



Modelisation of genomic selection in French dairy goats

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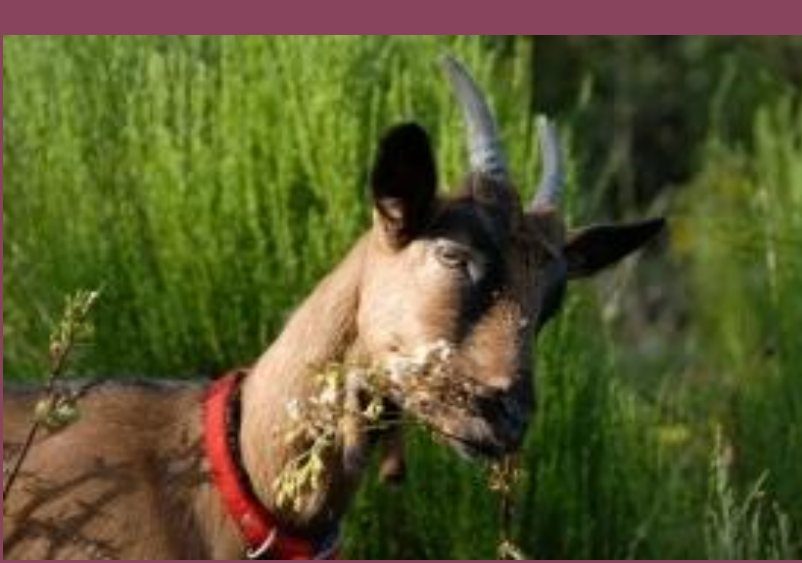
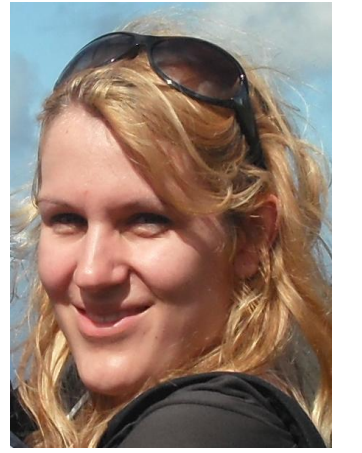
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Modelisation of genomic selection in French dairy goats

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Introduction

- Illumina 50K goat bead chip in 2011
- 2 **multi-breed** (Alpine and Saanen) populations with genotypes:
 - 1,985 **females** from commercial flocks born between 2008 and 2009 and their 20 sires
 - 657 artificial insemination **bucks** born between 1993 and 2009 and 148 young males born between 2010 and 2011
- Small generation interval (less than 4 years in sire-daughter pathway)
- High value of accuracy of young bucks at birth

Objectives and strategy

1

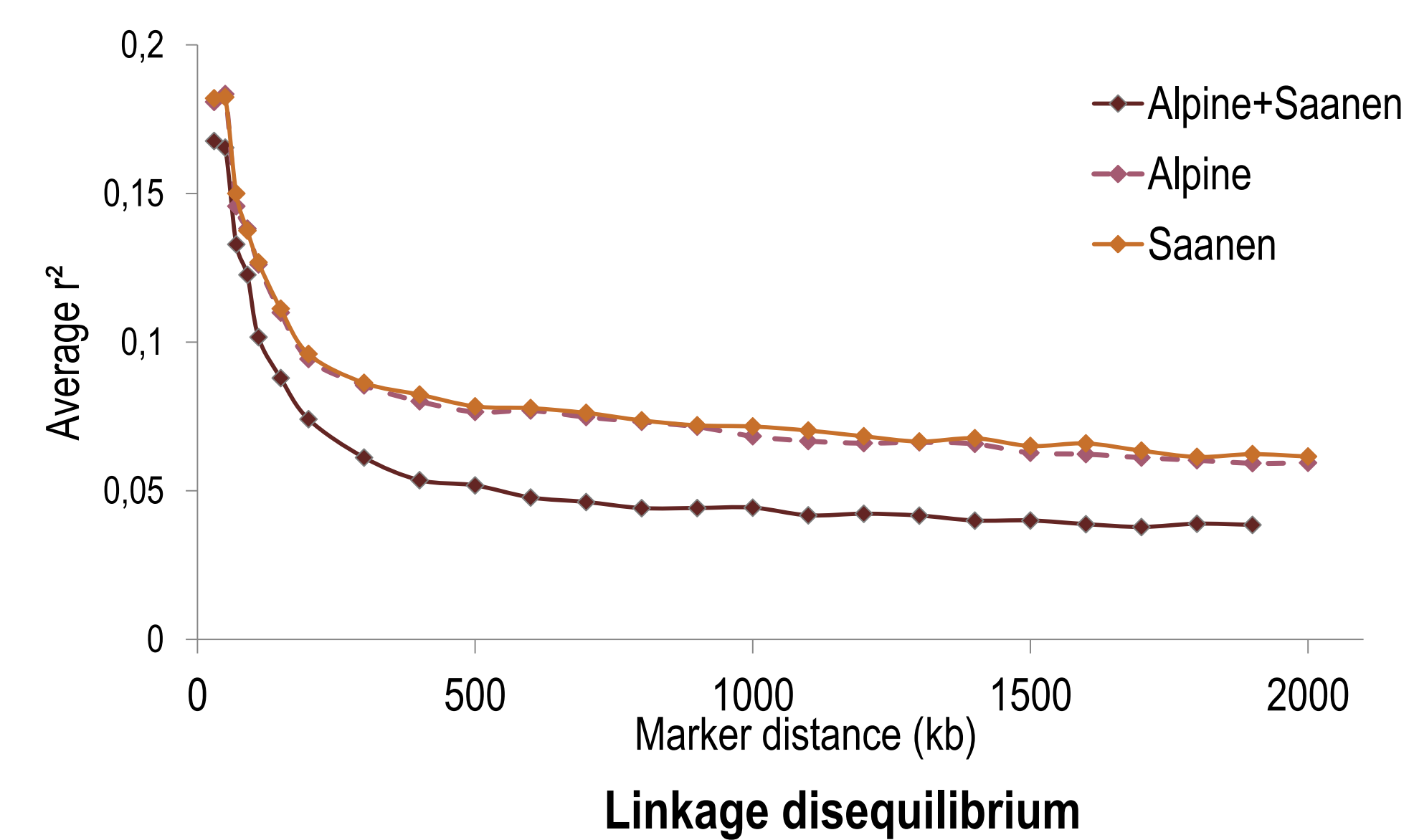
Characterization of reference population structure

Specificity: **Males and females**

Multi-breed

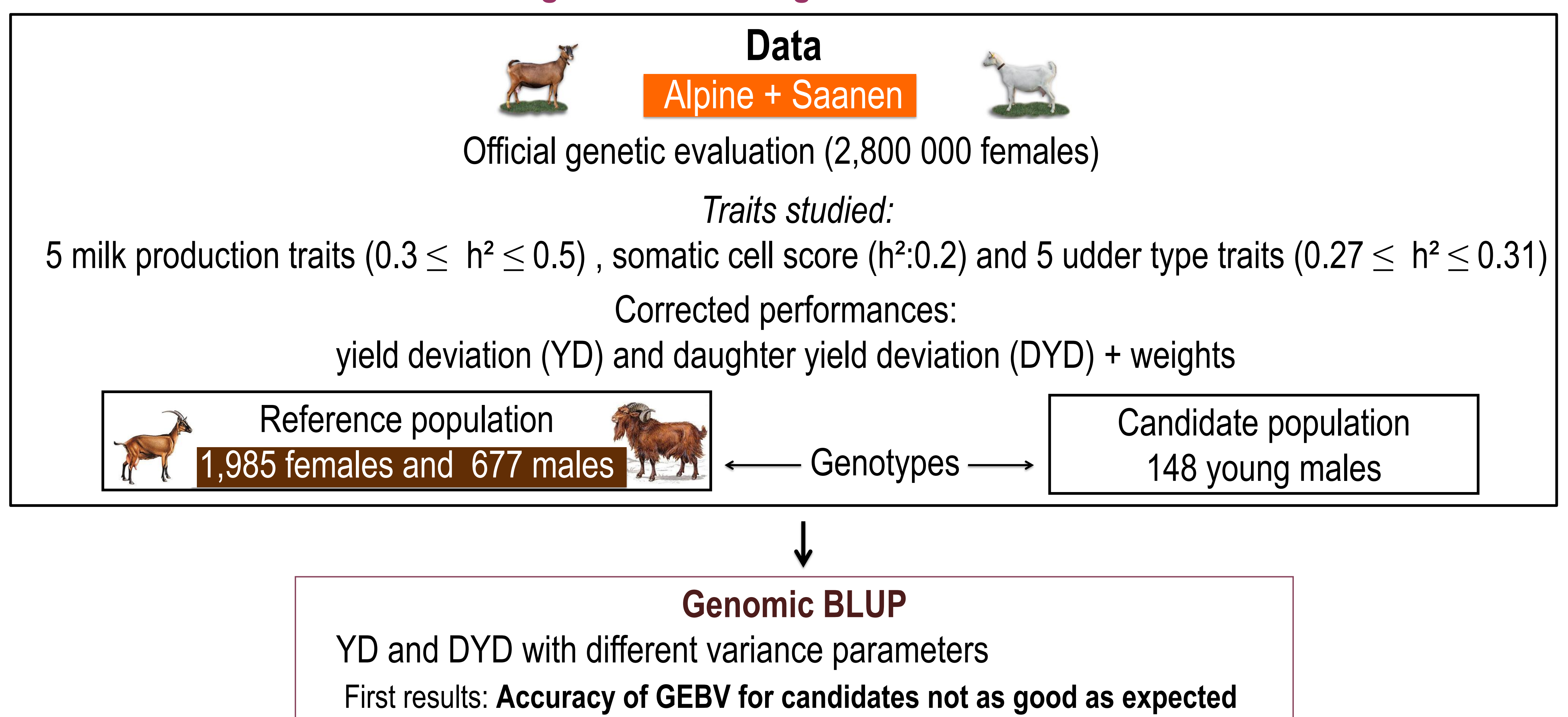
- Linkage disequilibrium
- Relationship (pedigree, genomic)

→ First results: **Not optimal for genomic selection**



2

Working on models for genomic evaluation



To be done

Multiple trait model

To take into account the variance components specific to each breed

Heteroskedastic genomic BLUP model:
heterogeneous variances

Single step model

Performances of all females
+ genotypes of males and females
+ pedigree information

Model using **haplotypes** instead of SNP by SNP

3

Advices and strategies for future

Identify the best suited genomic model, which animals should be genotyped, SNP with largest effects



Funding

Midi Pyrénées region
INRA with selGen program

Background

Master degree in animal breeding and genetics (AgroParis Tech)
Master degree in agronomic engineering (AgroSup Dijon)

■ 16^e Séminaire des thésards du Département de Génétique Animale ■ Amboise, 2 & 3 avril 2013 ■

