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

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

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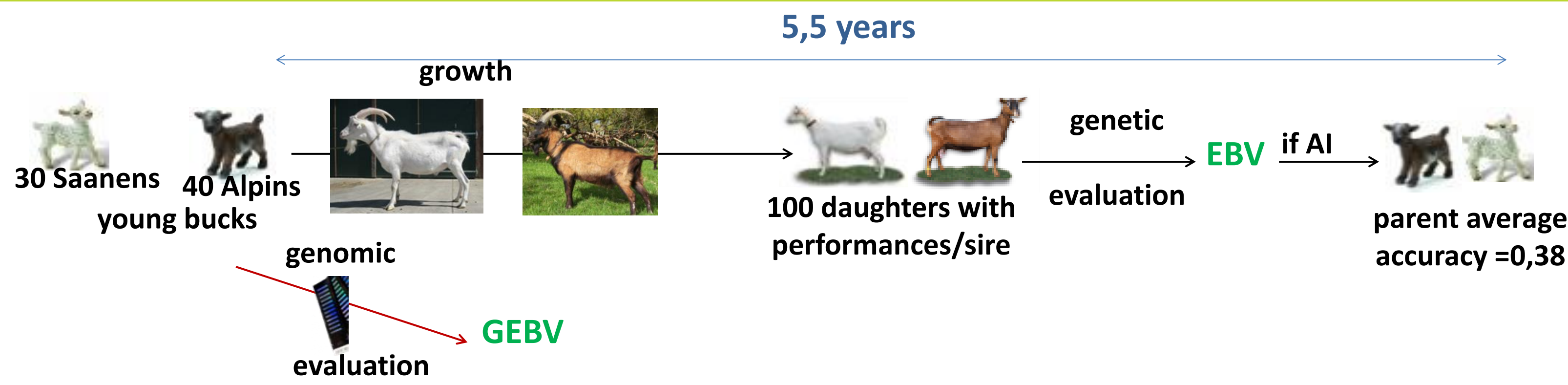
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Aim of genomic selection in French dairy goat



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

With genomic selection: \searrow generation interval
 \nearrow selection intensity, accuracy

To apply genomic selection we need:

GEBV accuracy \geq parent average for candidates

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

Method and models used

Single step : genomic evaluation based on female performances

Model A: Multi-breed Alpine + Saanen

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

y: female performances
 β : fixed effect of official evaluation + breed effect
u: genomic breeding value (GEBV)
p: effect of lactation repetition
H: genomic relationship matrix

Model B: per-breed Alpine or Saanen

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

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

alp: for Alpine breed
saa: for Saanen breed

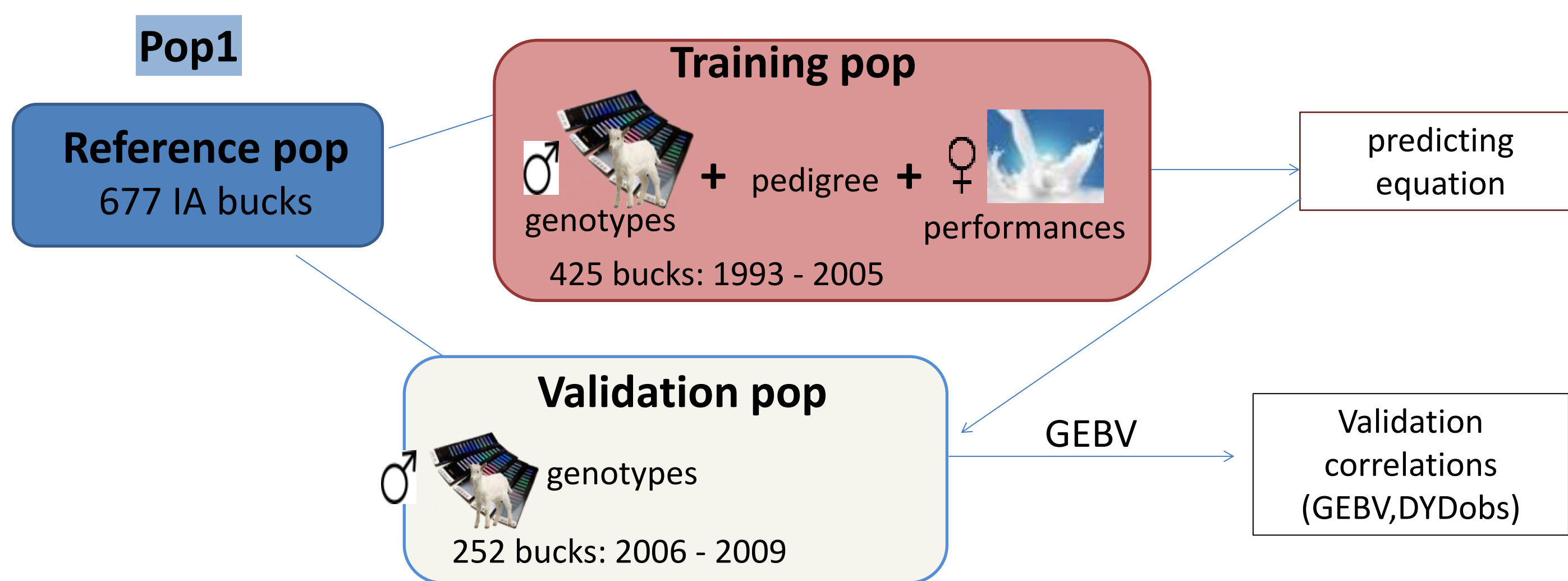
Model C: multiple trait Alpine \neq Saanen but correlated

$$\mathbf{y}_b = \mathbf{X}_b\boldsymbol{\beta}_b + \mathbf{Z}_b\mathbf{u}_b + \mathbf{W}_b\mathbf{p}_b + \boldsymbol{\varepsilon}_b$$

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

GEBV were estimated using blup90iod program thanks to I. Misztal

How do we evaluate model?



Pop2

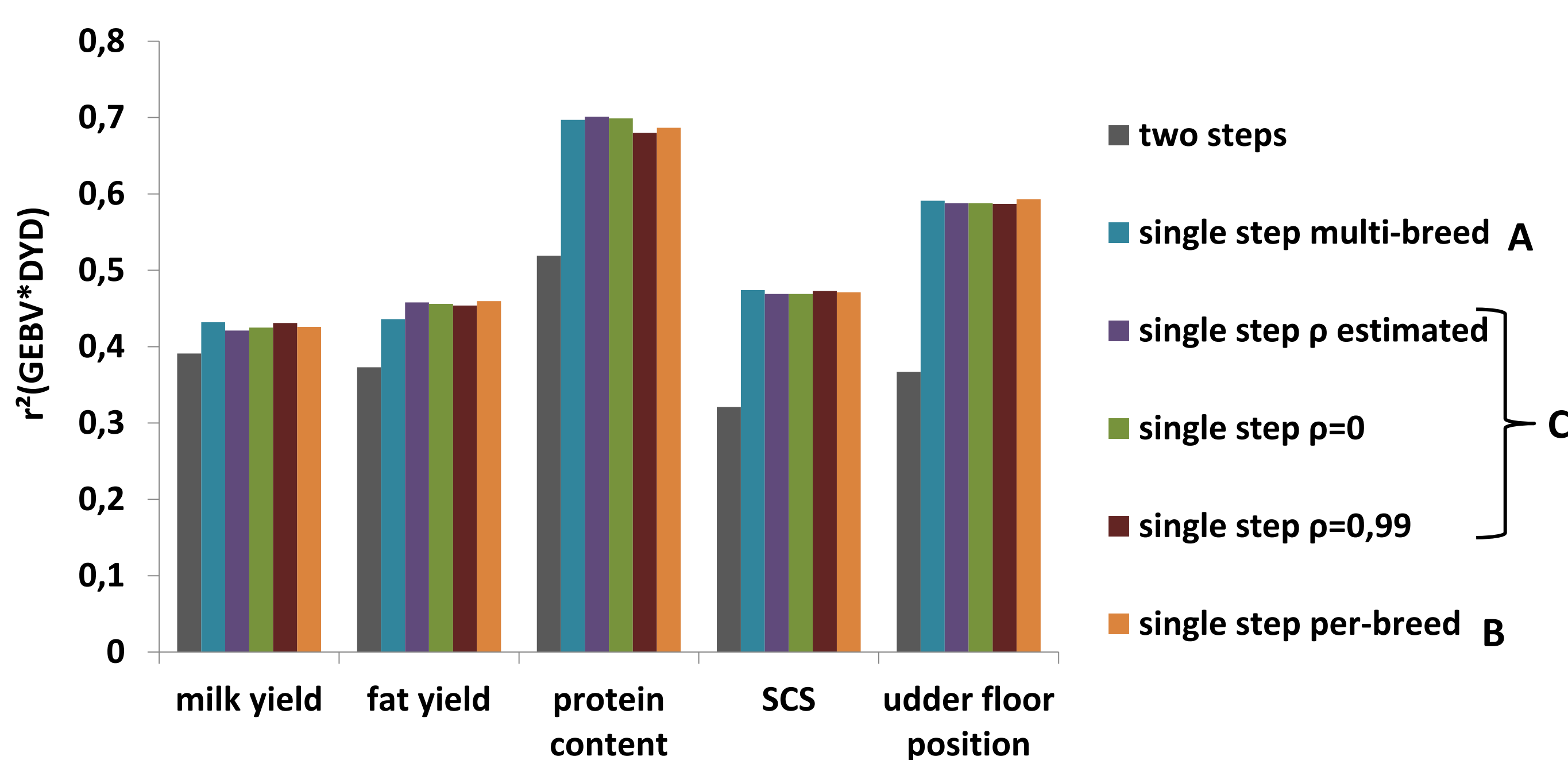
148 candidates without daughters born between 2010 and 2011

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

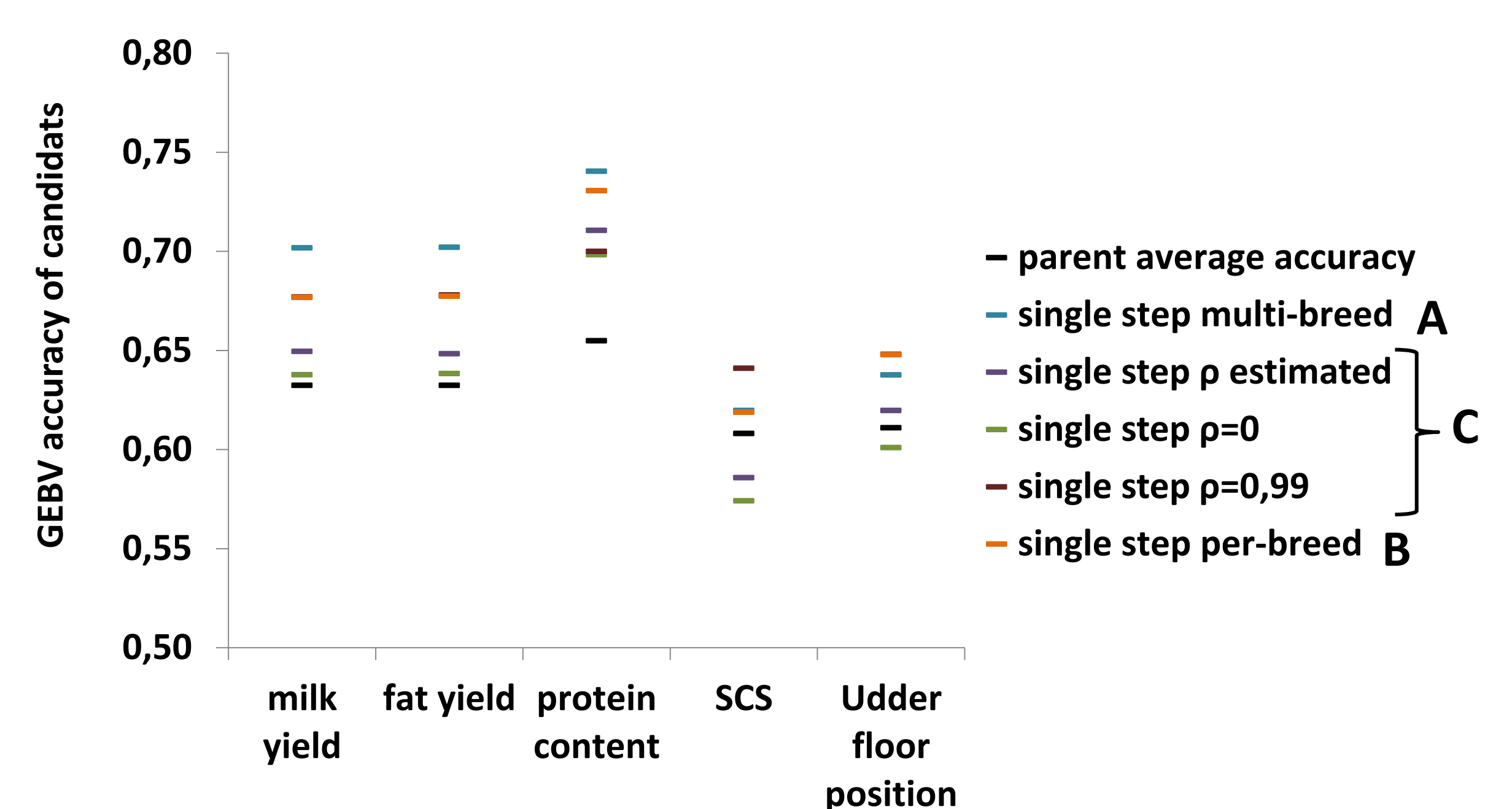
PEV: prediction error variance
 σ_u^2 : genetic variance

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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