



Update on the International Goat Genome Consortium Projects

Gwenola Tosser-Klopp, Max F Rothschild, Heather J Huson, Ezequiel Luis Nicolazzi, Tad S. Sonstegard, Marcel Amills, Penny Riggs, Curtis P van Tassell, P. Ajmone Marsan, Alexandra Stella, et al.

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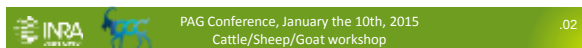


Update on the International Goat Genome Consortium Projects

Gwenola Tosser-Klopp, on behalf of IGGC

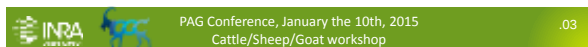
Outline

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



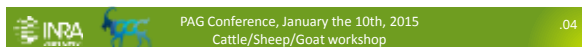
International Goat Genome Consortium

- 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

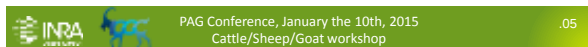
- First assembly published in December 2013, Yunnan Black Goat, constructed with Illumina reads and optical mapping data
- N50: 18,720 bp (39,408 contigs), 2.2Mb (344 scaffolds)
- New browser will be online soon
- Available from ncbi: http://www.ncbi.nlm.nih.gov/assembly/GCF_000317765.1



Goat genome assembly and annotation

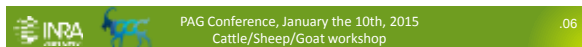
- Inbred San Clemente goat, PacBio reads, Hi-C technique, and RNA-seq data for *de novo* assembly and annotation
- 5,902 contigs in total, N50: 2.56 Mb
 Derek Bickhart, W144, Cattle/Sheep/Goat 2 workshop, Sunday 11th, 8:40 am
 Steven G. Schroeder, W440, IGGC workshop, Monday 12th, 5:10 pm
- 247 disagreements 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



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, 5:50 pm & Khanyisile Mladla, 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...)

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



PAG Conference, January the 10th, 2015
Cattle/Sheep/Goat workshop

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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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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, CLN, EHH, XP-EHH, Fst, etc)
 - Visible genetic profile (using pictures – Coat colour + Horns...)
- Breeding
 - Breeding and genetic improvement;

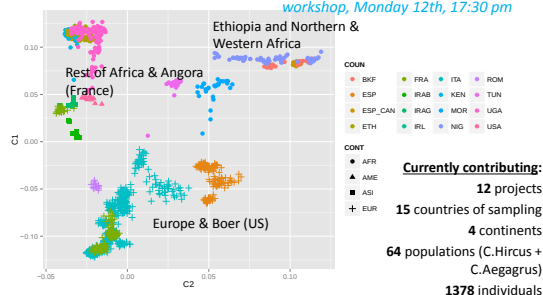


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ADAPTmap preliminary analysis

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

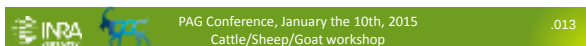


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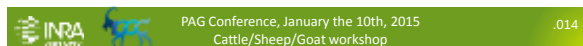
Conclusion

- 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)

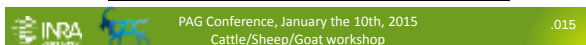


Acknowledgements

- **SNP discovery:**
 - 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



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



The authors:

Gwenola Tosser-Klopp, Max F. Rothschild, Heather J Huson, Ezequiel Luis Nicolazzi, Tad S. Sonstegard, Marcel Amills, Penny Riggs, Curtis P. VanTassell, Paolo Ajmone Marsan, Alessandra Stella, Brian Sayre, Wenguang Zhang, Rachel Rupp

thank you for your attention!

