Toward genomic breeding programs in French dairy sheep and goats

H. Larroque INRA – GenPhySE / 10th WCGALP – Vancouver, BC, Canada – August 17-22, 2014 - # 332

Introduction

Genomic selection: new perspectives for breeding programs of dairy ruminants

✓ Genomic selection is expected to:

↗ Accuracy EBV from birth

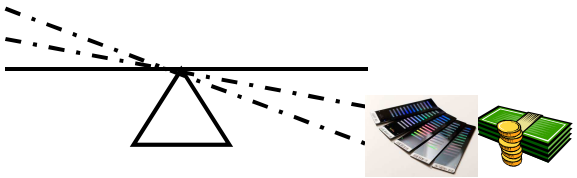
Progeny testing period ✗

} ↗ Annual genetic gain (**AGG**)

- **Dairy cattle**

↗ Accuracy (♂ at birth)
↗ Selection intensity
↘ Generation interval

↗↗ **AGG**



- **Small dairy ruminants**

AGG: Annual Genetic Gain

Introduction

Genomic selection for small dairy ruminants: a less favorable situation

✓ Higher **relative** cost of genotyping 

✓ Potential to ↗ **ΔG** :

- Intensity of genomic selection depends on:

↗ cost of genotyping ↘ artificial insemination livestock

↳ Fresh semen for AI in dairy sheep and demand highly concentrated in time

- Generation interval:

↳ Already short (4-5 years)

- Accuracy of GEBV depends on:
  - Characteristics of the reference population
  - Methods and evaluation models

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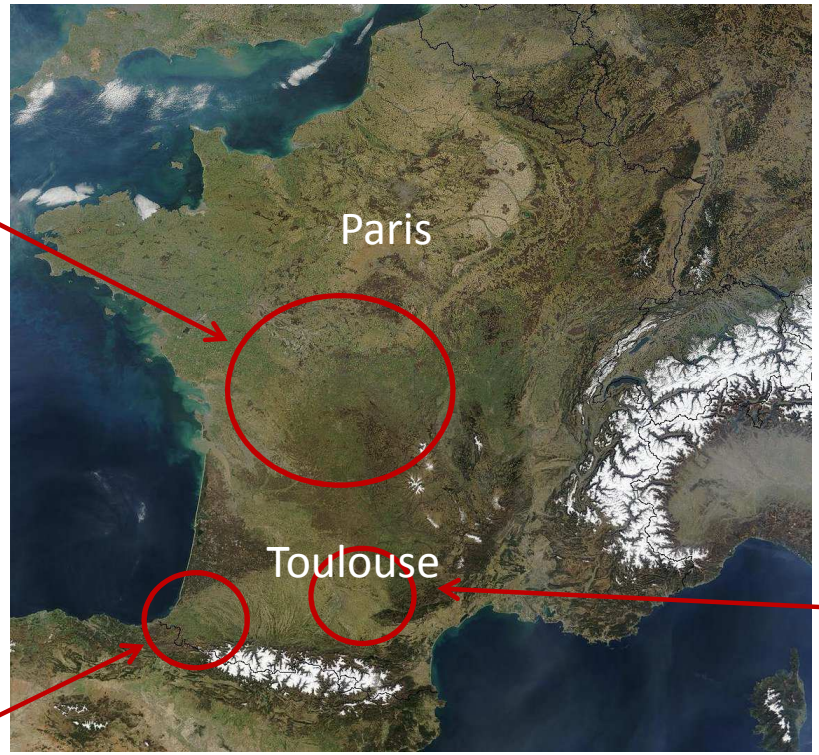
Populations

Populations

Breeding programs

Alpine (159,000)

Saanen (108,000)



Pyrenean sheep breeds:

Black-Faced Manech (13,000)

Basco-Béarnais (24,000)

Blond-Faced Manech (76,000)

Lacaune (170,000)

(♀ in official milk recording)

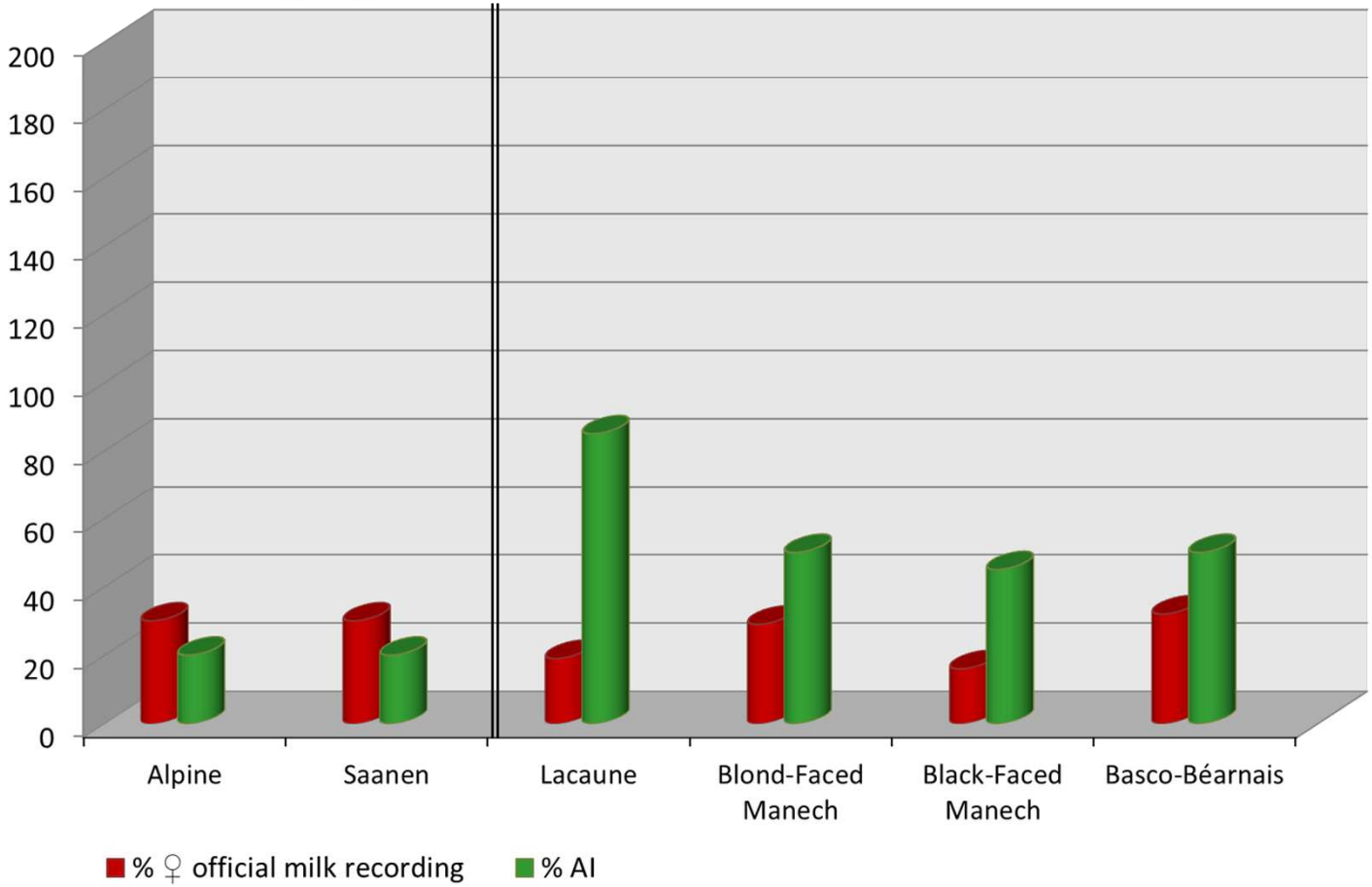
Photos: D. Hardy (La Chèvre); Upra Lacaune; Coram

Populations

Breeding programs

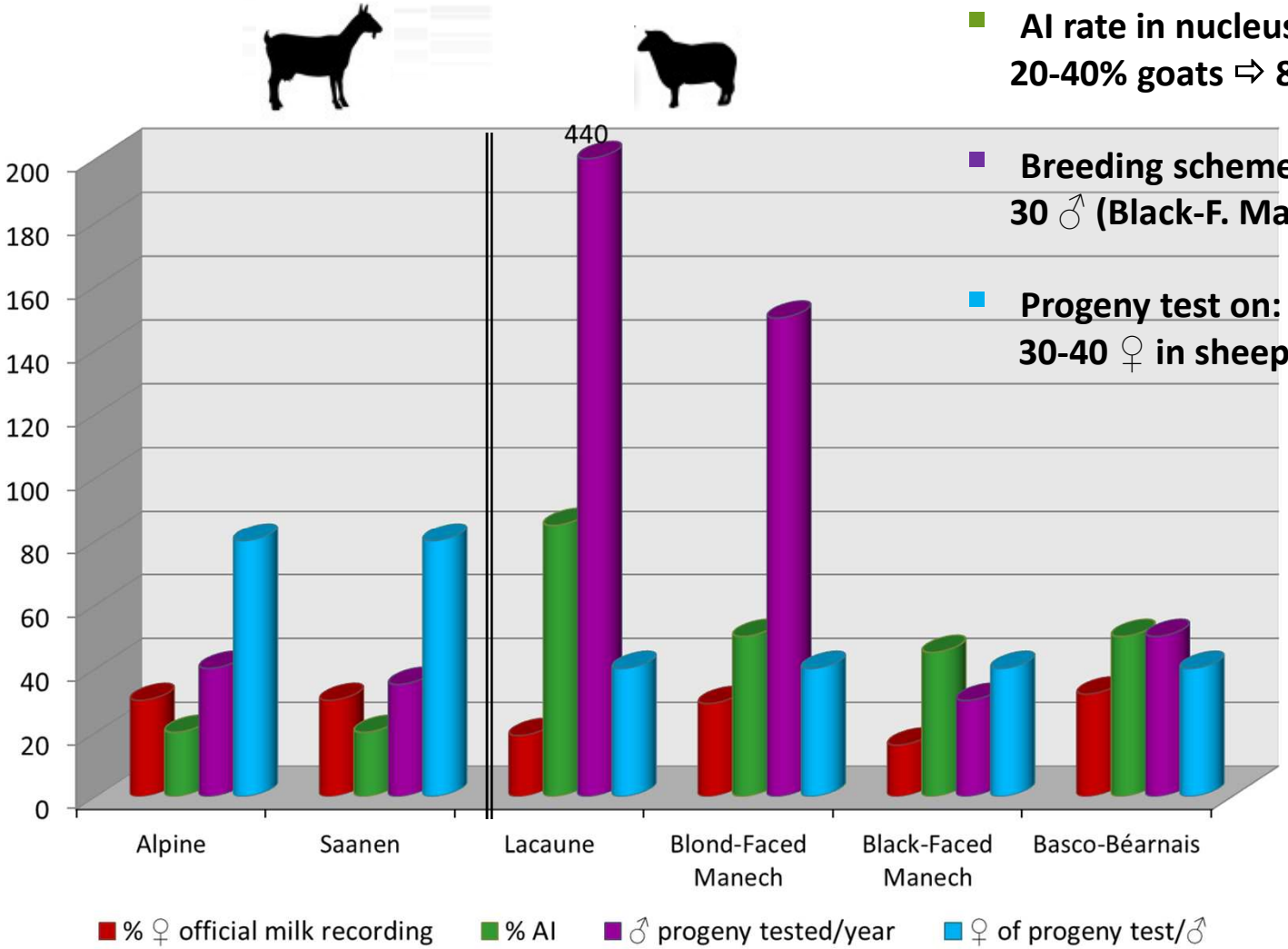
Characteristics

- **20-30% ♀ in official milk recording**
- **AI rate in nucleus:**
  20-40% goats ⇨ 85% (Lacaune)



Populations

Breeding programs

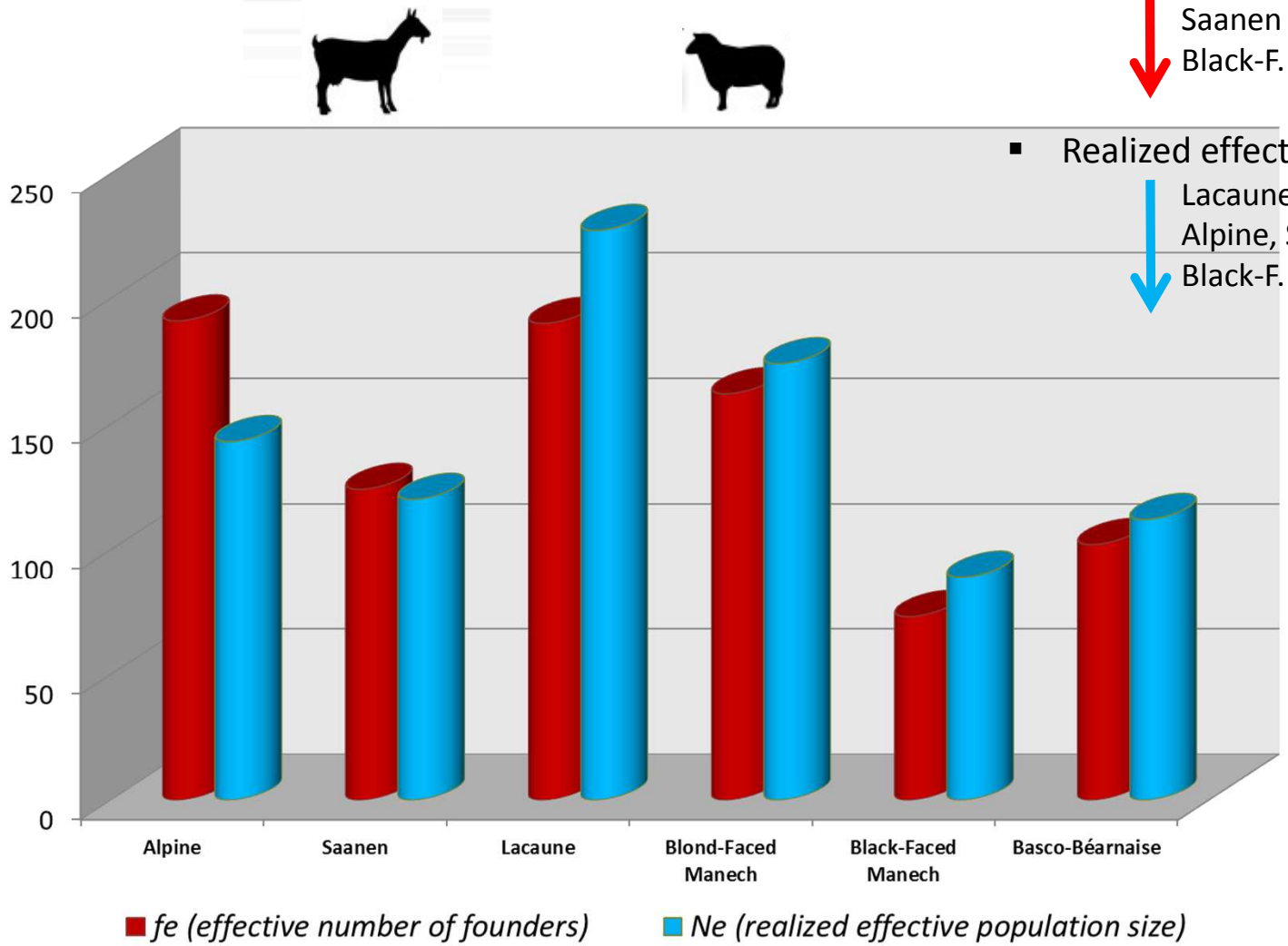


Characteristics

- **20-30% ♀ in official milk recording**
- **AI rate in nucleus:**
  20-40% goats ⇨ 85% (Lacaune)
- **Breeding schemes programs:**
  30 ♂ (Black-F. Manech)⇨ 440 ♂ (Lacaune)
- **Progeny test on:**
  30-40 ♀ in sheep ⇨ 80 ♀ in goats

Populations

Genetic diversity



Characteristics

- Effective number of founders (***fe***):
  - Alpine, Lacaune, Blond-F. Manech
  - Saanen
  - Black-F. Manech, Basco-Béarnaise
- Realized effective population size (***Ne***):
  - Lacaune, Blond-F. Manech
  - Alpine, Saanen
  - Black-F. Manech, Basco-Béarnaise

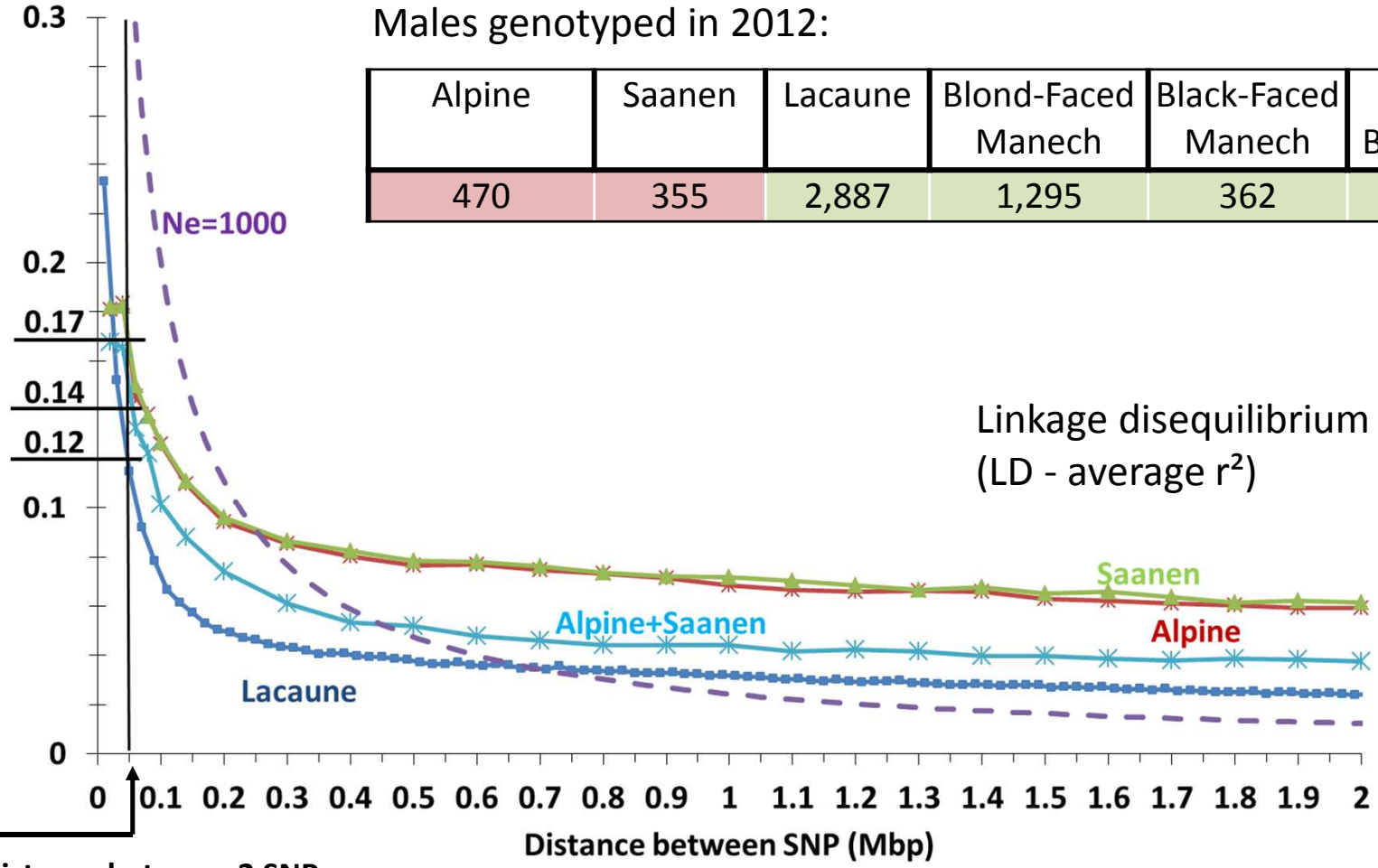
Danchin et al., 2011

Populations

Structure of the reference populations

Males genotyped in 2012:

Alpine	Saanen	Lacaune	Blond-Faced Manech	Black-Faced Manech	Basco-Béarnaise
470	355	2,887	1,295	362	281



Linkage disequilibrium
(LD - average r^2)

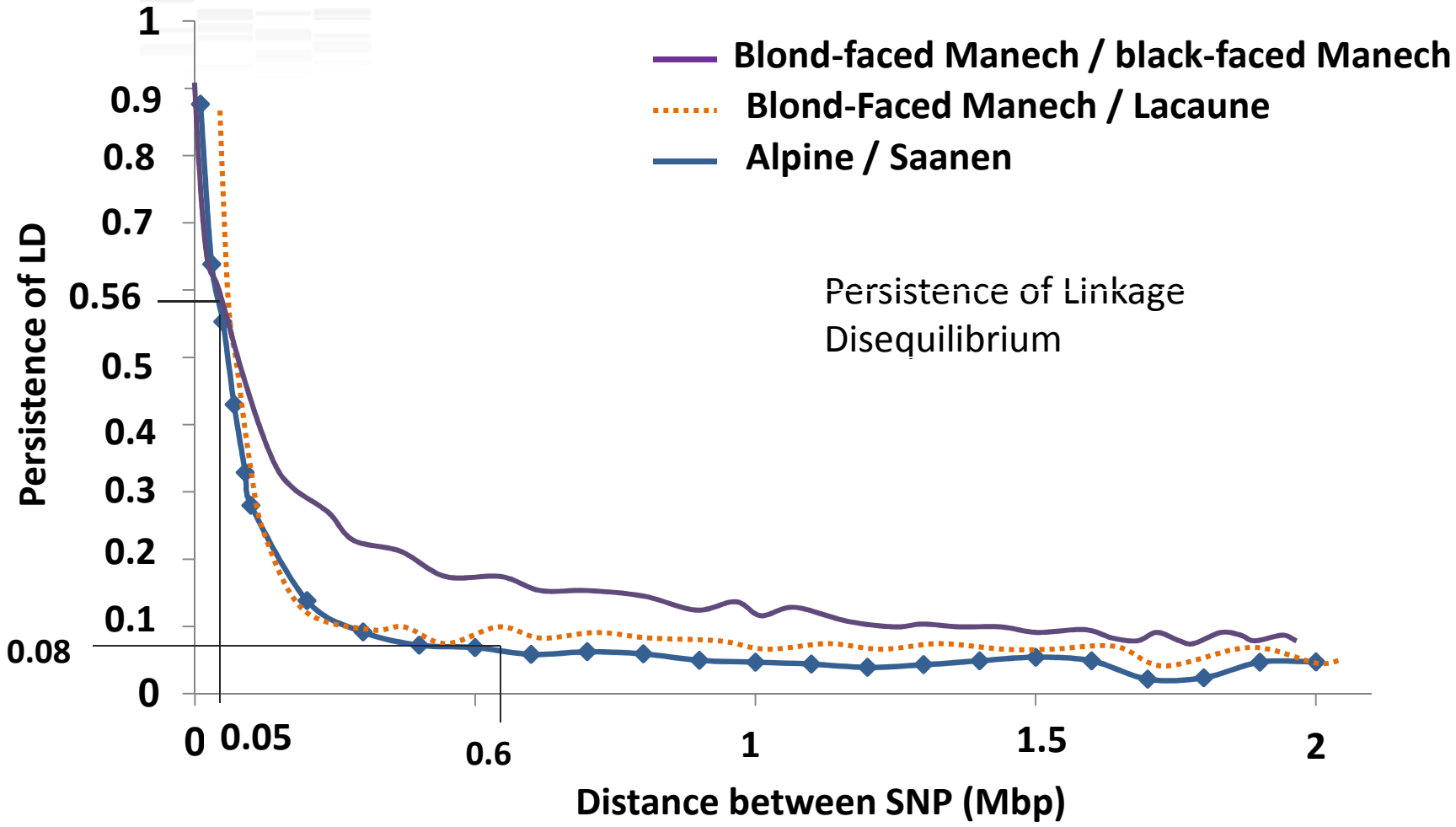
0.05

Average distance between 2 SNPs

Carillier et al., 2013; Baloche et al., 2013

Populations

Structure of the reference populations



Carillier et al., 2013

Populations

- ✓ Extent of LD and persistence of LD ⇨ not favourable to genomic selection

- ✓ Characteristics of the populations ⇨ 2 situations

1) Large size of reference population: ⇨ **single-breed approach**

   - ✓ Blond-Faced Manech
   - ✓ Lacaune

2) Small reference population : ⇨ **multiple-breed approach ?**
   + ↗ inbreeding + ↘ *Ne*

   - ✓ Alpine
   - ✓ Saanen
   - ✓ Black-Faced Manech
   - ✓ Basco-béarnais

   } ✓ *Accurate progeny test*

   ✓ ↘ *generation interval* + ↗ *AI rate*

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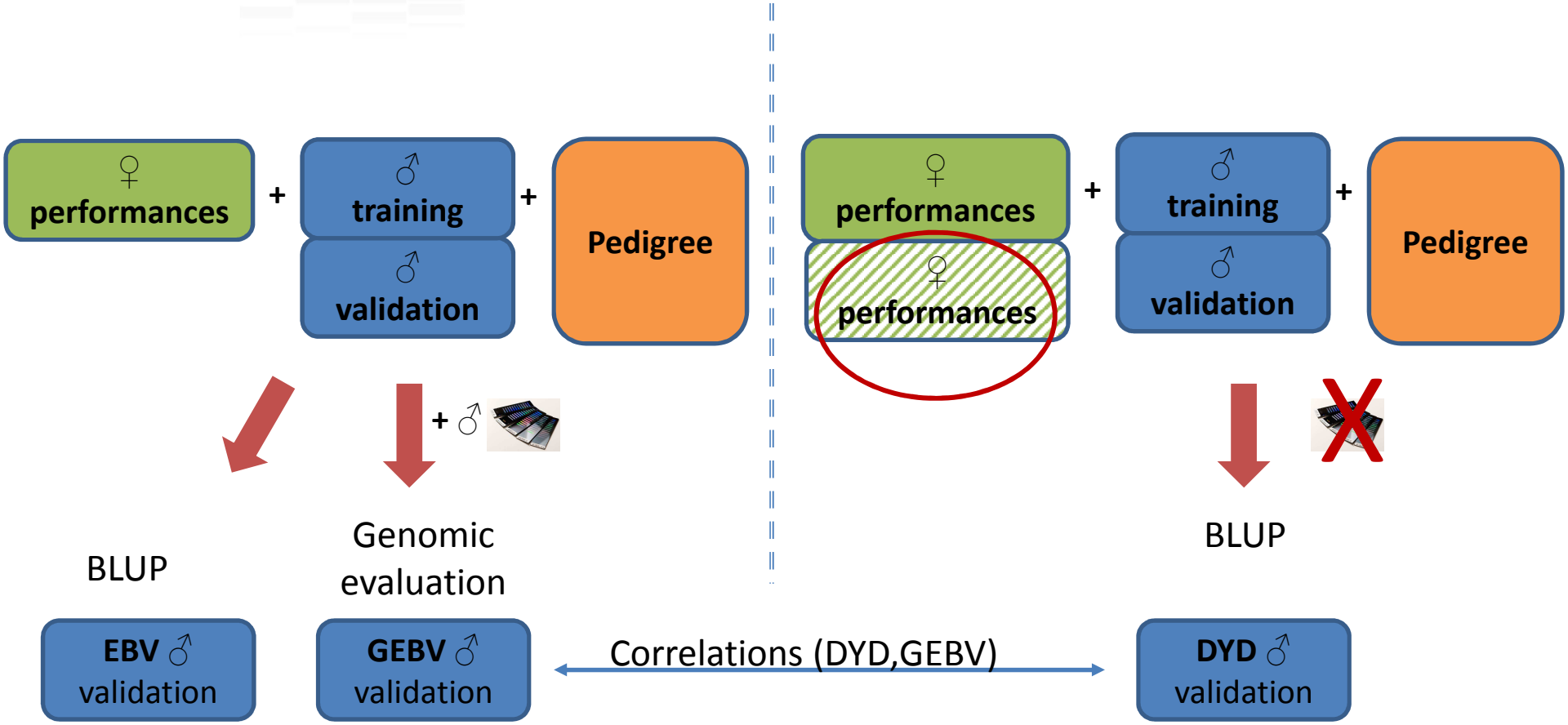
Improvement of genomic prediction quality

Improvement of genomic predictions quality

Principle of validation



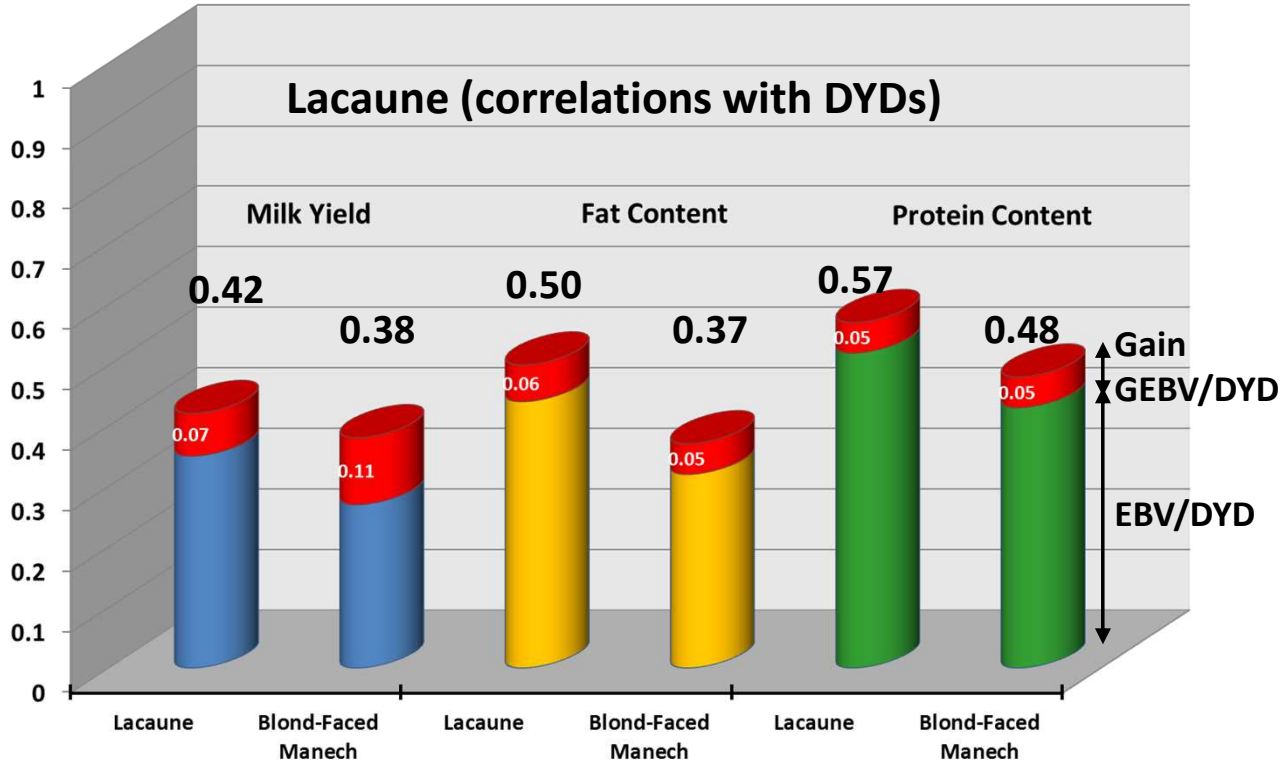
Improvement of genomic predictions quality

Single-breed context

Genomic evaluation: GBLUP two-step approach

BLUP ⇨ DYDs +  ⇨ GBLUP ⇨ GEBV

(♀ performances - training) (♂ genotyped) (♂ validation)



Astruc et al., 2012; Barillet et al., 2012

- **Correlations with DYDs:**

GEBVs>EBVs

Level:
Lacaune > level Blond-F. Manech

Gain for milk yield:
Blond-F. Manech> Lacaune

- **Other approaches:**

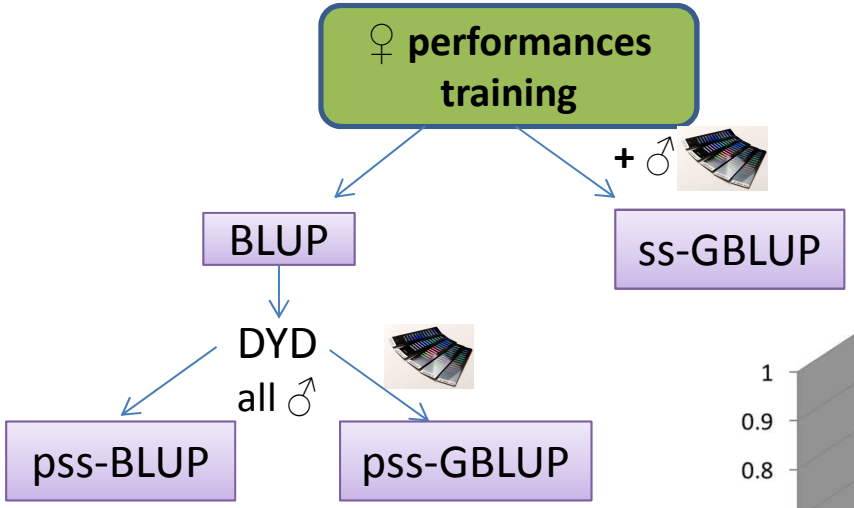
GBLUP≈ PLS ≈ SPLS<Bayes Cπ

Duchemin et al., 2012

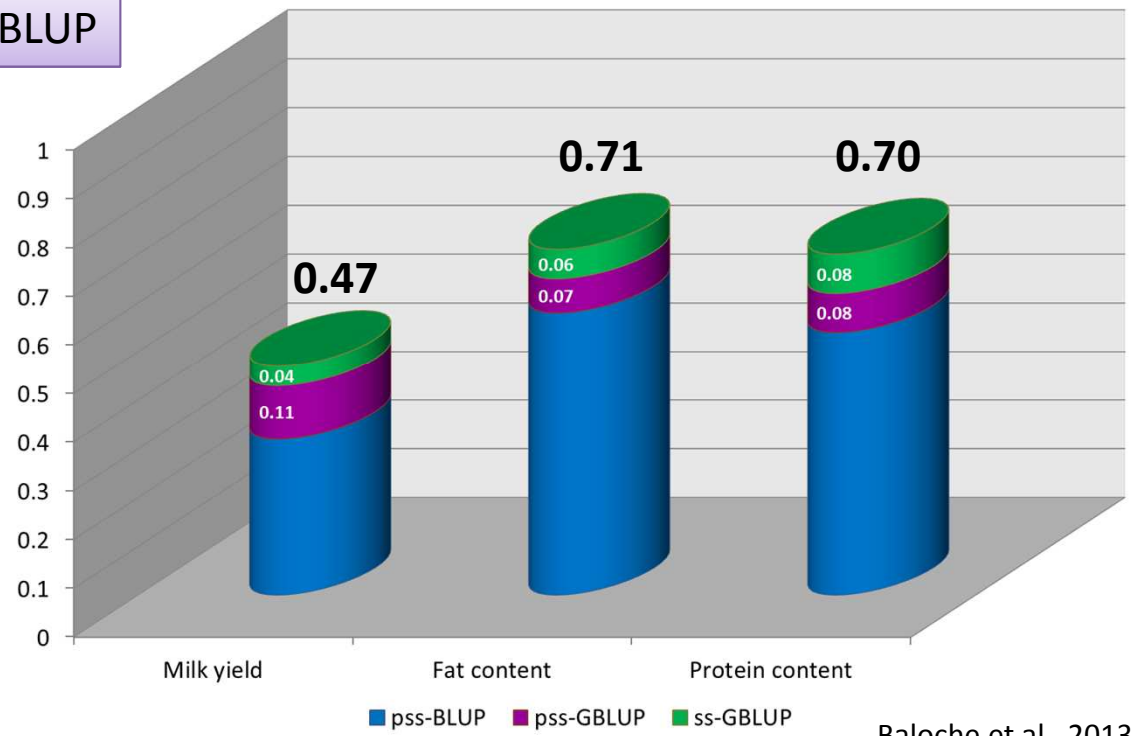
Improvement of genomic predictions quality

Single-breed context

Genomic evaluation: GBLUP single-step approach



Lacaune (genomic standardized accuracy)



Basco-Béarnais (genomic standardized accuracy for Milk yield):
0.46(pedigree)⇨ 0.52 (genomic)

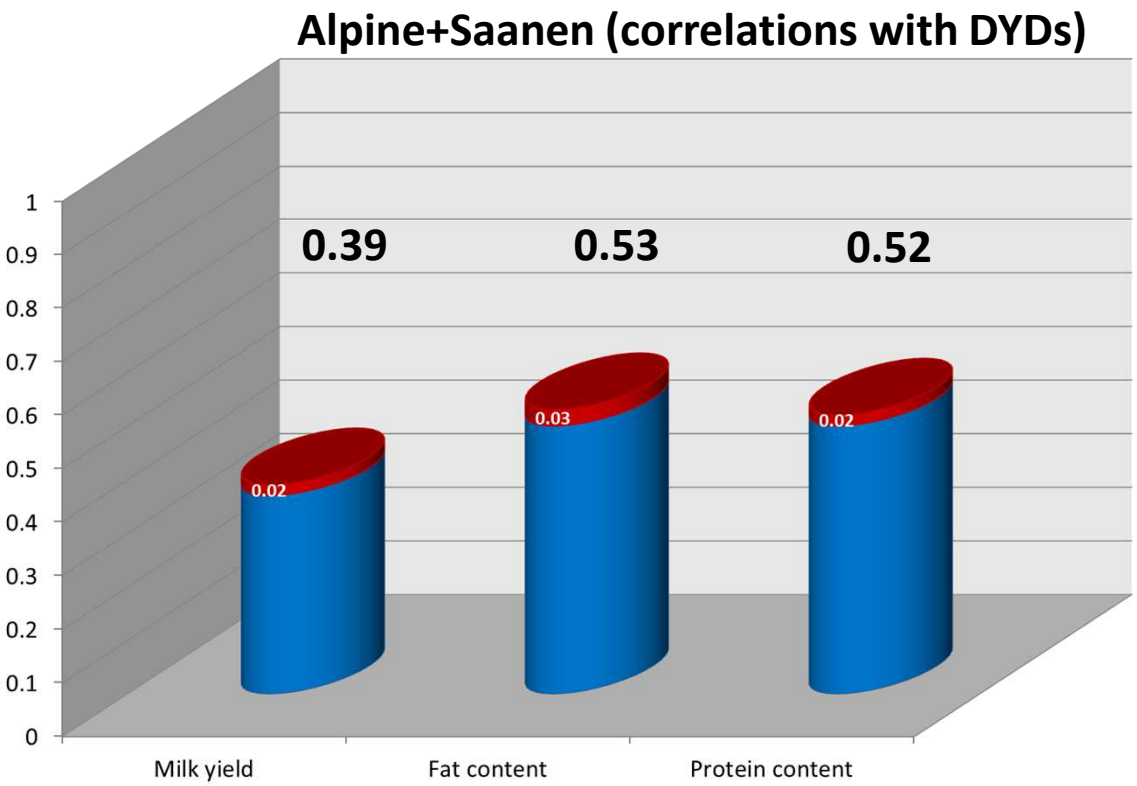
Legarra et al., 2014

Baloche et al., 2013

Improvement of genomic predictions quality

Multiple-breed context

Genomic evaluation: GBLUP two-step approach



- **Correlations with DYDs:**

GEBVs>EBVs

Small gains

- **Genomic accuracies of young bucks :**

Smaller than parent average accuracies

For Milk yield:

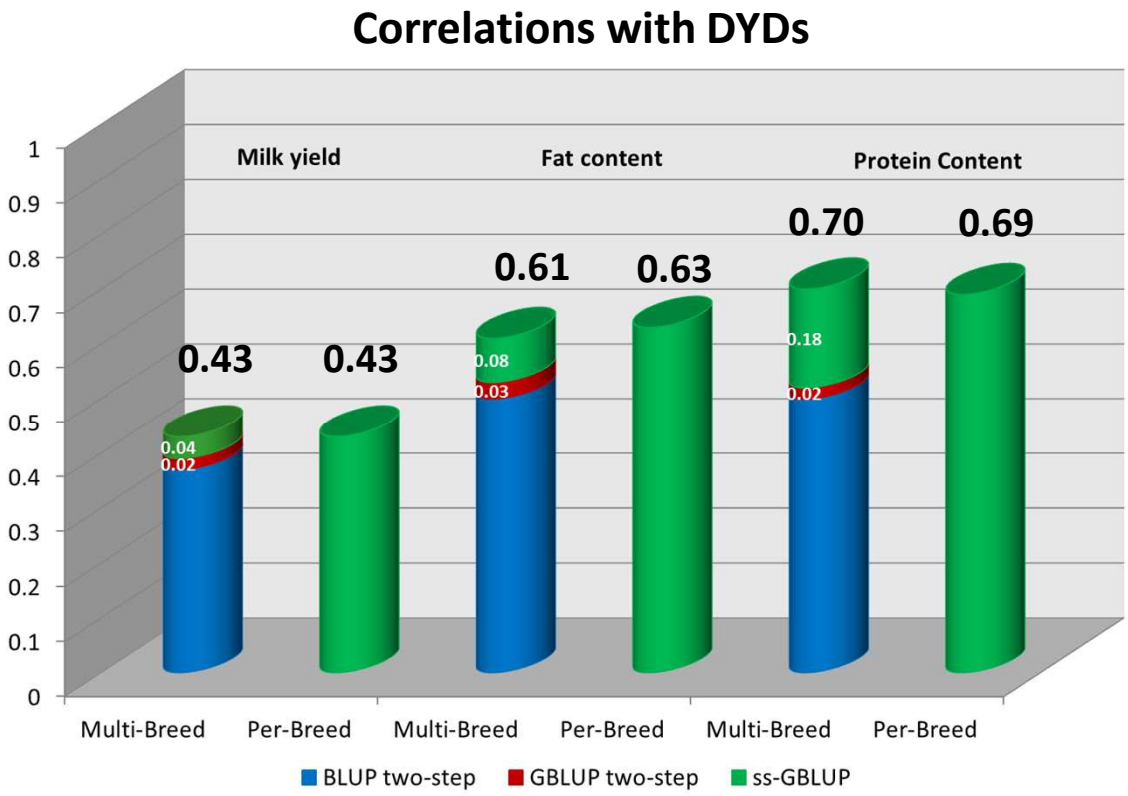
0.56 (genomic) < 0.62 (parent average)

Carillier et al., 2013

Improvement of genomic predictions quality

Multiple-breed context

Genomic evaluation: GBLUP single-step approach



Carillier et al., 2014

- **Single-Step models:**

Multi-Breed
Per-Breed
Multi-Trait

C. Carillier
WCGALP #337

- **Correlations with DYD:**

Single-step>>Two-step
Per-breed ≈ Multiple-Breed

- **Genomic accuracies of young bucks :**

Higher than parent average accuracies
For Milk yield:
0.70 (ssGBLUP multi-breed) > 0.62 (parent average)

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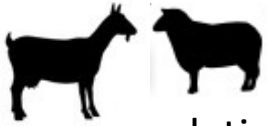
Learned lessons and prospects

Learned lessons and prospects

Quality of predictions

- Reliability of genomic evaluation:



<< Holstein 

≈ Montbéliarde, Normande

  - ✓ Small reference population
  - ✓ Low level of LD
  - ✓ Low accuracy of progeny testing → less precise reference population (sheep)

High accuracy of progeny testing (Goats)
Large inbreeding and small *Ne* (Basco-Béarnaise; Saanen)

- Single-Step approach **+++**, take into account:
  - ✓ ♀ information
  - ✓ Selection

✍ **Improvements:**

Slopes < 1 → overdispersion of EBV of youngest candidates
Heterogeneity of variance (herd's effect)
Major genes

Learned lessons and prospects

Quality of predictions

- Multiple-breed approach :

✓ Sheep:

Blond -Faced Manech + Latxa Cara Rubia

Reliability: Per-Breed ≈ Multiple-Breed

Blond-Faced Manech ⇨ already large reference population

Latxa Cara Rubia ⇨ small reference population

lack of intensive crossbreeding

Black-Faced Manech + Latxa Cara Negra Nevada

Reliability: slight ↗ with Multiple-Breed but low connections

Legarra et al., 2014

✓ Goats:

Alpine+Saanen

Reliability: Multiple-Breed ≈ Per-Breed (Saanen>Alpine)

GEBVs' accuracies of young bucks : Multiple-Breed > Per-Breed

Carillier et al., 2014

Learned lessons and prospects

Genomic breeding schemes

- Modeling Blond-Faced Manech and Alpine breeding schemes:
  dairy trait: h^2=0.30, 10 generations
  Best Genomic Scenario: Ne=200 ; nref=2000
  ↗↗ **AGG:** + 51.7% Blond-Faced Manech
  +26.2% Alpine

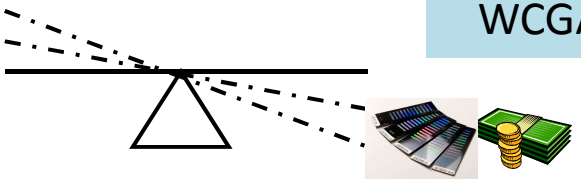
Shumbusho et al., 2013

- Genomic selection experiment in Lacaune:
  Genomic selection rate: 0.33
  Genomic Rams: +0.52 Total Merit Index (TMI) Std
  Progeny selection rate (on TMI threshold):
  0.76 Genomic Rams vs 0.52 Classical Rams

G. Baloche
WCGALP #335

- Genomic breeding schemes:
  Technically and economically feasible
  Lacaune: genomic selection rate: 0.3
  progeny selection rate: 0.8

↗↗ **AGG:+15%**



D. Buisson
WCGALP #898

AGG: Annual Genetic Gain; TMI: Total Merit Index

Learned lessons and prospects

Genomic breeding schemes: the future

- **Lacaune**: switch to genomic selection purebred in 2015 (↗ reference population: 4,841 ♂)
- **Pyrenean sheep breeds**: genomic selection purebred in the near future
  - Blond-Faced Manech: reliability as in Lacaune (↗ reference population: 1,424 ♂)
  - Basco-Béarnais: reference population 509 ♂ in 2013
  - Black-Faced Manech:

Genomic selection: ↘ complexity and number of rams in selection centers

- **Goats**: Single-step GBLUP ⇨ opportunity to genomic selection

Major genes: ⇨ to explore others genomic models

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