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## **Towards a high density SNP International Goat Chip**

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► **To cite this version:**

Gwenola Tosser-Klopp, Abdullah Johari Jiken, Philippe Bardou, Cédric Cabau, Patrice Dehais, et al.. Towards a high density SNP International Goat Chip. *Plant and Animal Genome*, Jan 2011, San Diégo, United States. hal-01194170

**HAL Id: hal-01194170**

**<https://hal.science/hal-01194170>**

Submitted on 6 Jun 2020

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# **Towards a high density SNP International Goat Chip**

Gwenola Tosser-Klopp  
on behalf of the International Goat  
Genome Consortium

# Outline

- Introduction
- Data
- Data processing
- Expected outcome
- Questions to be discussed

# High density SNP chips are useful

- Understanding species' evolution, domestication...
- Dissecting genetic mechanisms of complex agronomic traits
- Improving selection methods

# SNP chips in many species

- SNP chips are available in several species
  - Humans
  - Model animals : mouse, rat
  - domestic species : chicken, dog, horse, cattle, sheep, pig
- Affymetrix and Illumina technologies are mainly used
- 20 K <density<1.1 M

# Several SNP discovery projects for goats in the world

- University of Utrecht, Netherlands (H. Heuven / M.Groenen)
  - Reduced Representation Libraries of 17 dairy goats. 120 millions of 32bp paired-ends sequences = 3 Gb
- Malaysian Agricultural Research and Development Institute, Malaysia & DNA Landmarks, Canada (JJ Abdullah / TP Yu)
  - Whole genome sequencing of 3\*20 Boer, Savanna and Kacang meat and indigenous goats = >210 Gb
- French National Institute for Agricultural Research (INRA), France (Ph. Mulsant / R. Rupp / C.Moreno):
  - RRL of 6 goats and whole genome sequencing of 13 Alpine, Saanen and Creole goats = >150 Gb

# Goat genomic tools in progress

- Reference sequence : see W. Zhang presentation
- RH map in progress : see B. Sayre presentation
- 20K SNP chip: see poster P198
- International resequencing project of 25 goat breeds will also give more SNPs
- Several projects around expressed sequences (France, China)

# We propose to federate these data

- Centralisation of the data at INRA
- Data processing with INRA pipeline
- [www.sigenae.org](http://www.sigenae.org) & T.Faraut
- Data access to all partners



# Steps of the Bioinformatic process

- alignment of the different sequences on *de novo* assembled goat contigs (BWA software)
- ordering of contigs on ovine or bovine genome reference sequence
- SNP discovery and annotation
- small set SNP test generation
- determination of the final SNP panel

# Web interface

- Data visualisation with Ensembl



- Data extraction with Biomart : select SNP on different criteria = chromosome, specific contig, dataset



Based on Ensembl release 40 - Aug 2006

putative SNP:  
snp\_EE760096\_333

[snp\\_EE760096\\_333 - SHP info](#)

CD285973.p.ov.8  
106 - 306

- [Graphical view](#)
- [Polymorphism view](#)
- [Export information about region](#)
- [Export sequence as FASTA](#)
- [Export EMBL file](#)

Use Ensembl to...

- [Search Contig Browser](#)
- [Data mining \[BioMart\]](#)
- [Export data](#)
- [Download data](#)
- [Digital Differential Display](#)
- [Venn Diagrams](#)

Docs and downloads

- [About Contig Browser](#)
- [Contig Browser data](#)

Other links

- [Home](#)
- [Sigenae](#)
- [Agenae](#)



### SNP Report

SNP	snp_EE760096_333 (putativeSNP1)
Synonyms	None currently in the database
Alleles	C/T (ambiguity code: Y)
Validation status	Unknown
Linkage disequilibrium data	No linkage data for this SNP
Sequence region	<pre> GGACGACCCCTGGAGATGATCGAACCGCCACGCTGAAATACAAAGCTACTGGAACTGTT YTGCTCTGGGCAAGGAGCGAATTGCTGCTGTGGATATCGGCTCCGAGTGAAGGCTGCT G      (SNP highlighted)           </pre>

60b+SNP+60b

#### Genotype frequencies per population

This SNP has not been genotyped in a population.

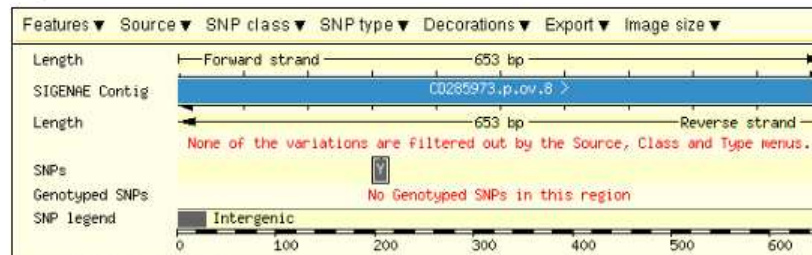
#### Allele frequencies per population

This SNP has no allele frequencies per population.

#### SNP snp\_EE760096\_333 is located in the following transcripts

There are no transcripts that contain this SNP.

#### SNP Context - contig CD285973.p.ov.8 206



#### Individual genotypes for SNP snp\_EE760096\_333



# Criteria for SNP selection (1/2)

- Good sequence quality around the SNP
- Each allele of the SNP is included in at least 2 reads
- No repetitive elements surrounding the SNP (within 100bp)
- The SNP must be predicted by a minimum of 6 reads
- No overlap with complex regions

Ref : Matukumalli, 2009 & Ramos, 2009

# Criteria for SNP selection (2/2)

- Representativity of the whole genome
- Also take SNPs in the regions that are not mapped on the genome
- Intra-species polymorphism in a maximum number of breeds
- Other criteria (to be defined)?

# Expected outcomes

- Millions of SNPs
- A majority will be mapped on the genome
- Annotation will be facilitated by RNA seq data
- A first international chip order is planned at autumn 2011

# Open questions

- Density of the chip
- Technology to be used
- The price depends on the interest of the goat community for this tool :
  - for example, Illumina's price is between \$130 and \$300 for a 50K SNP chip (20000 or 5000 chips)

# PAG is an opportunity to join the project

- Contact to join IGGC and the HD SNP chip project :  
[gwenola.tosser@toulouse.inra.fr](mailto:gwenola.tosser@toulouse.inra.fr)
- Website : [www.goatgenome.org](http://www.goatgenome.org)
- Illumina meeting at 12.30 today



# Acknowledgements

- UNCEIA, Capgenes and Apis-gene (French breeding organizations)

I thank you for your attention