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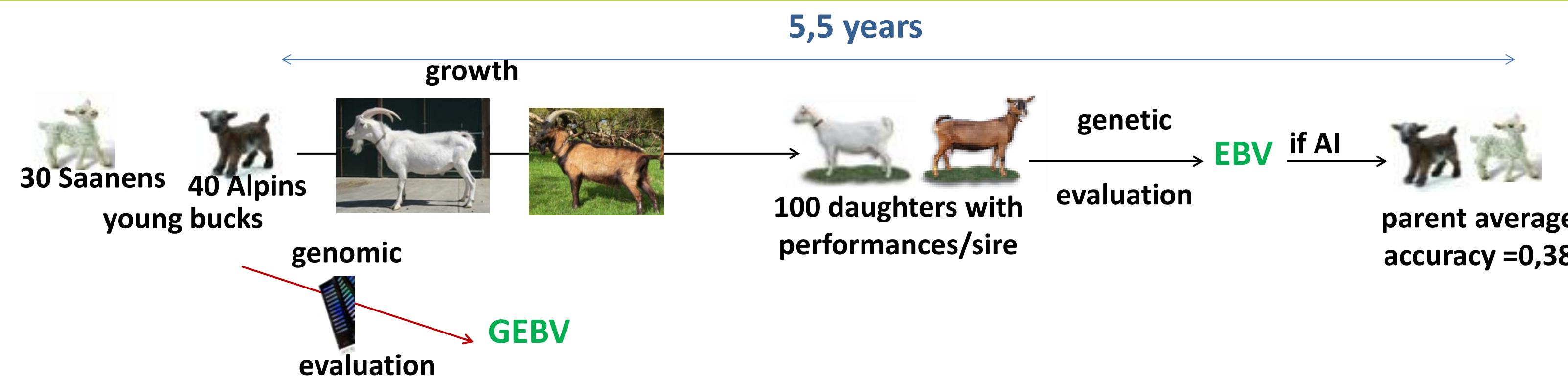
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# Comparison of multi-breed and within-breed genomic evaluation in French dairy goat

Céline Carillier, Hélène Larroque, Christèle Robert-Granié, INRA - UMR1388 GenPhySE - Castanet-Tolosan, FRANCE

## Aim of genomic selection in French dairy goat



$$\text{annual genetic gain} = \frac{\text{selection intensity} \times \text{accuracy} \times \sigma_u}{\text{generation interval}}$$

With genomic selection: ↓ generation interval  
↗ selection intensity, accuracy

To apply genomic selection we need:  
GEBV accuracy ≥ parent average for candidates

Genomic selection with two steps approach (using DYD): GEBV accuracy of candidates < parent average accuracy (Carillier et al 2013)  
→ Find a more accurate approach

## Method and models used

Single step : genomic evaluation based on female performances

### Model A: Multi-breed Alpine + Saanen

$$\mathbf{y} = \mathbf{X}\beta + \mathbf{Z}\mathbf{u} + \mathbf{W}\mathbf{p} + \mathbf{e} \quad \mathbf{u} \sim N(\mathbf{0}, \mathbf{H}\sigma_u^2)$$

y: female performances  
 $\beta$ : fixed effect of official evaluation + breed effect  
 $\mathbf{u}$ : genomic breeding value (GEBV)  
 $\mathbf{p}$ : effect of lactation repetition  
 $\mathbf{H}$ : genomic relationship matrix

GEBV were estimated using blup90iod program thanks to I. Misztal

### Model B: per-breed Alpine or Saanen

$$\mathbf{y}_{alp} = \mathbf{X}_{alp}\beta_{alp} + \mathbf{Z}_{alp}\mathbf{u}_{alp} + \mathbf{W}_{alp}\mathbf{p}_{alp} + \mathbf{e}_{alp} \quad \mathbf{u}_{alp} \sim N(\mathbf{0}, \mathbf{H}_{alp}\sigma_{u_{alp}}^2)$$

$$\mathbf{y}_{saa} = \mathbf{X}_{saa}\beta_{saa} + \mathbf{Z}_{saa}\mathbf{u}_{saa} + \mathbf{W}_{saa}\mathbf{p}_{saa} + \mathbf{e}_{saa} \quad \mathbf{u}_{saa} \sim N(\mathbf{0}, \mathbf{H}_{saa}\sigma_{u_{saa}}^2)$$

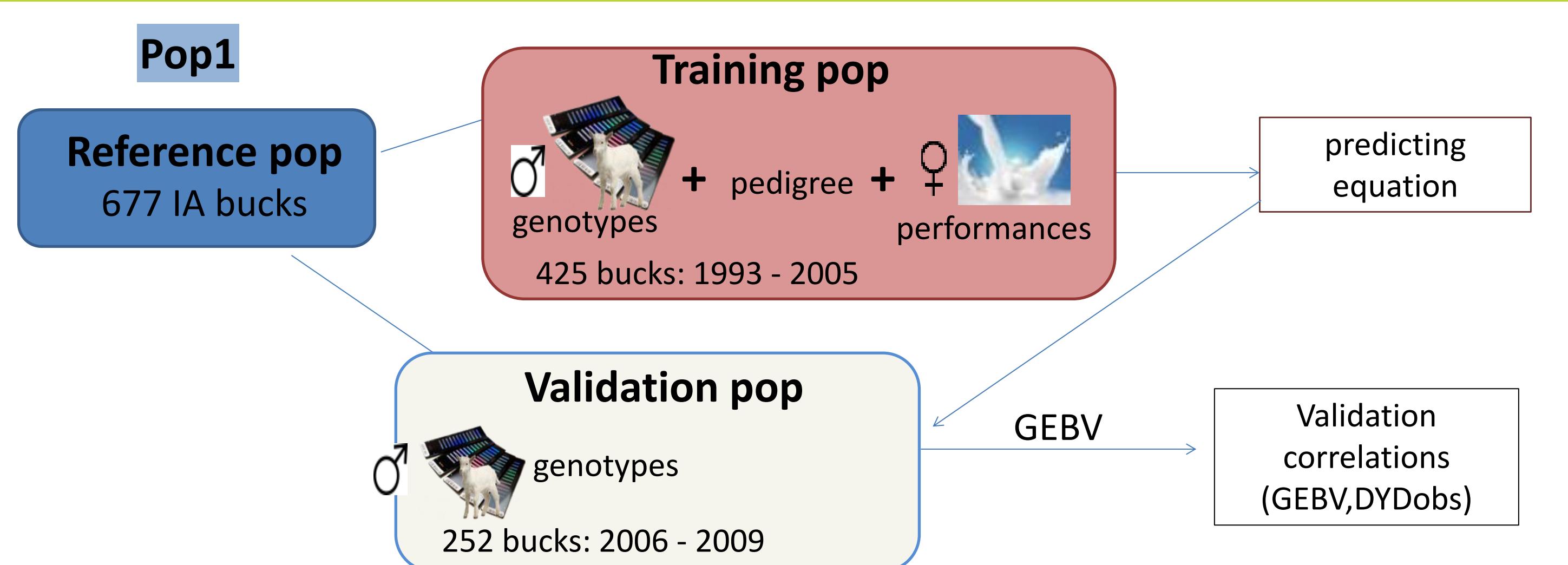
alp: for Alpine breed  
saa: for Saanen breed

### Model C: multiple trait Alpine≠Saanen but correlated

$$\mathbf{y}_b = \mathbf{X}_b\beta_b + \mathbf{Z}_b\mathbf{u}_b + \mathbf{W}_b\mathbf{p}_b + \mathbf{e}_b$$

$$\sigma_{u_{alp,saa}} \begin{cases} \text{estimated} \\ \rho = 0 \\ \rho = 0.99 \end{cases} \quad \mathbf{u}_b = \begin{cases} \mathbf{u}_{saa} \\ \mathbf{u}_{alp} \end{cases} \sim N \left[ \begin{pmatrix} \mathbf{0} \\ \mathbf{0} \end{pmatrix}, \begin{pmatrix} \sigma_{u_{alp}}^2 & \sigma_{u_{alp,saa}} \\ \sigma_{u_{alp,saa}} & \sigma_{u_{saa}}^2 \end{pmatrix} \otimes \mathbf{H} \right]$$

## How do we evaluate model?



### Pop2

148 candidates without daughters born between 2010 and 2011

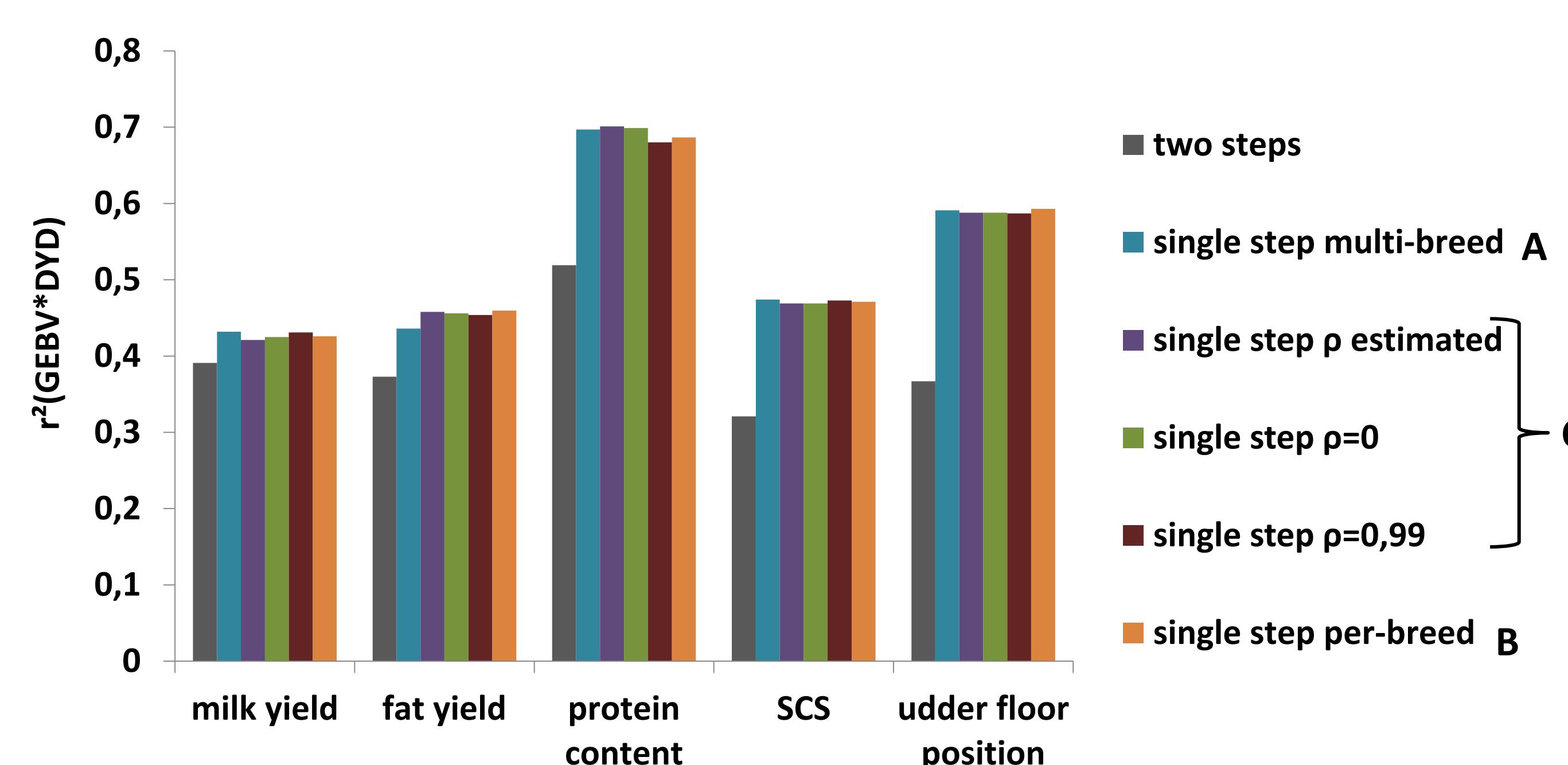
$$\text{GEBV accuracy} = \sqrt{\frac{\sigma_u^2 - PEV}{\sigma_u^2}}$$

PEV: prediction error variance

$\sigma_u^2$ : genetic variance

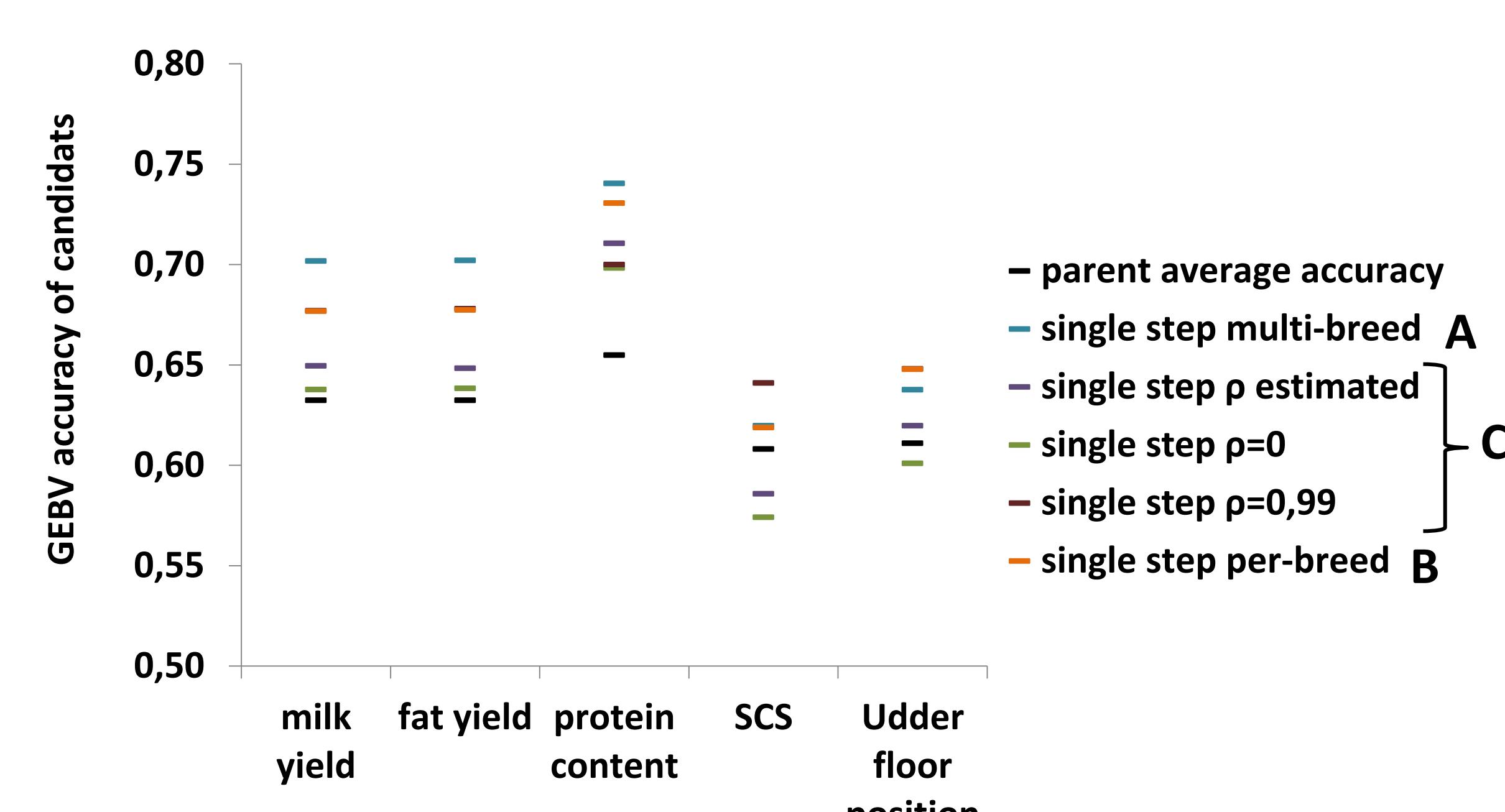
## Results

### Pop1 validation correlations similar with all models used



### Pop2

### genomic accuracy >> parent average accuracy



## Conclusions

- Genomic selection is feasible in French dairy goat
- Per-breed model is a good one given small population sizes
- Perspectives: integrate major gene in genomic selection models

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