



Toward genomic selection in French dairy goats

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Toward genomic selection in French dairy goats

Céline Carillier

Christèle Robert-Granié.

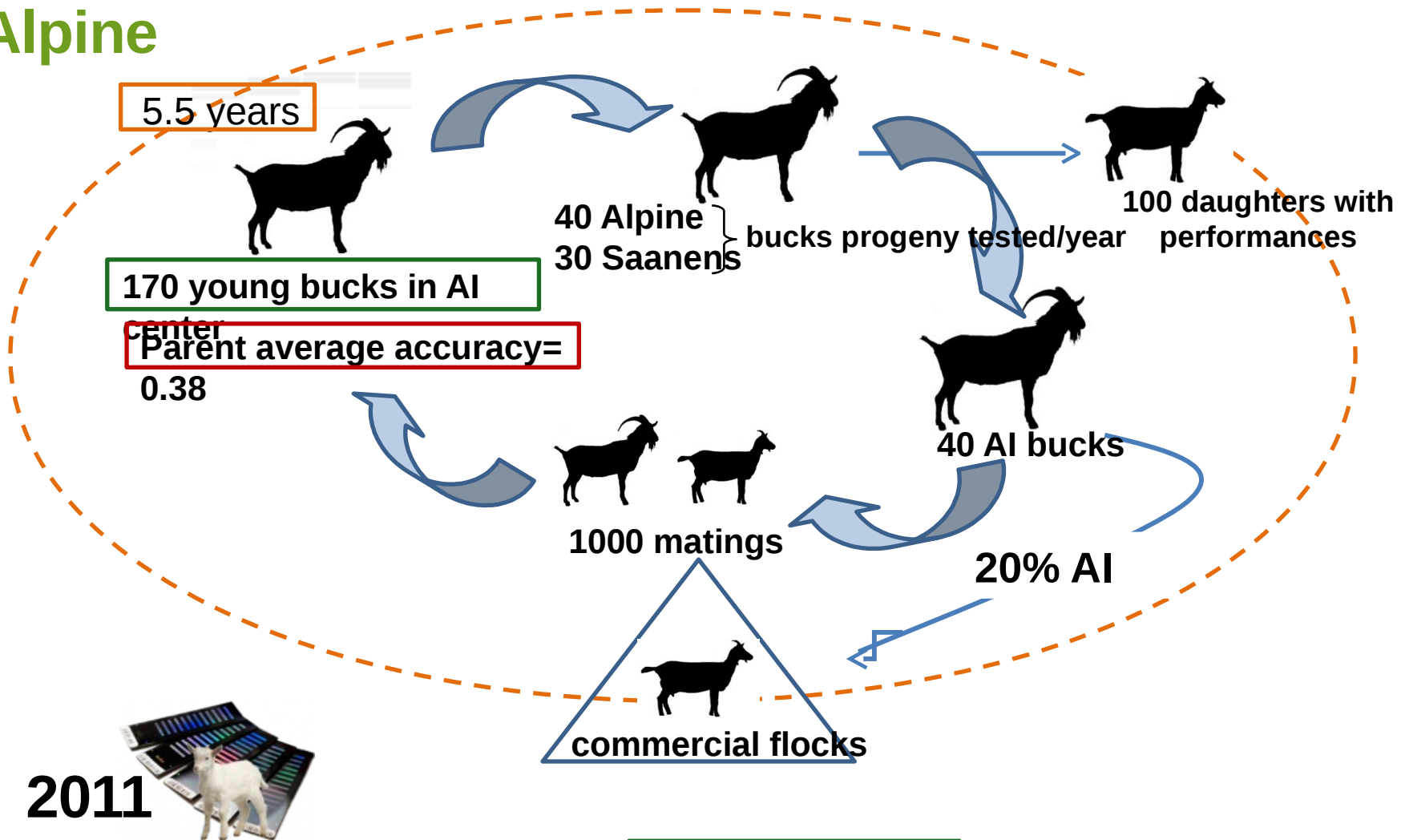
Hélène Larroque

INRA-GenPhySE. Toulouse. France



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

Classical breeding scheme in French Saanen and Alpine



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

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

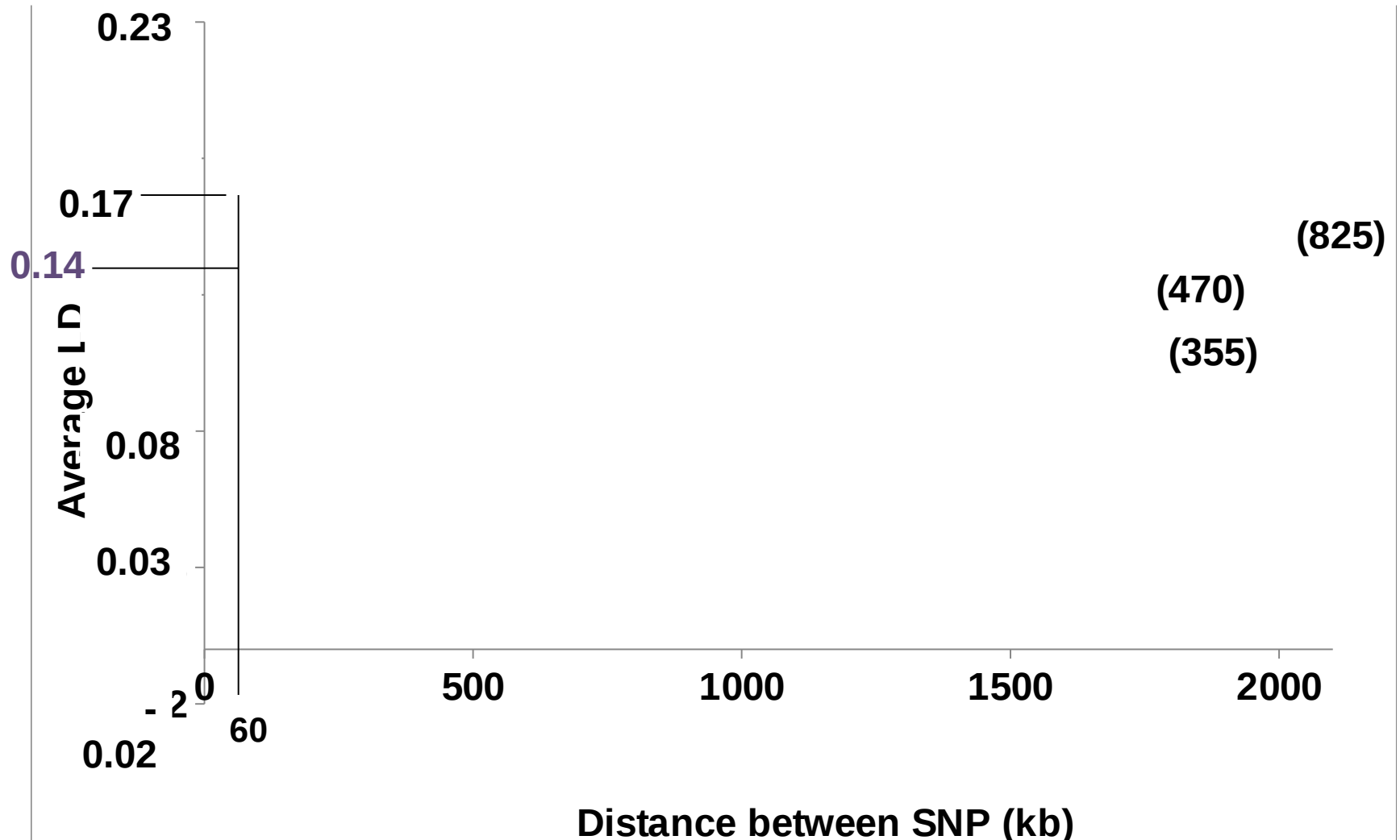


61 Saanens



Genotype population structure

Low average linkage disequilibrium between SNP in dairy goats



Good genetic diversity in Alpine and Saanen breeds

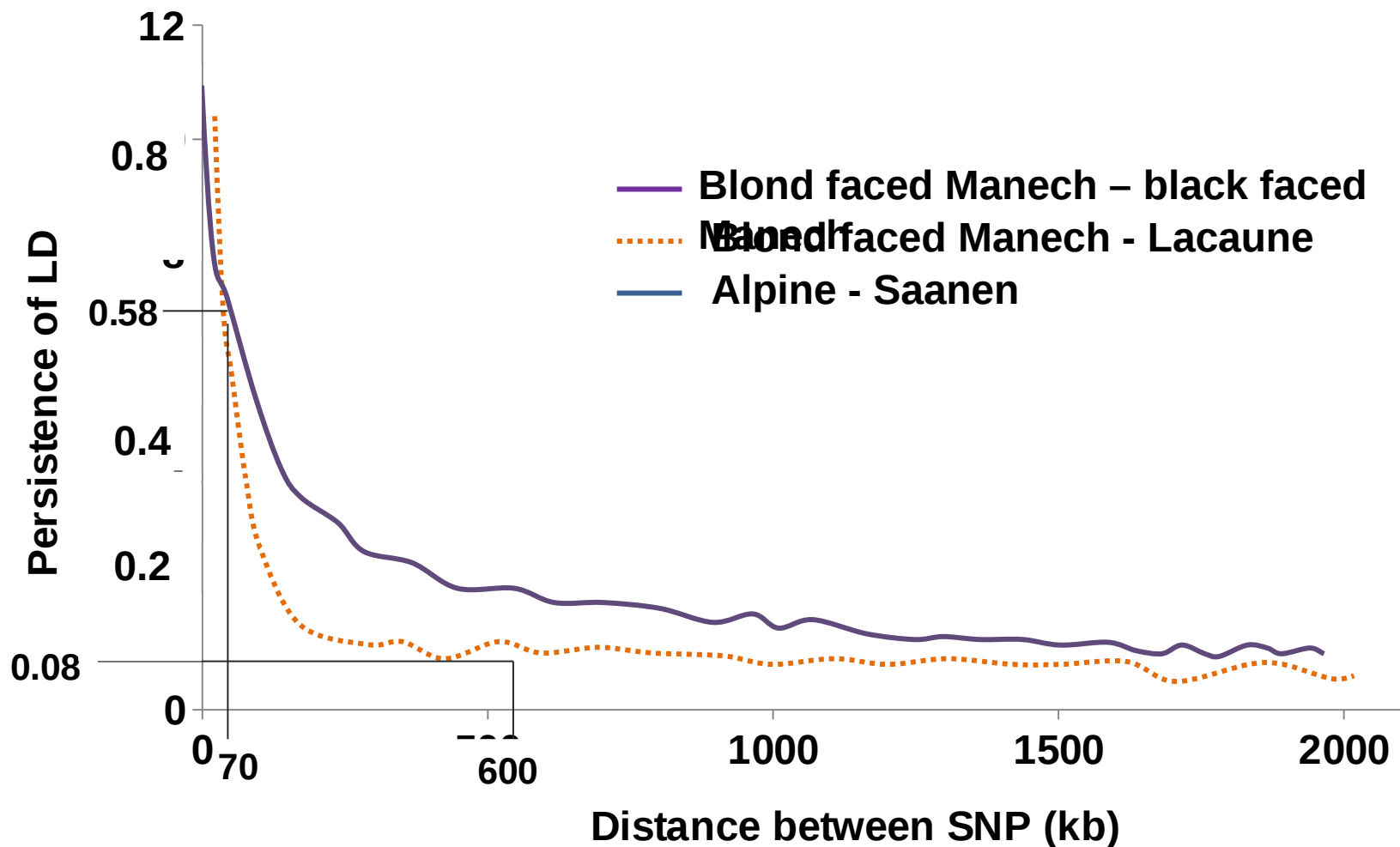


		Alpine	Saanen	<i>Multi-breed</i>
inbreeding	reference population	1.8	2.3	2.1
kinship	between reference and candidates	1.1	2.4	0.7

- ❖ 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**

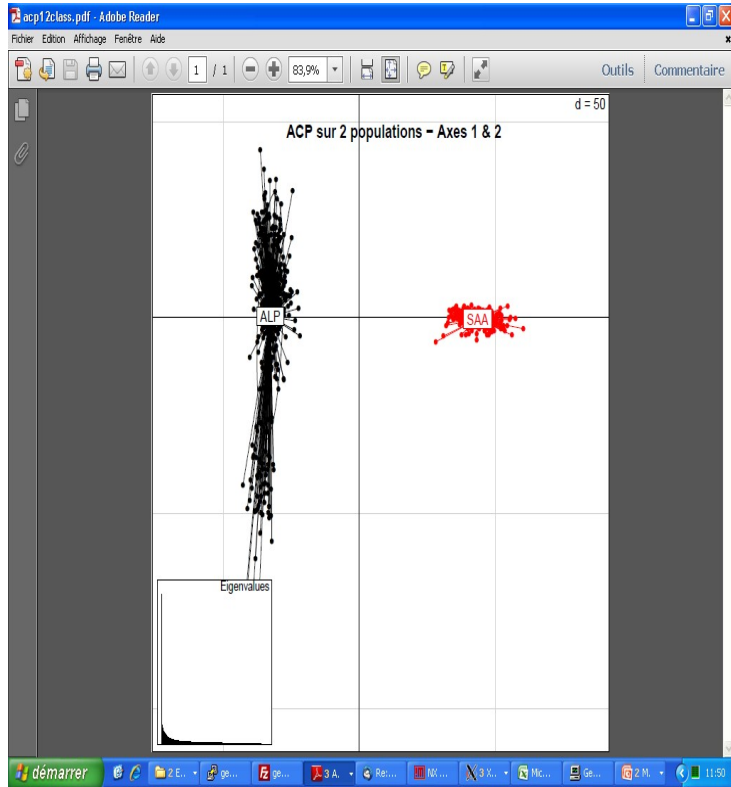
Alpine and Saanen two different breeds according to persistence of LD



Alpine genomic structure different from Saanen one

Allele frequency correlation between Saanen and Alpine breeds:

Males: 0.69
Female 0.85
S:

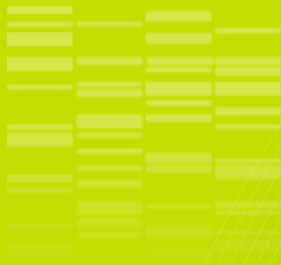


- ❖ Low persistence of LD between Alpine and Saanen
- ❖ Low correlation between allele frequencies

☐ **Alpine and Saanen = two different breeds**

PCA on genotypes, factor =
breed

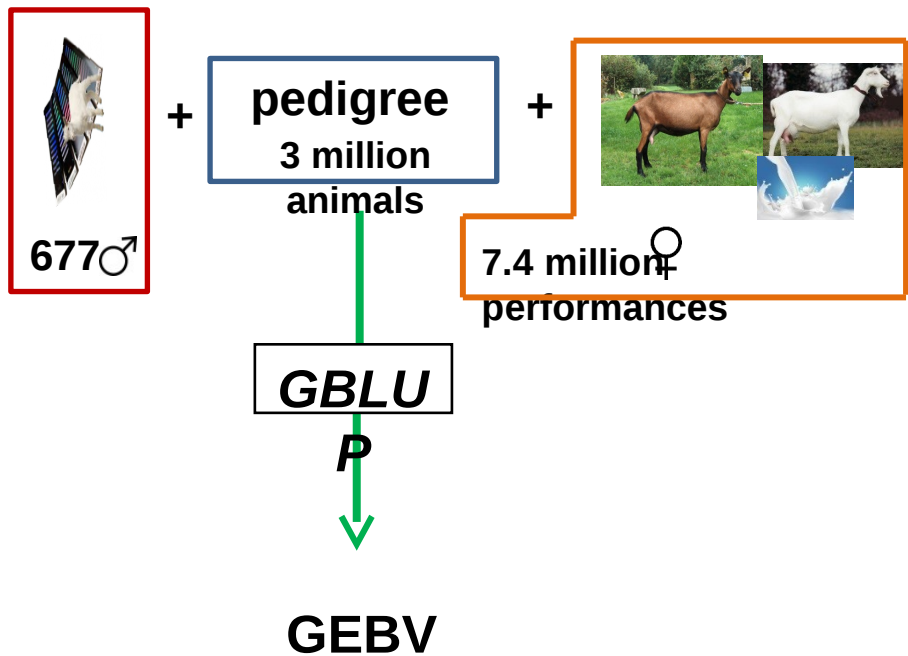
Axis 1 and 2



Genomic selection

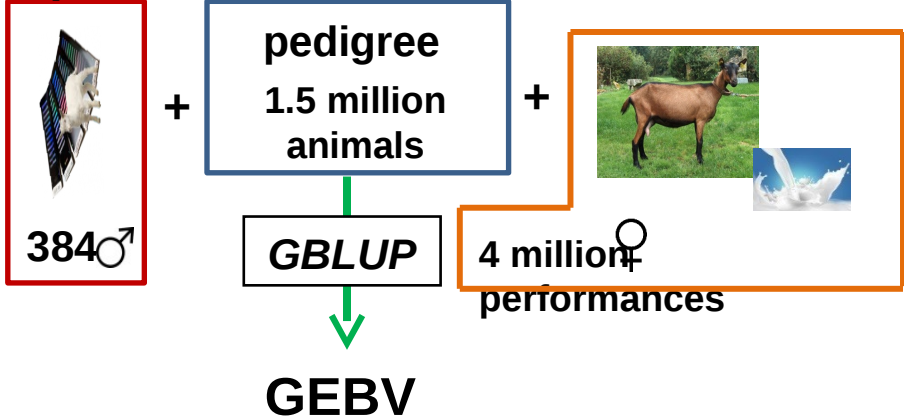
Per-breed vs multi-breed genomic selection

Multi-breed

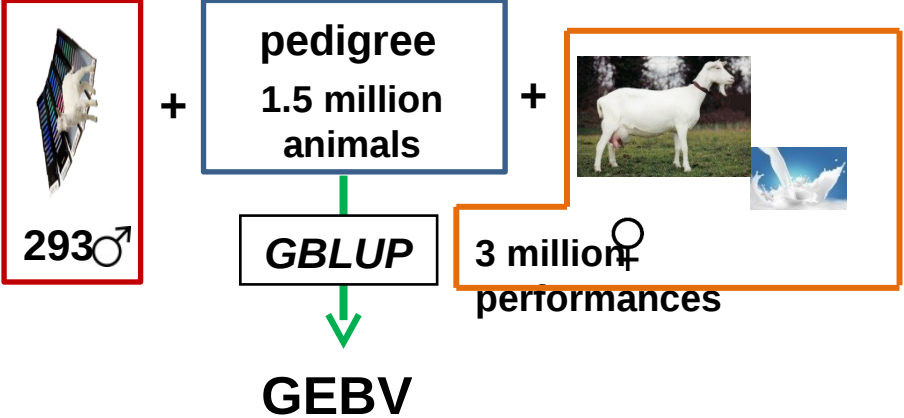


Per-breed

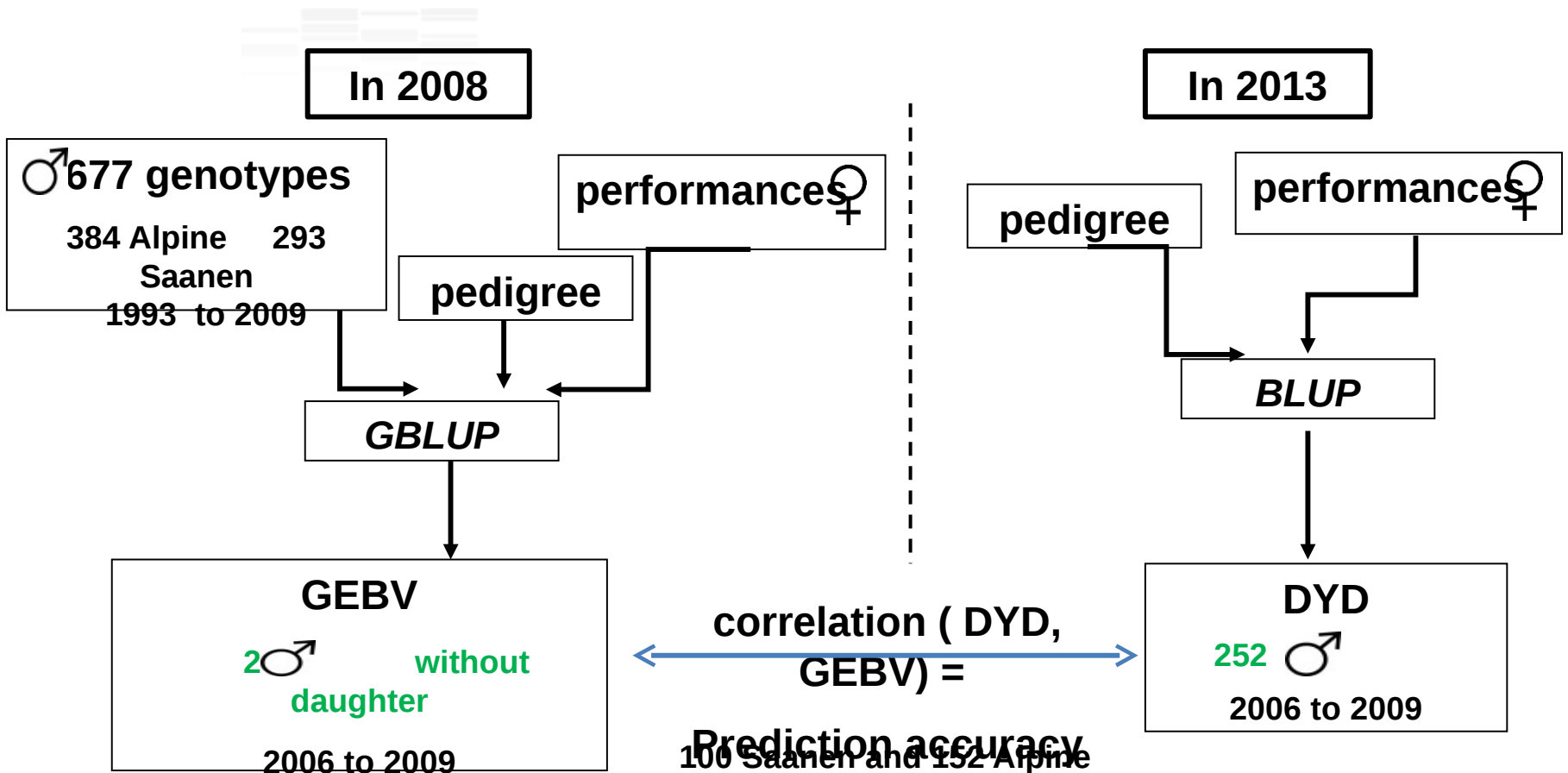
Alpine



Saanen

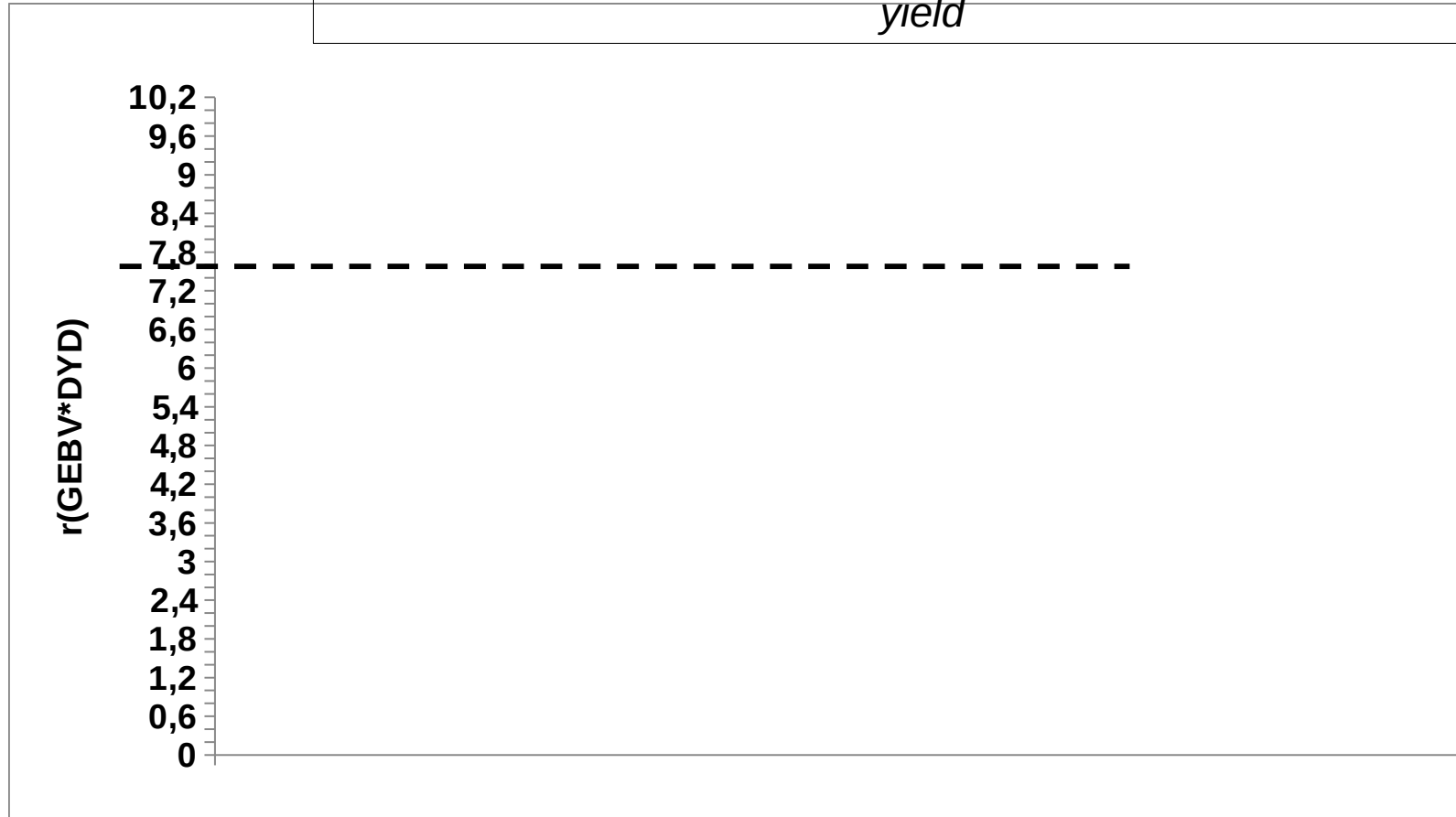


Evaluation of prediction quality of genomic selection

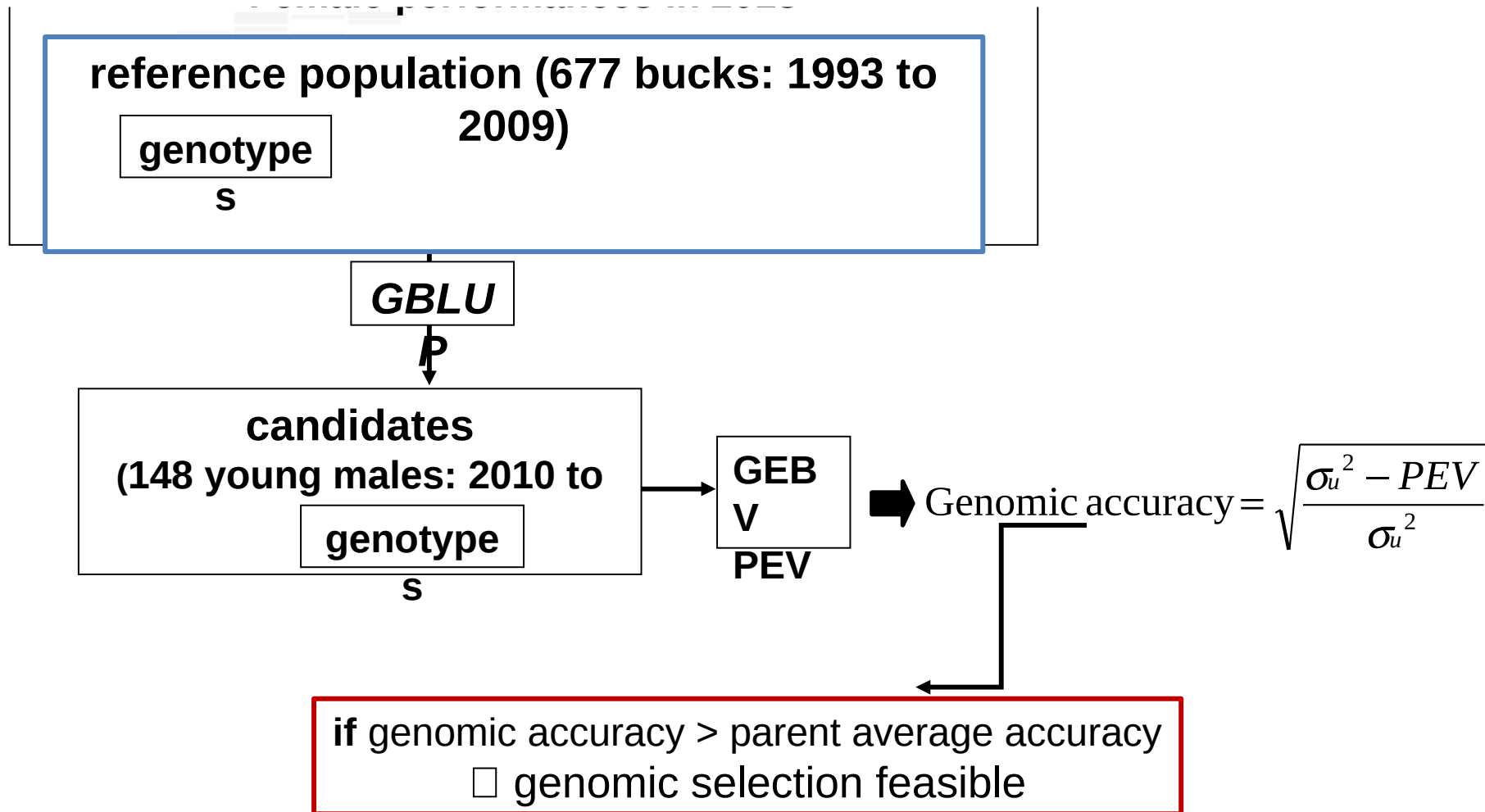


Similar prediction accuracies whatever the model used

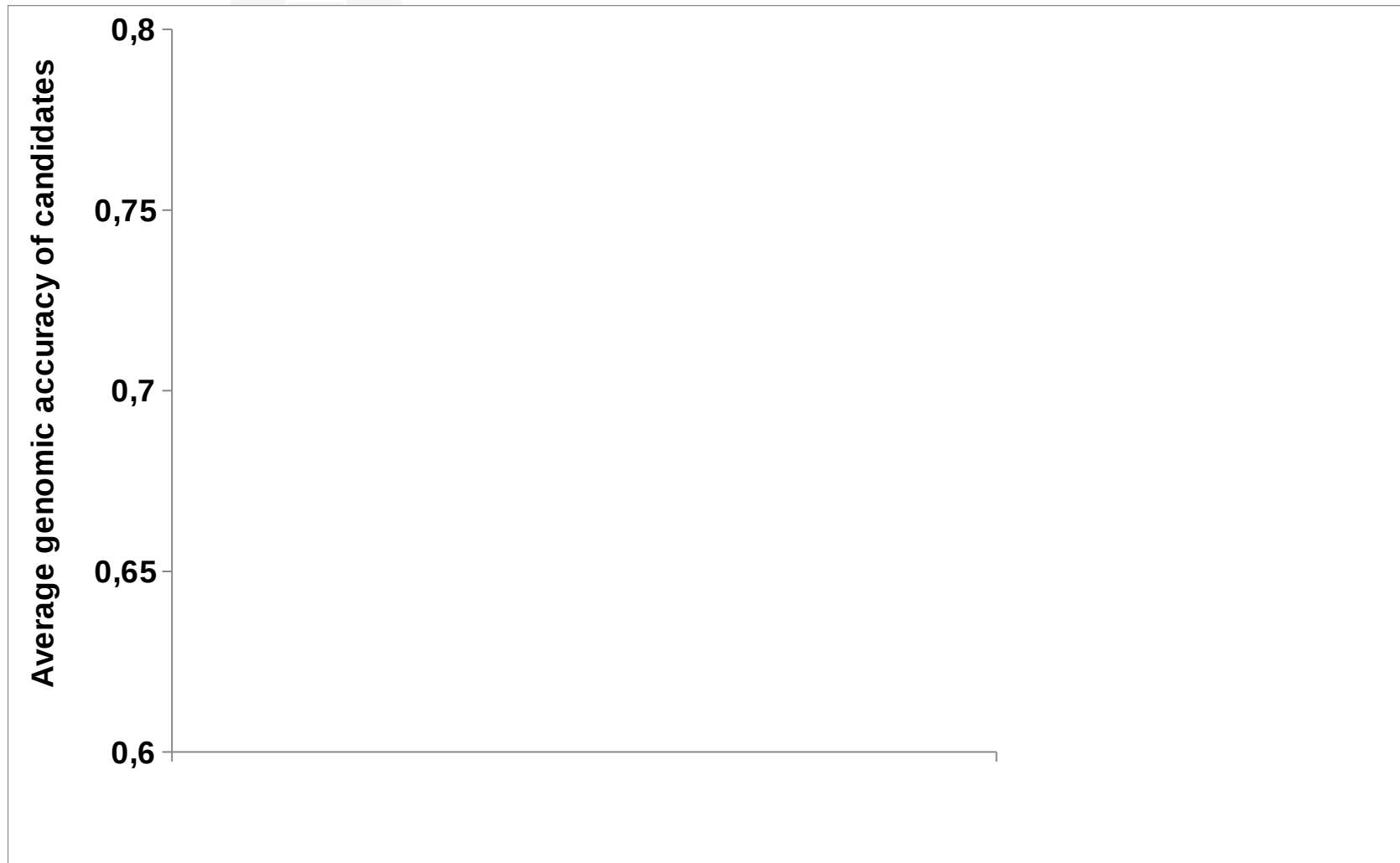
Lacaune dairy sheep and Montbéliarde dairy cattle: 0.47 on milk yield



A way to estimate feasibility of genomic selection



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