Update on the International Goat Genome Consortium Projects

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Slide 1

Update on the International Goat Genome Consortium Projects

Gwenola Tosser-Klopp, on behalf of IGGC

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Slide 2 — Outline

- History and coordination of IGGC

- Projects underway
  - Goat genome assembly
  - 100 breeds resequencing
  - SNP chips
  - ADAPTMAP project

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Slide 3 — International Goat Genome Consortium

- Created in March, 2010
- www.goatgenome.org
- Coordination: Wenguang Zhang & Gwenola Tosser-Klopp
- More than 10 Countries and 20 teams involved
- Open for new participants
- Workshop on Monday afternoon (5pm : 8pm, Sunrise)

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Slide 4 — Goat genome assembly and Annotation

- First assembly published in December 2013, Yunnling Black Goat, constructed with Illumina reads and optical mapping data
- N50: 18,720 bp (39,408 contigs), 2.2Mb (344 scaffolds)
- New browser will be online soon
- Available from ncbi: http://www.ncbi.nlm.nih.gov/assembly/GCF_000317765.1

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Slide 5 — Goat genome assembly and annotation

- Inbred San Clemente goat, PacBio reads, Hi-C technique, and RNA-seq data for *de novo* assembly and annotation
- 5,902 contigs in total, N50: 2.56 Mb
Derek Bickhart, W144, Cattle/Sheep/Goat 2 workshop, Sunday 11th, 8:40 am
Steven G. Schroeder, W440, IGGC workshop, Monday 12th, 5:10 pm
- 247 disagreements between the two assemblies = 123 inversions and 124 chromosome relocalisations
- FR-AgENCODE project to improve annotation of goat genome (and other species)
Sylvain Foissac, W445, IGGC workshop, Monday 12th 6:50 pm

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Slide 6 — Resequencing

- Resequencing of >100 goats from several international breeds

- Selective sweeps study

- Cashmere yield determism

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Design of new SNP chips

- First SNP design = 54K
- Illumina, available since Dec 2011
- Tosser-Klopp et al., 2014, PlosOne
- SNP details were released in dbSNP 138 build (Dec, 2012)
- Already used for genetic diversity studies, GWAS & QTL studies and genomic selection evaluation

Marcel Amills, W442, IGGC workshop, Monday 12th, 5:50 pm & Khanyisile Mdladla, W443, IGGC workshop, Monday 12th, 6:10 pm, Céline Carillier, W444, IGGC workshop, Monday 12th, 6:30 pm

- Further needs to be discussed by the community (higher density? more breeds to be represented, different MAF range…)

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http://bioinformatics.tecnoparco.org/SNPchimp/index.php/browse

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ADAPTmap objectives

- Centralized data sharing: for greater understanding of the goat genome and its multi-purpose use with a strong emphasis on adaptation to local environments
  - Breeding perspective
    - Selection and conservation
      - Adaptive variation
    - Production environment descriptors
      - Feedback to FAO on PEDs
  - Ecology perspective
    - Climate change
- Keywords: integration of people and data

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ADAPTmap: Contributing projects

- The beginning:

- The consortium grows larger…and more to come!

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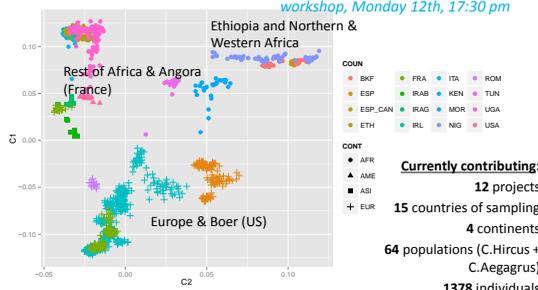Cattle/Sheep/Goat workshop
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ADAPTmap tasks

- Reference genome
  - improvement of genome assembly;
  - genome annotation;
  - comparative genomics (with other ruminants);
- SNP panels
  - Study of the possibility to improve the current SNP panel;
  - Identification of parentage SNP panel;
- Domestication and diversity
  - Integration and standardization of phenotypic data;
  - population genetics analyses and population history (domestication reconstruction);
  - Selection signatures (landscape genomics, iHS, CLL, EHH, XP-EHH, Fst, etc)
  - Visible genetic profile (using pictures – Coat colour + Horns…)
- Breeding
  - Breeding and genetic improvement;

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ADAPTmap preliminary analysis

Ezequiel L. Nicolazzi, W441, IGGC workshop, Monday 12th, 17:30 pm

Currently contributing:
12 projects
15 countries of sampling
4 continents
64 populations (C.Hircus + C.Aegagrus)
1378 individuals

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Conclusion

- IGGC federates groups working on goat genomics
- Open for new participants
- Tools are being shared (assembly data, SNP chips…)
- Data sharing in ADAPTMAP will allow meta data analysis
- Workshop on Monday afternoon (5pm : 8pm, Sunrise)

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  – INRA-Toulouse, MARDI-Malaysia, Utrecht University, French breeding organizations (see publication for complete list of contributors)
- Genome sequence & resequencing:
  – Jun Wang, Wen Wang, Wenguang Zhang, KIZ, BGI
  – Derek Bickhart , Steven G. Schroeder, Tad Sonstegard, Curt Van Tassell, USDA
- Illumina: André Eggen, Cindy Lawley, Karine Viaud
- ADAPTMAP:
  – Alessandra Stella, Ezequiel Nicolazzi
- Advice and support: monthly phone conference group, ISGC key members: John McEwan, James Kijas

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In memory of the victims of the attack at Charlie Hebdo (and all other terrorist attacks)

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thank you for your attention!

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