman^{8¤}

- 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

Molecular tools and analytical approaches for the characterization of farm animal genetic diversity

J. A. Lenstra^{*}, L. F. Groeneveld[†], H. Eding[‡], J. Kantanen[§], J. L. Williams[¶], P. Taberlet^{**}, E. L. Nicolazzi^{††}, J. Sölkner^{‡‡}, H. Simianer^{§§}, E. Ciani^{¶¶}, J. F. Garcia^{***}, M. W. Bruford^{†††}, P. Ajmone-Marsan^{††} and S. Weigend[†]

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

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PLOS BIOLOGY

Genome-Wide Analysis of the World's Sheep Breeds Reveals High Levels of Historic Mixture and Strong Recent Selection

James W. Kijas¹*, Johannes A. Lenstra², Ben Hayes³, Simon Boitard⁴, Laercio R. Porto Neto¹, Magali San Cristobal⁴, Bertrand Servin⁴, Russell McCulloch¹, Vicki Whan¹, Kimberly Gietzen⁵, Samuel Paiva⁶, William Barendse¹, Elena Ciani⁷, Herman Raadsma⁸, John McEwan⁹, Brian Dalrymple¹, other members of the International Sheep Genomics Consortium¹⁰

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



Review

On the Breeds of Cattle—Historic and Current Classifications

Marleen Felius ¹, Peter A. Koolmees ², Bert Theunissen ², European Cattle Genetic Diversity Consortium [†] and Johannes A. Lenstra ^{2,*}

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

P. J. Boettcher^{*}, M. Tixier-Boichard[†], M.A. Toro[‡], H. Simianer[§], H. Eding[¶], G. Gandini^{**}, S. Joost^{††}, D. Garcia^{±‡}, L. Colli^{§§}, P. Ajmone-Marsan^{§§} and the GLOBALDIV Consortium

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
 - partioning 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