GENOME-WIDE STUDY FINDS A QTL WITH PLEOTROPIC EFFECT ON SEMEN AND PRODUCTION TRAITS IN SAANEN GOATS









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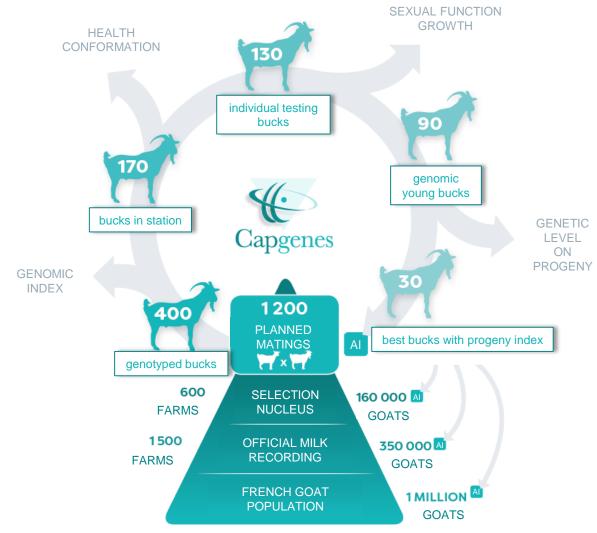
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OGET Claire

Background



FRENCH DAIRY GOAT SELECTION SCHEME IN 2018 (CAPGENES)



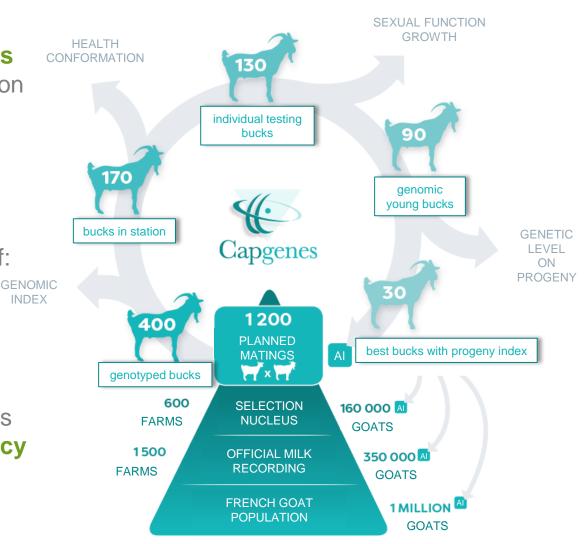
Background

- In France, major role of bucks from performance testing station in selection efficiency and costs
- Large number of bucks eliminated before progeny testing (47%) due to issues of:

Health

Conformation

- Behaviour
- Semen quality
- How can genetic impact on this major issue to ensure efficiency of selection scheme?



FRENCH DAIRY GOAT SELECTION SCHEME IN 2018 (CAPGENES)



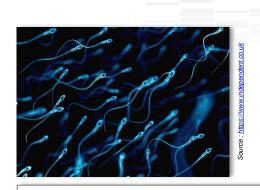




__01 __MATERIALS & METHODS







MALE TRAITS

5 reproduction traits:

- Semen concentration
- Semen volume
- Number of spermatozoa
- Percentage of livingspermatozoa after thawing
- Spermatozoa motility after thawing

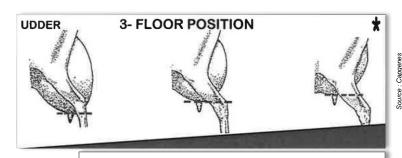




MALE TRAITS

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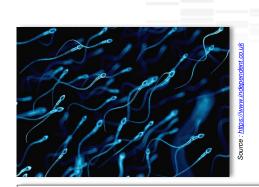
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FEMALE TRAITS

- 11 udder type and body condition traits
- 5 milk production traits
- **Lifespan** of livestock
- Somatic Cell Score (SCS), related to health



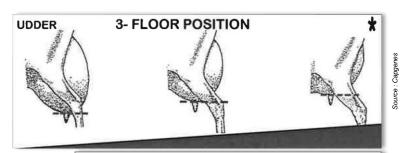


MALE TRAITS

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Bucks in performance testing stations genotyped with the 50K SNPs Goat Chip



FEMALE TRAITS

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Computing phenotypes for bucks



- Male reproduction traits:
 - Repeated data (from 1 to 447 repetitions / buck): Yield Deviations (YD)
 - Corrected for environmental effects: age, month and year of sampling, duration between sampling
 - Phenotypes used in the analyses: mean of corrected data for each individual
- Female production traits and SCS:
 - Repeated data (number of female lactations)
 - Daughter Yield Deviations (DYD) from official genetic evaluation
 - Average performance of daughters corrected for environmental effects and genetic value of their dam



Genome Wide Association Study (GWAS)

- Linear mixed model, with genomic kinship matrix
- ❖ Single SNP tests using GEMMA software (Zhou and Stephens, 2012)
- Correction for multiple tests: Bonferroni threshold
- Bucks in performance testing stations genotyped with the 50K SNPs Goat Chip (Tosser-Klopp et al., 2014)

	With male reproduction traits	With Female production traits and SCS
Alpine	672	597
Saanen	519	460







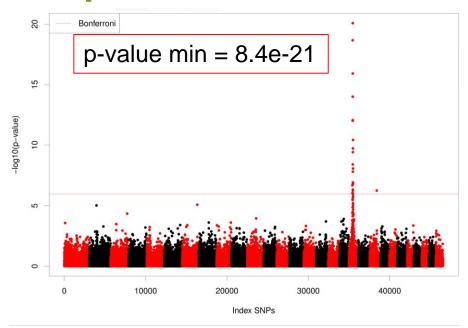
__02 RESULTS & DISCUSSION



Discovery of a QTL (Quantitative Trait Loci) for semen production in the Saanen breed

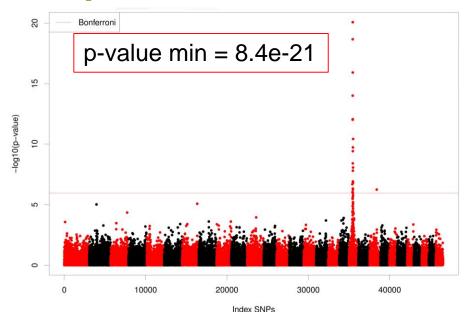


Discovery of a QTL (Quantitative Trait Loci) for semen production in the Saanen breed



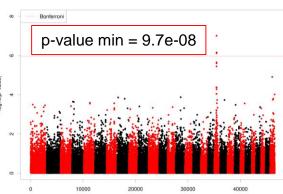
Manhattan plot: Semen volume

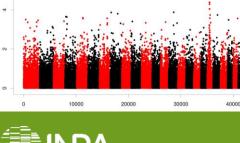
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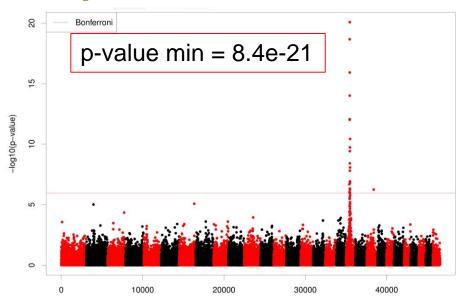
Manhattan plot: Semen volume

Semen concentration





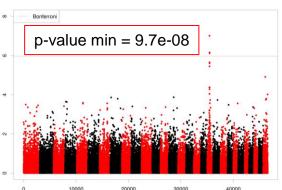
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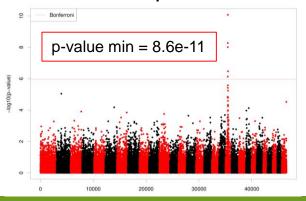
Index SNPs

Manhattan plot: Semen volume



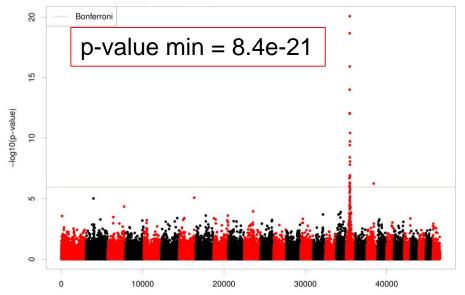


Number of spermatozoa



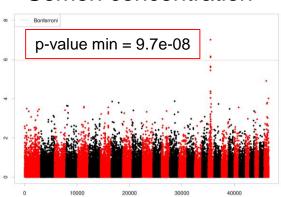


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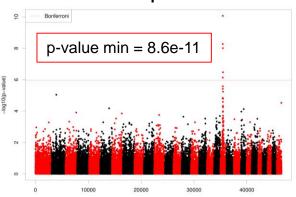


Manhattan plot: Semen volume

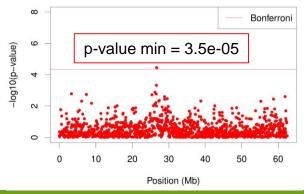
Semen concentration



Number of spermatozoa



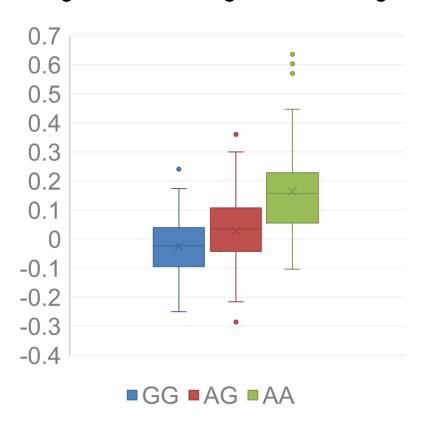
Percentage of living spermatozoa after thawing (CHR19 level)





One significant SNP effect on semen production

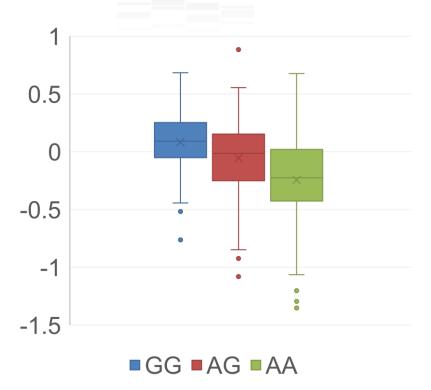
DYD for semen volume according to the most significant SNP genotype



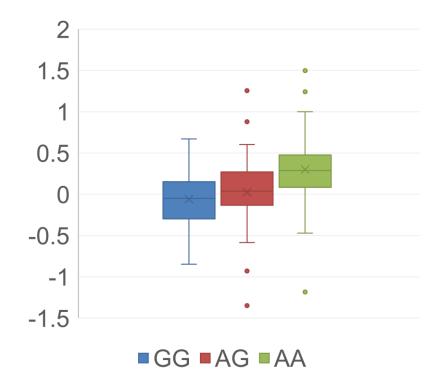
- ANOVA highly significant
- The most significant SNP has an additive effect on semen volume
- An individual carrying the A allele has a higher semen volume
- In Saanen, the frequency of this allele is close to 50%
- ❖ In Alpine, the frequency is less than 2% → lower semen volume

One significant SNP effect on semen production

DYD for semen concentration



DYD for number of spermatozoa

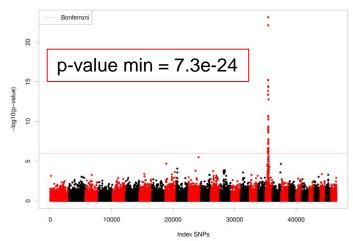


An individual carrying the A allele has a lower semen concentration but a higher number of spermatozoa

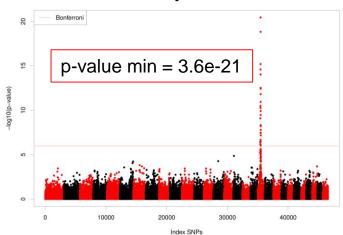
The QTL also associated with production traits in the Saanen breed Udder floor

- QTL for 14 of the 23 studied traits within all categories:
 - All the reproduction traits
 - Udder type traits: udder rear attachment, udder front, udder floor position, chest size
 - Milk production traits: milk, fat and protein yields
 - Lifespan of livestock
 - Trait related to health: SCS
- These results confirm the adverse pleiotropic QTL region for milk production and udder traits found by Martin et al. (2018)
- We did not find this QTL in the Alpine breed suggesting a breed-specific control

Udder floor position



Milk yield





Fine mapping of the QTL on CHR19 using sequence data

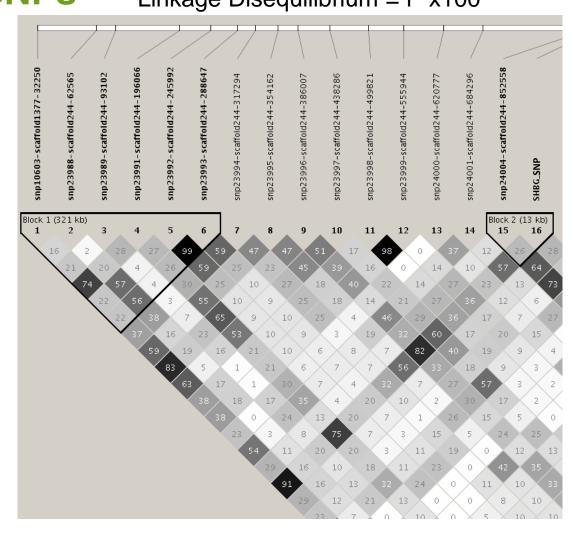
- In the Saanen breed:
 - Significant region on chromosome 19
 - > 238 candidate genes
 - Highest p-values position ≈ 26.61 Mb

20 sequenced bucks:

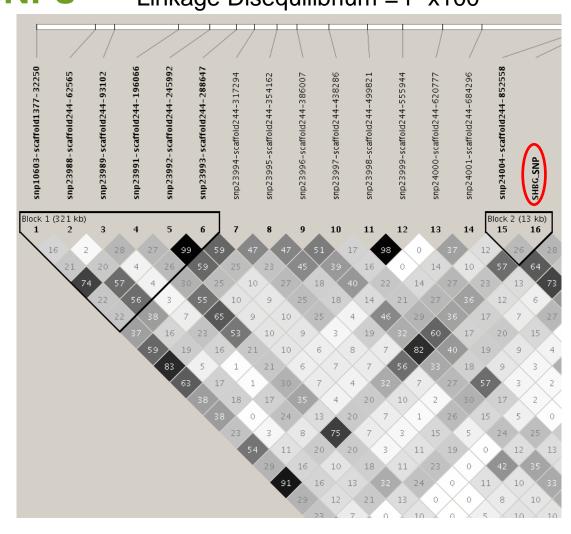
- Search for differences of allele frequencies between the Alpine and Saanen sequences in the significant region
- Aim: to find a mutation in the Saanen population at the origin of the strong association of this region with several male reproductive traits
- ❖ A candidate mutation found in the SHBG gene (Sex Hormone Binding Globulin)
 - An exonic SNP that modifies the amino acid sequence
 - Functions of SHBG: androgen transport protein, but may also be involved in steroid receptor mediated processes



- SHBG_SNP genotyped for 342 Saanen bucks
- Closely linked to the both most significant SNPs of the CHI 19 region in the GWAS

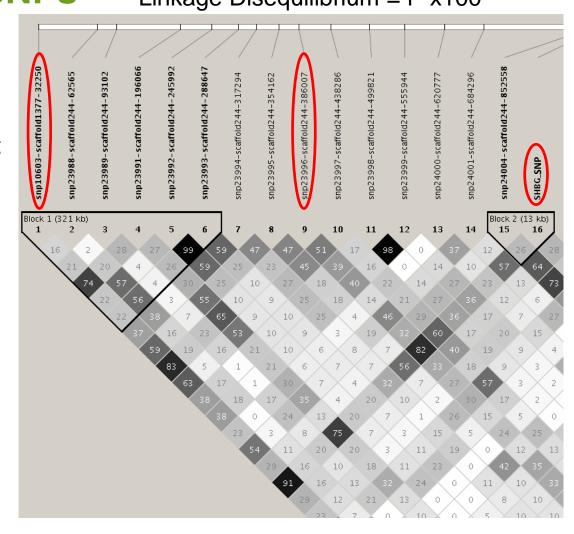


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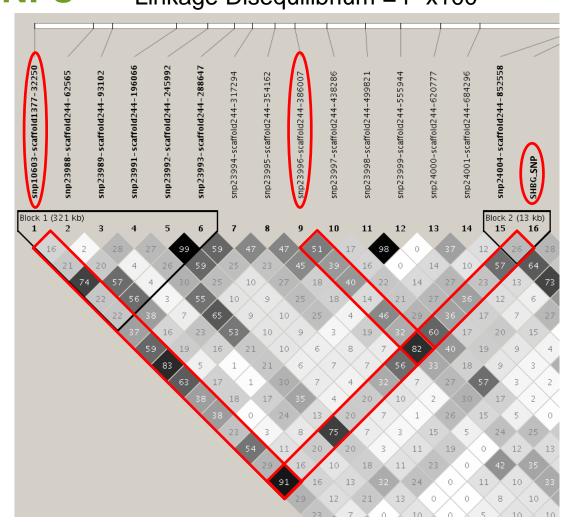




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TAKE HOME MESSAGE

- ❖ Highly significant QTL on chromosome 19 (22.8 28.9 Mb) in the Saanen breed for semen production and production traits
- The mutation has a favorable additive effect on semen production and is also linked to production traits (favorable effect for milk production) and adversly to udder traits (unfavorable effect for SCS and type traits)
- Candidate causal mutation in the Sex Hormone Binding Globulin (SHBG) gene





Thank you for your attention!

Any questions?









