Update on the International Goat Genome Consortium Projects
Gwenola Tosser-Klopp, on behalf of IGGC

Outline
• History and coordination of IGGC
• Projects underway
  – Goat genome assembly
  – 100 breeds resequencing
  – SNP chips
  – ADAPTMAP project

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)

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), 2.2 Mb (344 scaffolds)
• New browser will be online soon
• Available from ncbi: http://www.ncbi.nlm.nih.gov/assembly/GCF_000317765.1

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
  • 247 disagreements between the two assemblies = 123 inversions and 124 chromosome relocisations
  • FR-AgENCODE project to improve annotation of goat genome (and other species)

Resequencing
• Resequencing of >100 goats from several international breeds
• Selective sweeps study
• Cashmere yield determinism
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, 5:30 pm & Khanyisile Mabola, W443, IGGC workshop, Monday 12th, 6:10 pm

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

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
    - Adaptation variation
    - Production environment descriptors
  - Ecology perspective
  - Climate change
- Keywords: integration of people and data

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, Hap, CIL, ENH, XP-DER, F4, etc)
  - Visible genetic profile (using pictures – Coat colour + Horns...)
- Breeding
  - Breeding and genetic improvement;

ADAPTmap: Contributing projects

- The beginning:
  - The consortium grows larger...and more to come!

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
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)

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

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- ADAPTMAP:
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thank you for your attention!