Modelisation of genomic selection in French dairy goats

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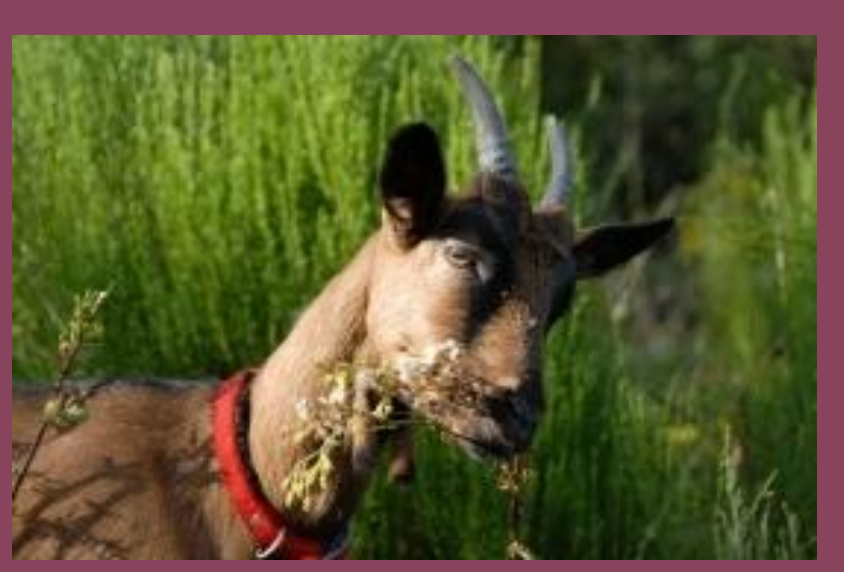
Introduction

- 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
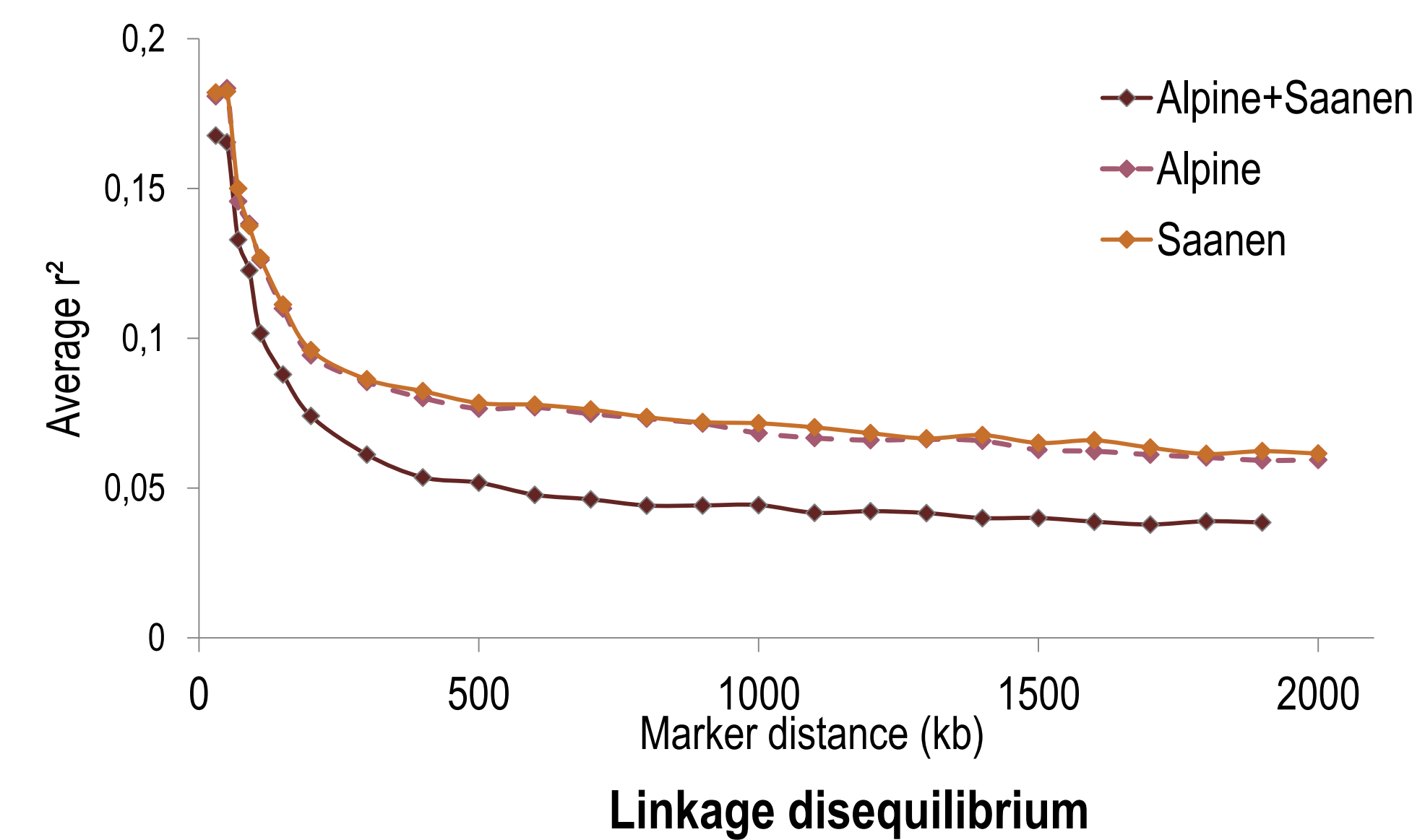
Objectives and strategy

1

Characterization of reference population structure
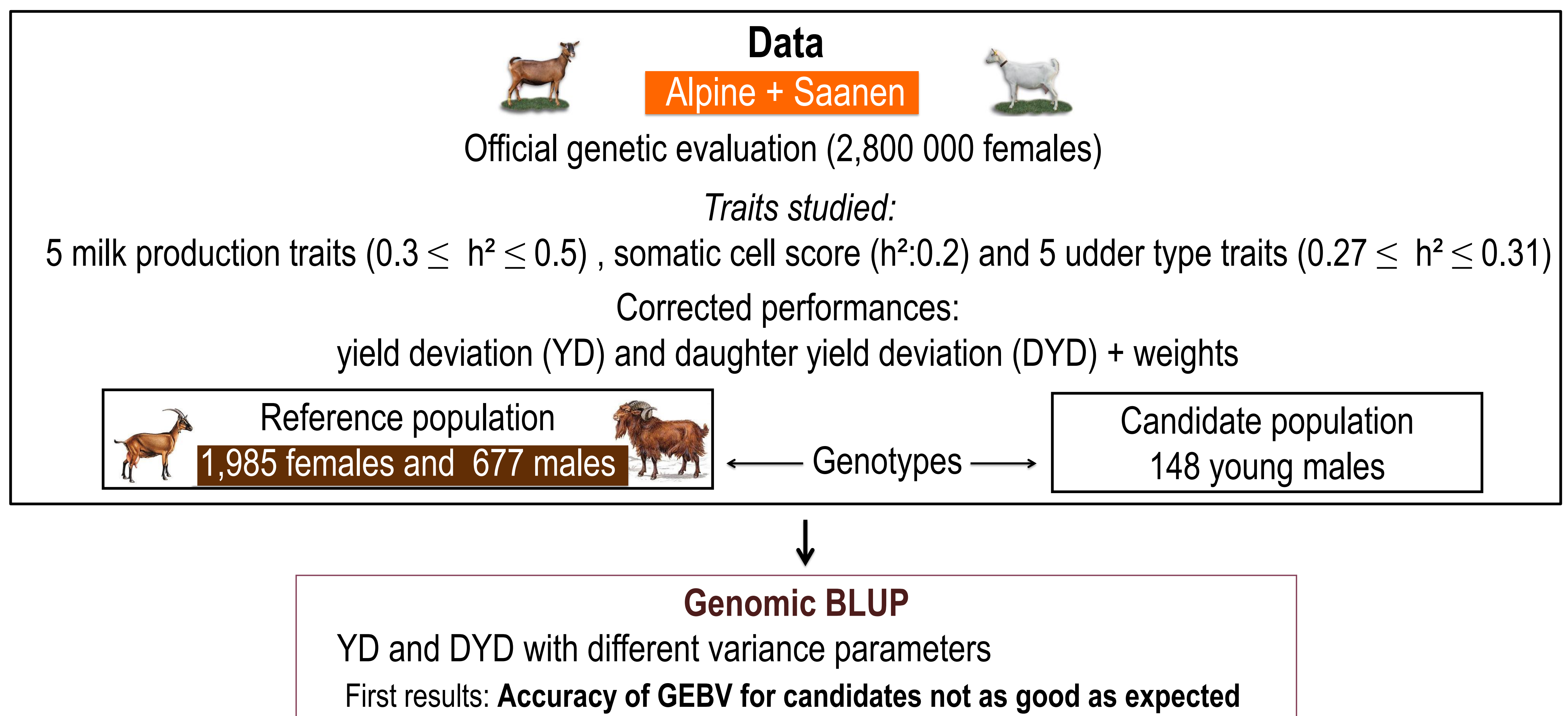
Specificity: **Males and females**

Multi-breed

- Linkage disequilibrium
- Relationship (pedigree, genomic)

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

Linkage disequilibrium

2 **Working on models for genomic evaluation**

Data

Alpine + Saanen

Official genetic evaluation (2,800 000 females)

Traits studied:

5 milk production traits $(0.3 \leq h^2 \leq 0.5)$, somatic cell score $(h^2:0.2)$ and 5 udder type traits $(0.27 \leq h^2 \leq 0.31)$

Corrected performances:

yield deviation (YD) and daughter yield deviation (DYD) + weights

Reference population
1,985 females and 677 males ← Genotypes → Candidate population
148 young males

Genomic BLUP

YD and DYD with different variance parameters

First results: **Accuracy of GEBV for candidates not as good as expected**

-- To be done --

Multiple trait model
To take into account the variance components specific to each breed

Single step model
Performances of all females
+ genotypes of males and females
+ pedigree information

Heteroskedastic genomic BLUP model:
heterogeneous variances

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)

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

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