Toward genomic selection in French dairy goats

Céline Carillier, Helene H. Larroque, Christèle Robert-Granié

Céline Carillier, Helene H. Larroque, Christèle Robert-Granié. Toward genomic selection in French dairy goats. 23. International Plant and Animal Genome, Jan 2015, San Diego, United States. pp.1. hal-02792341

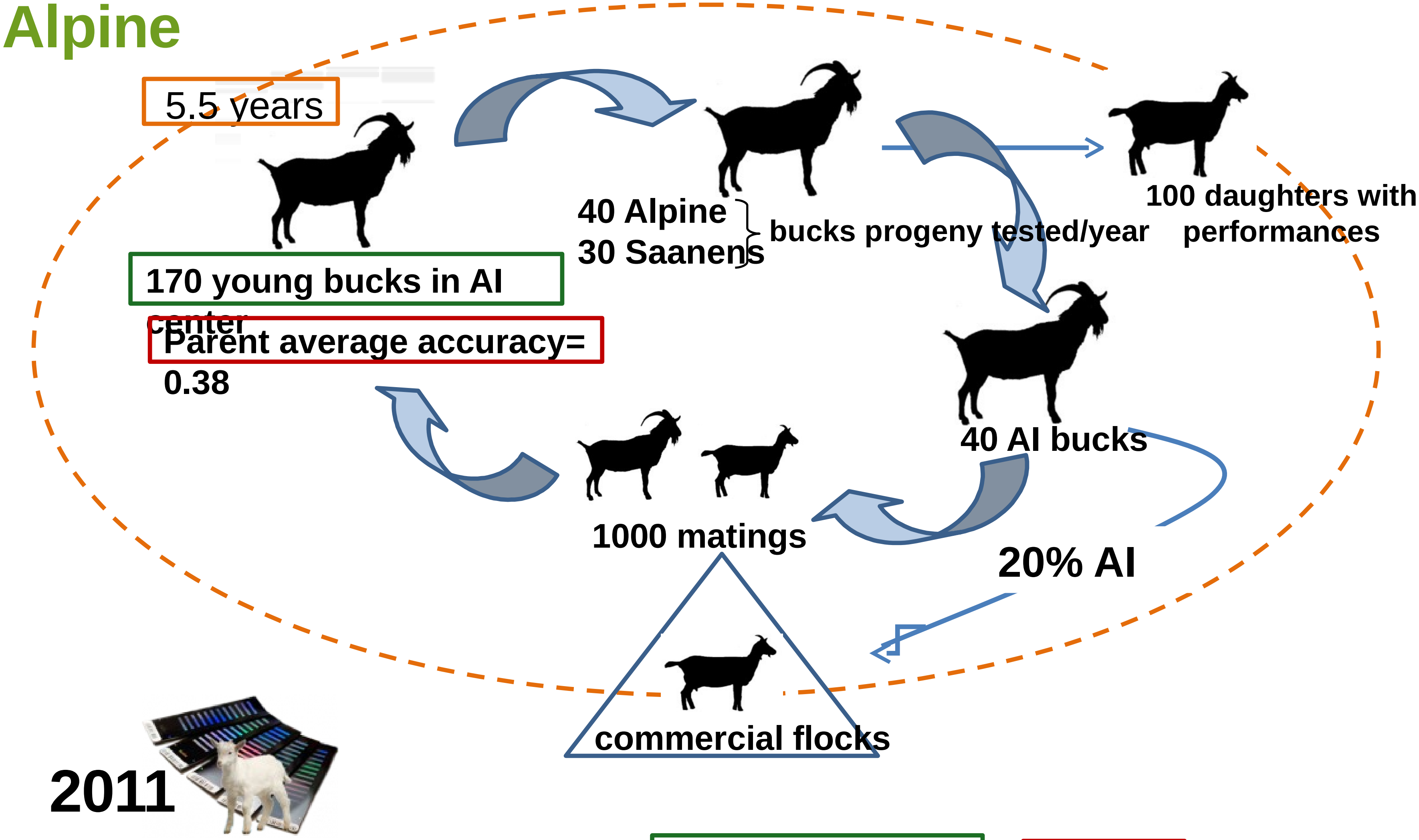
Toward genomic selection in French dairy goats

Céline Carillier
Christèle Robert-Granié.
Hélène Larroque

INRA-GenPhySE. Toulouse. France

PAG XXIII. IGGC. January 12th 2015. San Diego. USA

Classical breeding scheme in French Saanen and Alpine



5.5 years

170 young bucks in AI center

Parent average accuracy= 0.38

40 Alpine
30 Saanens } bucks progeny tested/year

100 daughters with performances

40 AI bucks

20% AI

1000 matings

commercial flocks

2011

$$\text{Annual genetic gain} = \frac{\boxed{\text{selection intensity}} \times \boxed{\text{accuracy}} \times \sigma_A}{\boxed{\text{generation interval}}}$$

The French dairy goat population: small size, 2 breeds

46 959 SNP after quality control

reference population

677 ♂

all♂ progeny tested since 1993

232 Alpines	**training set 425**	**193 Saanens**
152 Alpines	**validation set 252**	**100 Saanens**

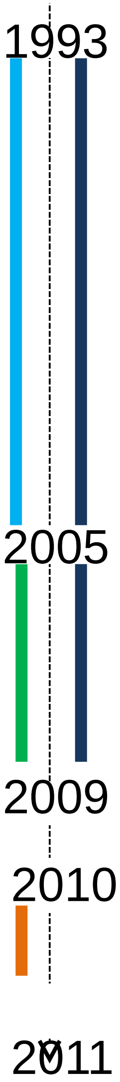
87 Alpines

candidates

148 ♂

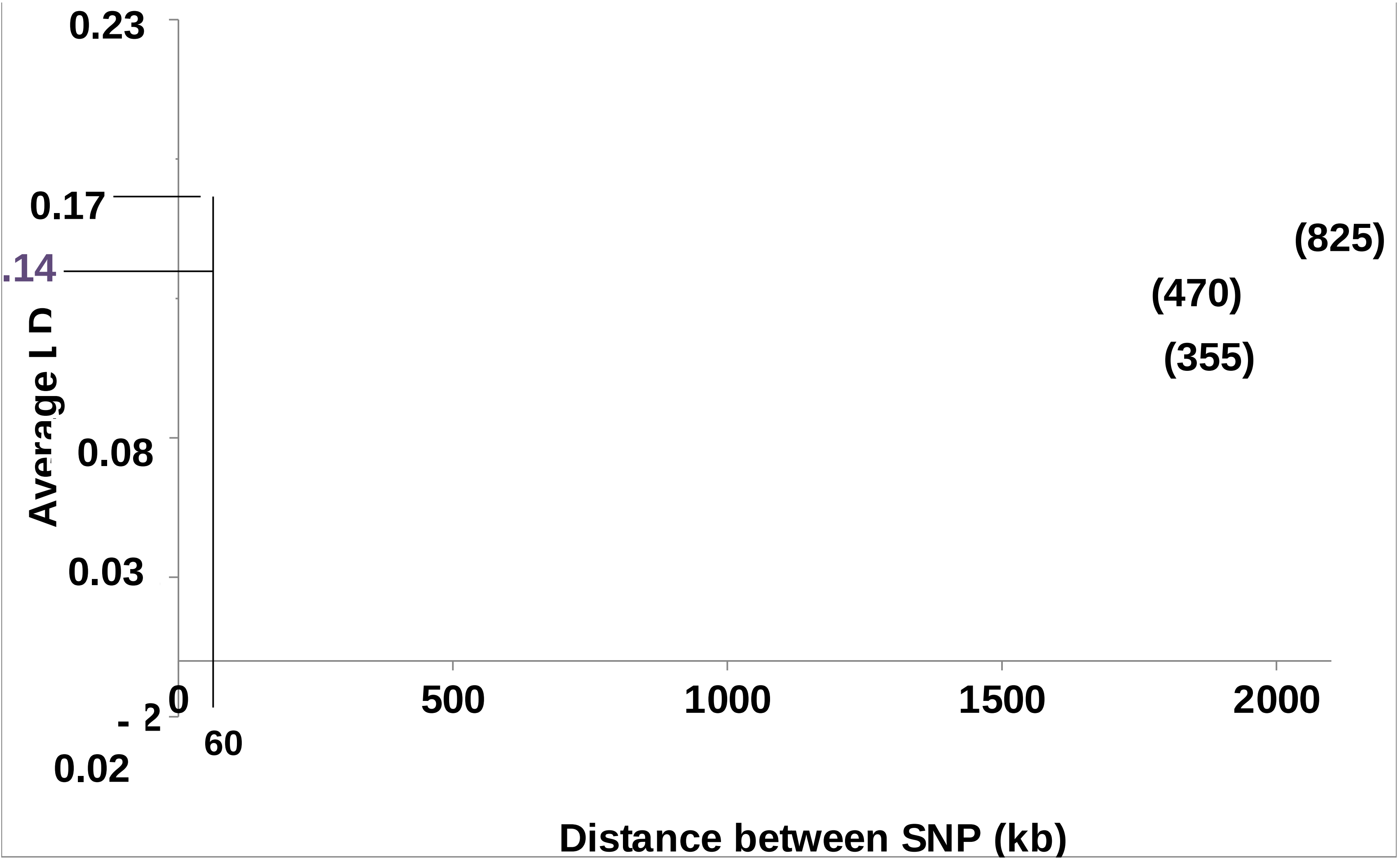
not progeny tested yet

61 Saanens



Genotype population structure

Low average linkage disequilibrium between SNP in dairy goats



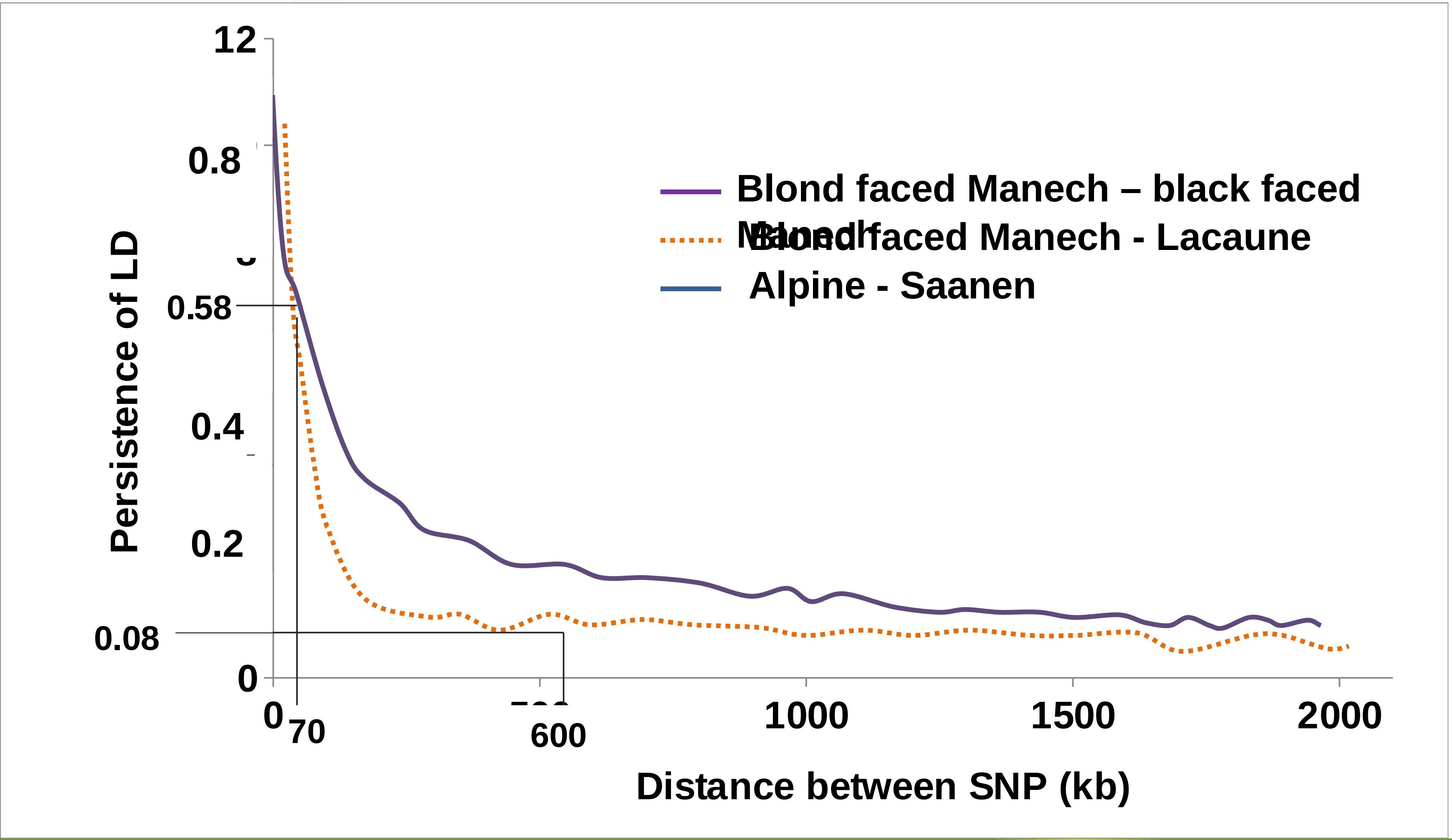
Good genetic diversity in Alpine and Saanen breeds

		Alpine	**Saanen**	***Multi-breed***
inbreeding	**reference population**	**1.8**	**2.3**	***2.1***
kinship	**between reference and candidates**	**1.1**	**2.4**	***0.7***

- high genetic diversity compare to dairy cattle or Lacaune dairy sheep
- Low LD between 2 SNP
- Low relationship between candidate and reference populations for Alpine

 Difficulties for genomic prediction

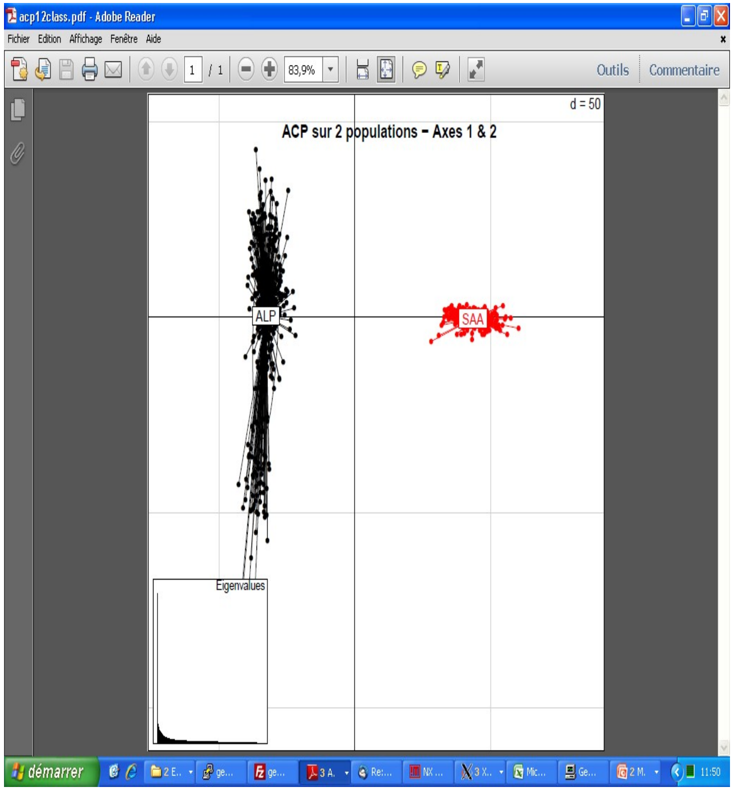
Alpine and Saanen two different breeds according to persistence of LD



Alpine genomic structure different from Saanen one

Allele frequency correlation between Saanen and Alpine breeds:

Males:	**0.69**
Females:	**0.85**



- Low persistence of LD between Alpine and Saanen
- Low correlation between allele frequencies

 Alpine and Saanen = two different breeds

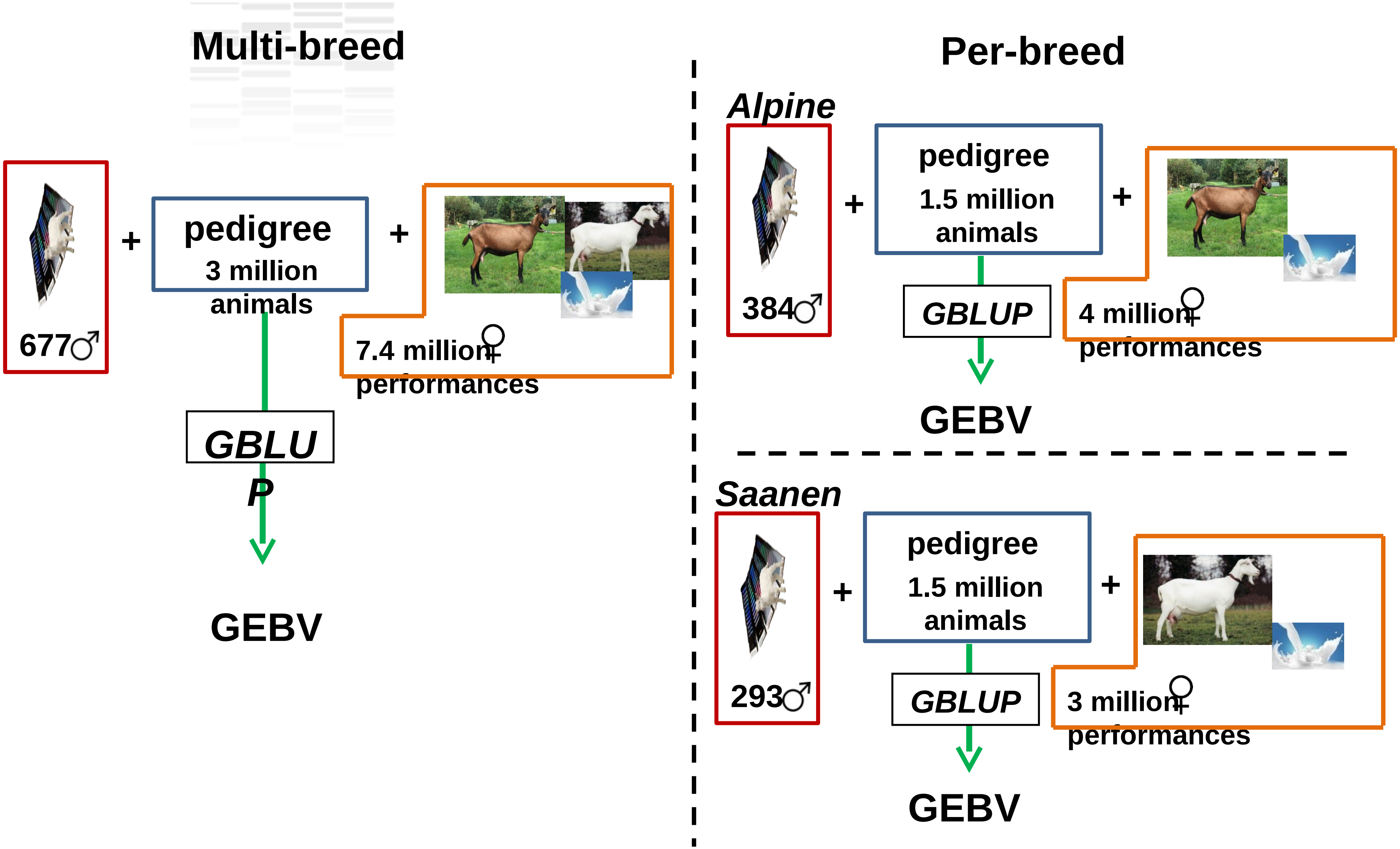
PCA on genotypes, factor = breed

Axis 1 and 2

Genomic selection

INRA
SCIENCE & IMPACT

Per-breed vs multi-breed genomic selection



Multi-breed

677♂ + **pedigree** 3 million animals + 7.4 million♀ performances

GBLUP

GEBV

Per-breed

Alpine

384♂ + **pedigree** 1.5 million animals + 4 million♀ performances

GBLUP

GEBV

Saanen

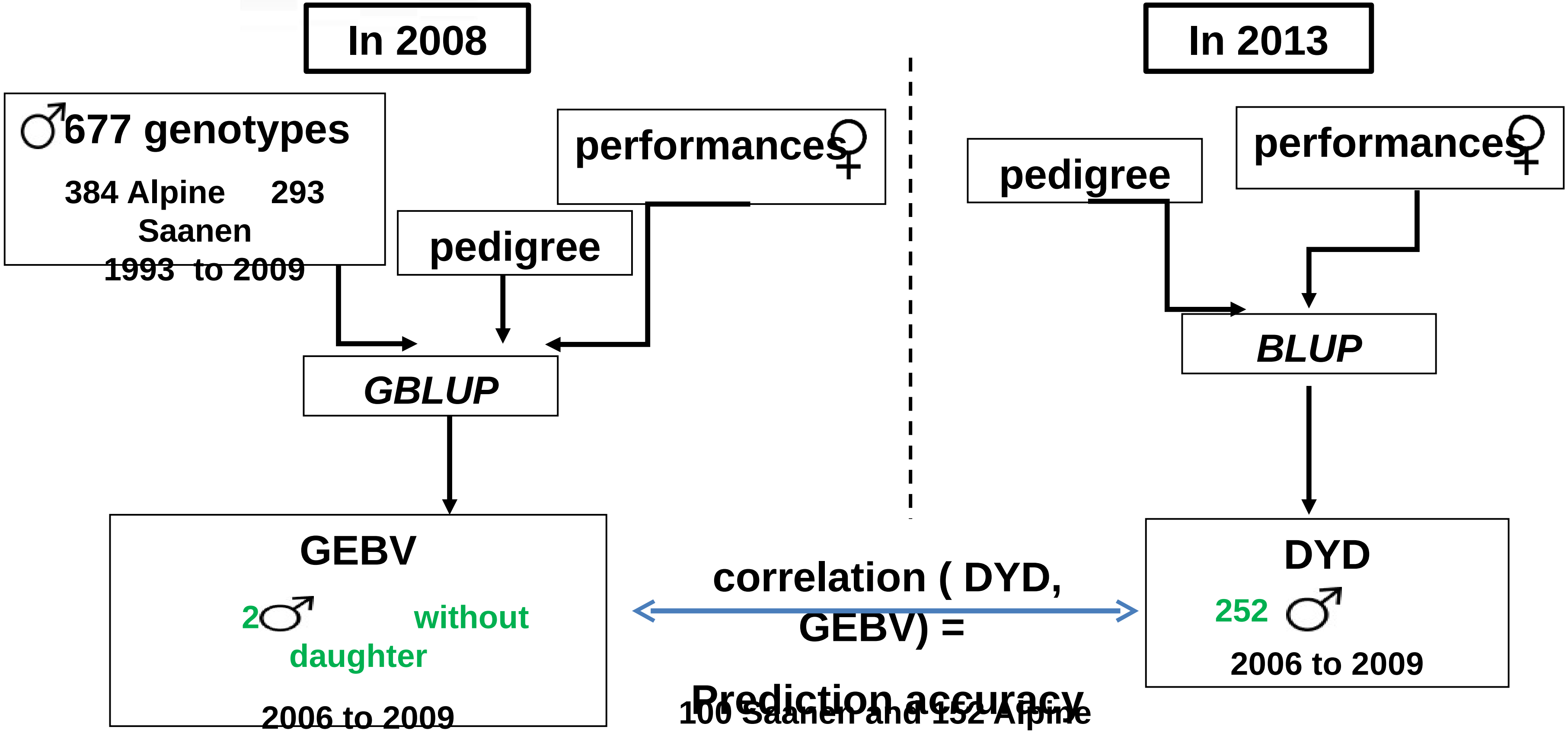
293♂ + **pedigree** 1.5 million animals + 3 million♀ performances

GBLUP

GEBV

GEBV= genomic estimated breeding value

Evaluation of prediction quality of genomic selection



In 2008

♂677 genotypes

384 Alpine 293 Saanen

1993 to 2009

performances♀

pedigree

GBLUP

GEBV

2♂ without daughter

2006 to 2009

correlation (DYD, GEBV) =

Prediction accuracy

100 Saanen and 152 Alpine

In 2013

pedigree

performances♀

BLUP

DYD

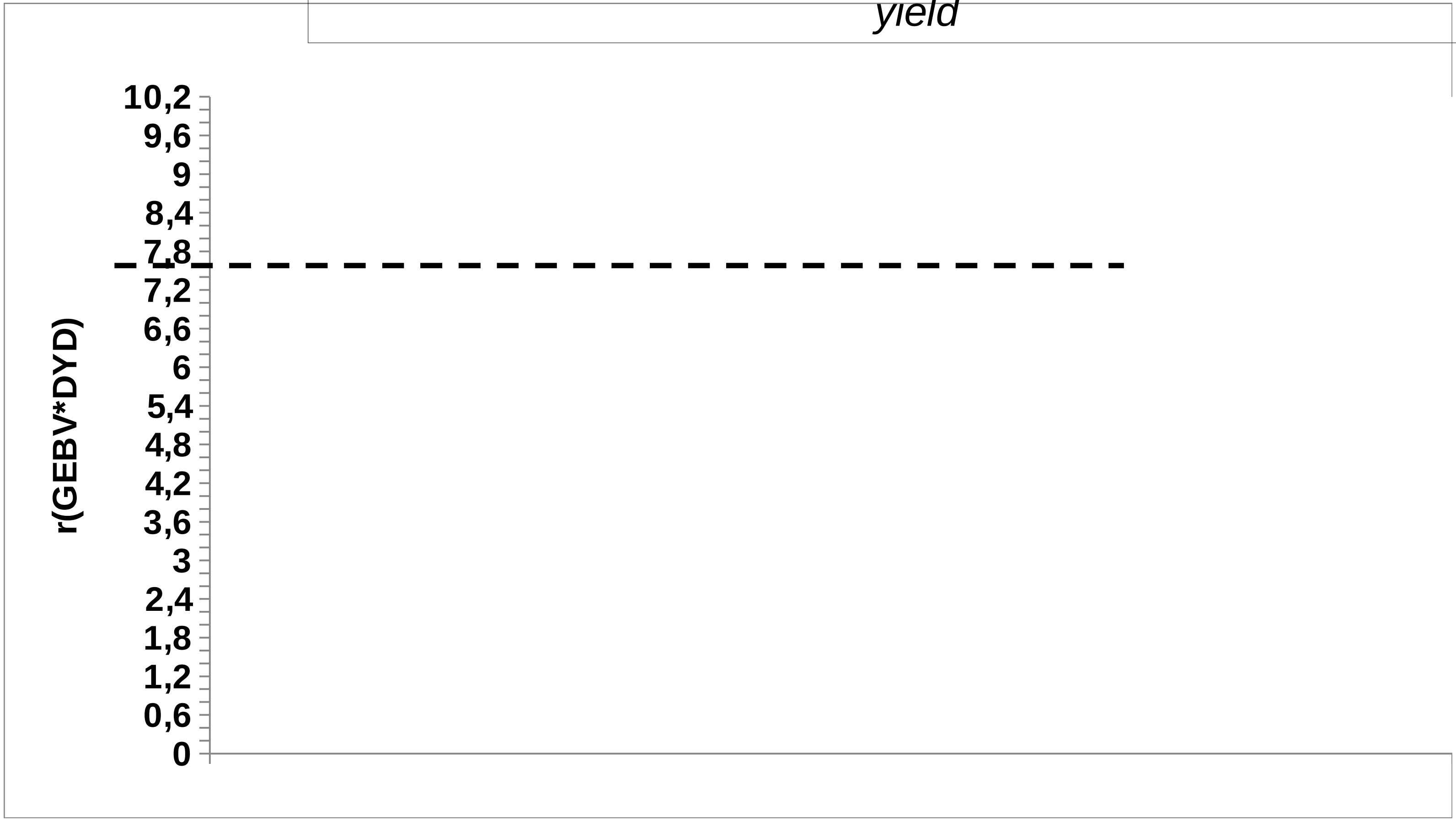
252 ♂

2006 to 2009

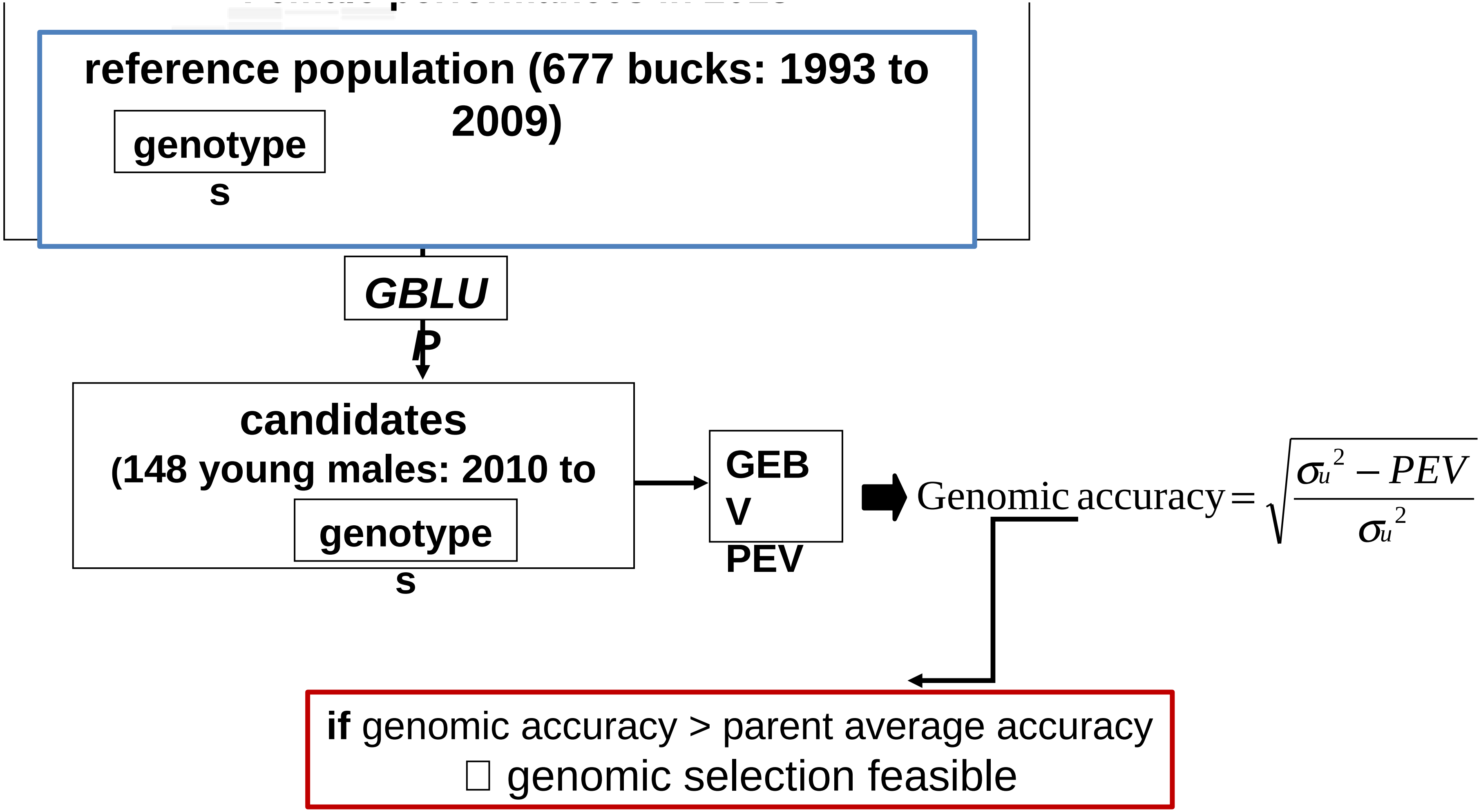
GEBV= genomic estimated breeding value
DYD=daughter yield deviation

Similar prediction accuracies whatever the model used

Lacaune dairy sheep and Montbéliarde dairy cattle: 0.47 on milk yield



A way to estimate feasibility of genomic selection



reference population (677 bucks: 1993 to 2009)

genotypes

GBLUP

candidates

(148 young males: 2010 to

genotypes

GEBV

PEV

$$\text{Genomic accuracy} = \sqrt{\frac{\sigma_u^2 - PEV}{\sigma_u^2}}$$

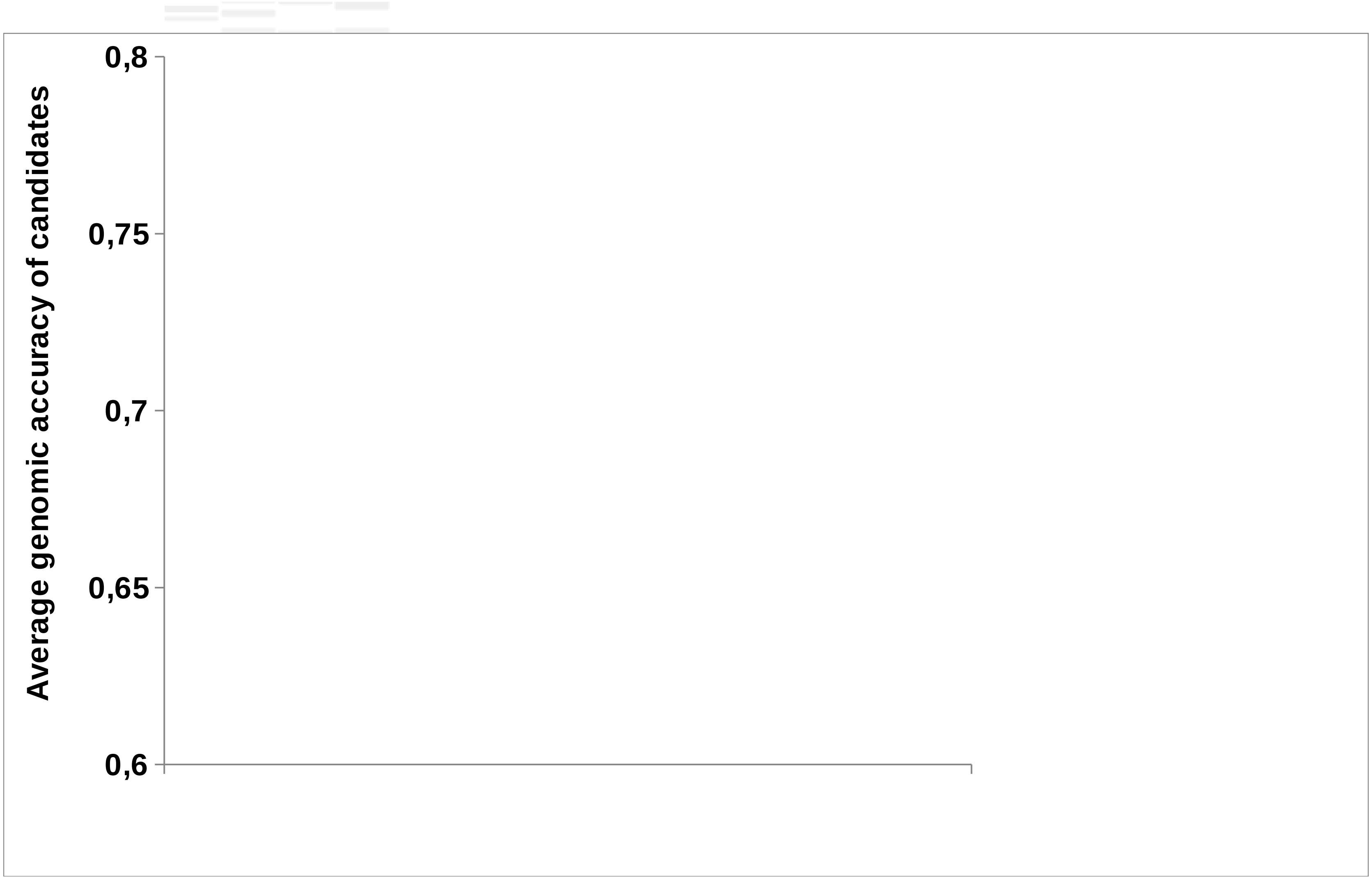
if genomic accuracy > parent average accuracy

 genomic selection feasible

GEBV= genomic estimated breeding value

PEV=prediction error variance

Genomic accuracy of candidates exceeds parent average one



Genomic selection with single-step is feasible in goats

population

- **677♂ genotyped and phenotyped**
- **2 different breeds**
- **high genetic diversity, low LD**

Genomic evaluation*

prediction quality : - no difference between models
- not bad results with per-breed model

genomic accuracy > ascendance accuracy

➡ genomic selection feasible

Prospects

- **Evaluation of efficiency and cost of "genomic" breeding schemes** (with breeding organism)
- **Including major gene** (casein, DGAT1) **in genomic selection model**
- **Using other genomic tools:** Low density bead chip (females)
  High density bead chip (multi-breed)
  Sequence data

* Carillier et al. 2014. Genetic Selection Evolution. 46:67.