

A single-step, multiple-trait genomic evaluation model increase the accuracy for suckling performance in beef cows



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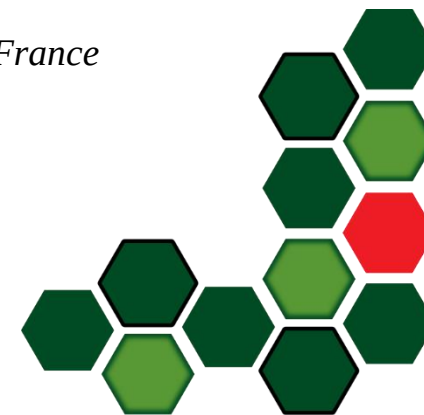
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Context

- Income of livestock farmers depends greatly on the suckling performance of beef cows
- Lack of accurate selection index to improve maternal weaning weight (WWm) and milk yield (MY)
 - Testing station since 1978 (8 bulls/year)
- French National Evaluation (IBOVAL) since 1993

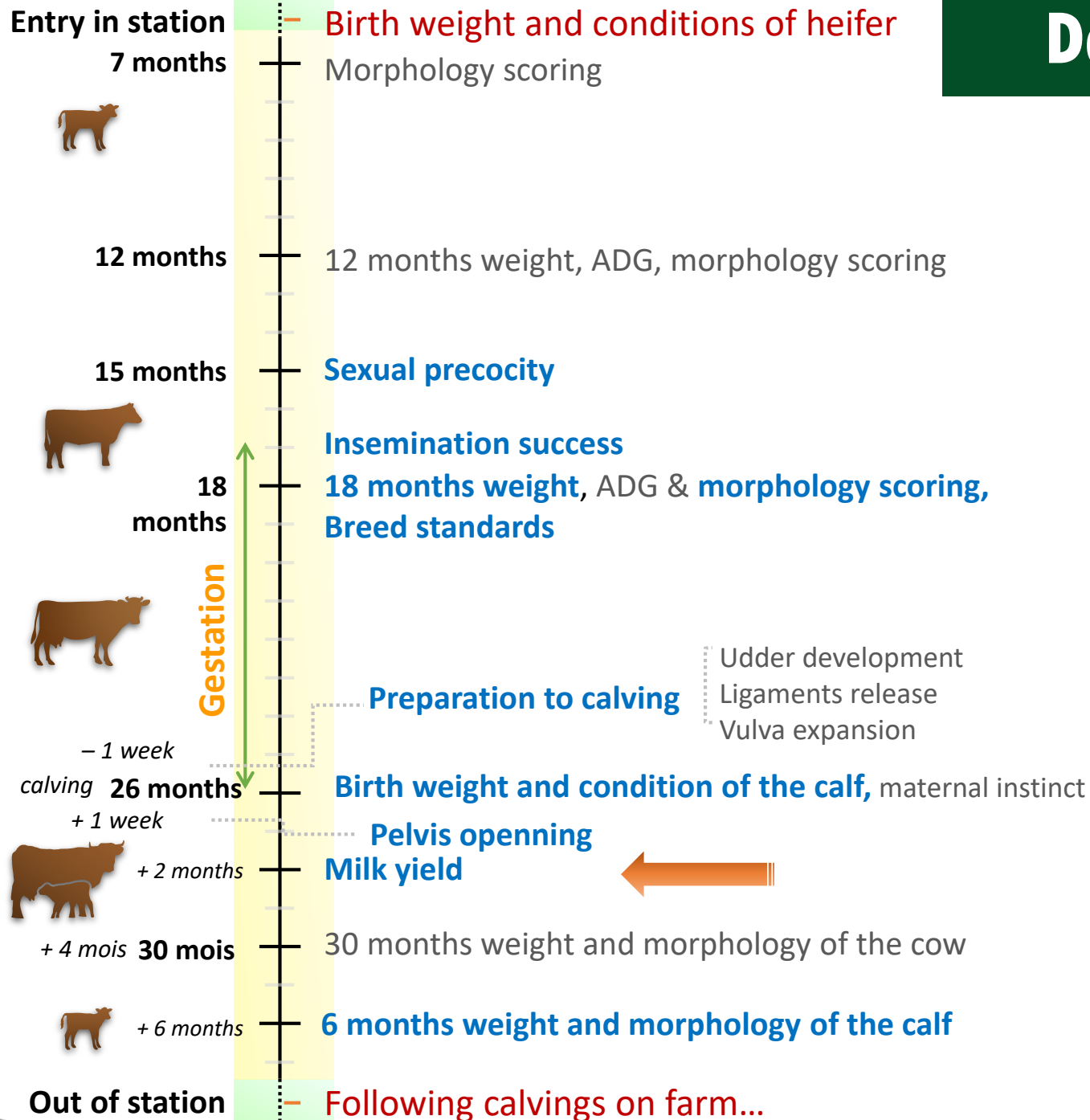


Blonde d'Aquitaine breed



Objective: Assess the interest of a single-step and multiple-trait genomic model to accurately estimate breeding values for maternal suckling traits

Data record in station



Published trait

Trait not published

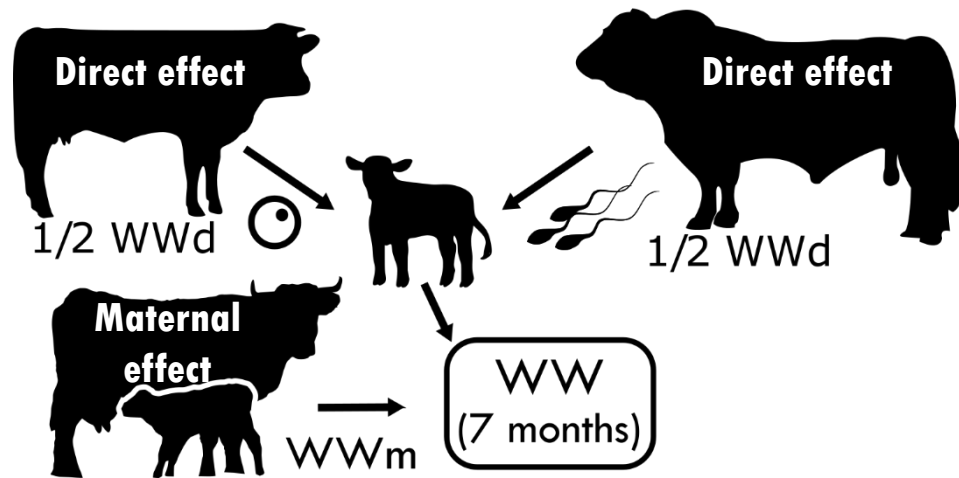
Farm recording



Material and methods

Phenotypes

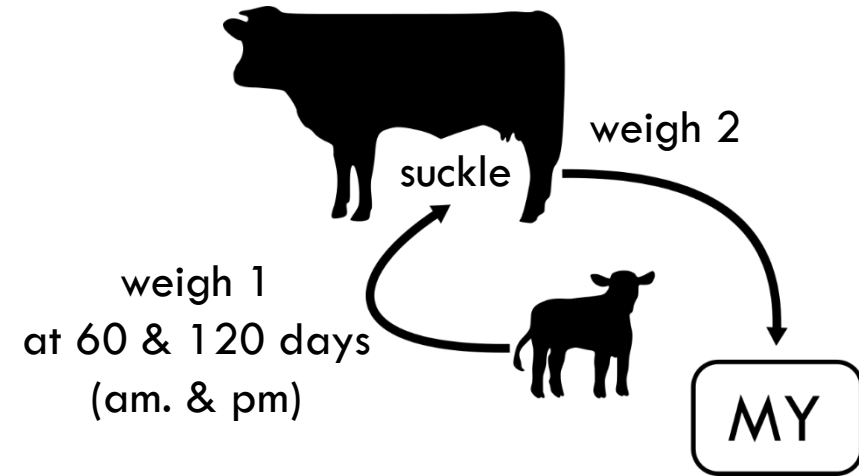
On-farm records



For weaning weight (WW)

137,943 performance records in 484 herds
Mean= 285.4 kg, standard deviation= 45.1kg

Station records



For milk yield (MY)

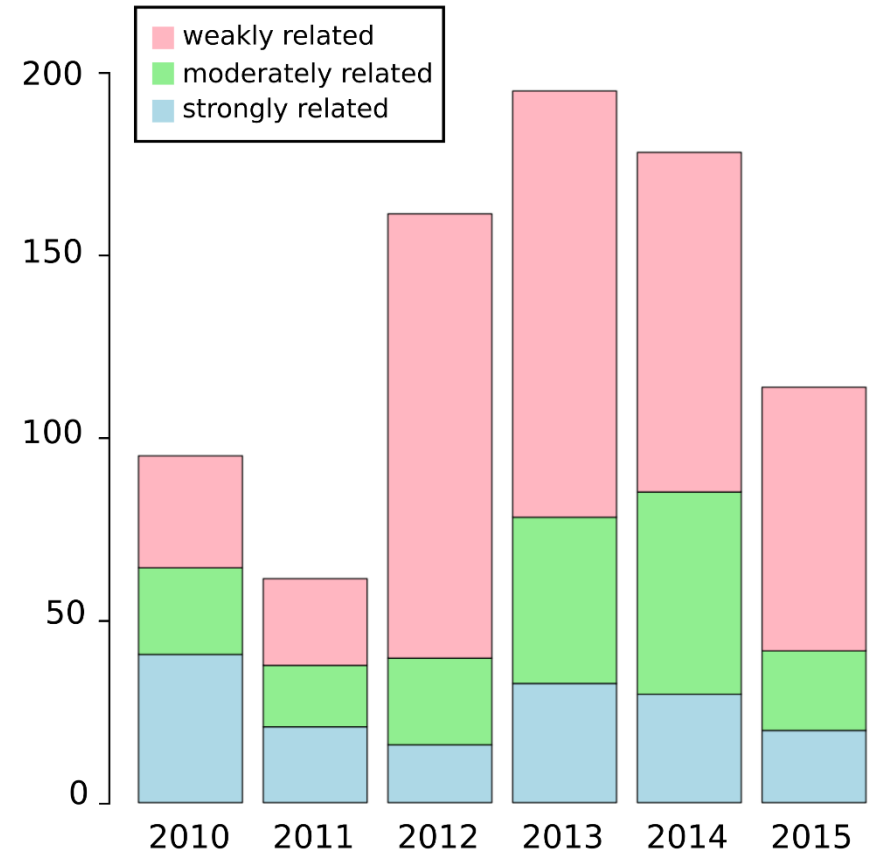
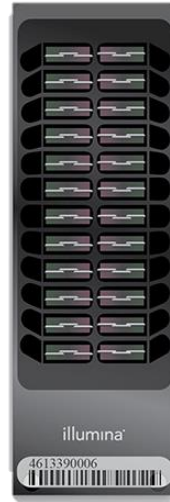
2403 performance records in station
Mean= 5.66kg, standard deviation= 1.46kg

Material and methods

Genotypes

3,007 Blonde d'Aquitaine animals
truly genotyped (58%)
or imputed on SNP50 BeadChip®

- 1,155 females recorded for MY
(station reference population)
- 1,039 animals with WW data
(farm reference population)
- 813 candidates for selection



Distribution of the population of candidates for selection according to their birth year and their degree of relationship with the station reference population



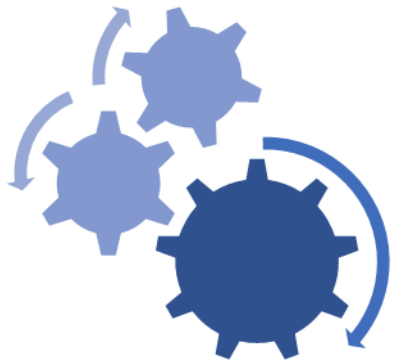
Material and methods

Model

$$y = X\beta + Z_1u + Z_2m + Z_3p + e$$

y : performance vector | β : fixed effects | u : direct genetic effects (WWd, MY) |
 m : maternal genetic effect (WWm) | p : permanent environmental random effect |
 e : residuals of the model | X, Z_1, Z_2, Z_3 : incidence matrices for β, u, m, p respectively

Fixed effects: MY: contemporary group, calving difficulty, age of the heifer at calving
 WW: calf contemporary group, calf birth season, dam parity



Software:

BLUPF90 (Misztal et al., 2002)
for genetic parameters, pedigree BLUP and ssGBLUP



Results

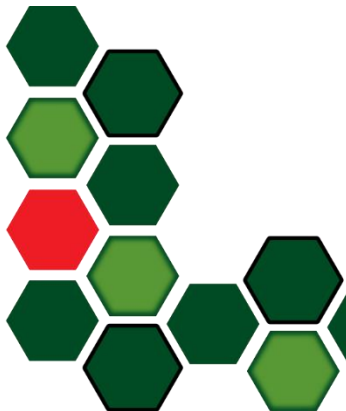
Genetic parameters

	MY	WWd	WWm
MY	0.41 (0.07) ¹	0.01 (0.12)	0.75 (0.10)
WWd		0.30 (0.02)	-0.39 (0.04) statistical artifact
WWm			0.09 (0.01)

¹Heritabilities in bold on the diagonal, genetic correlations above the diagonal (standard errors in brackets)

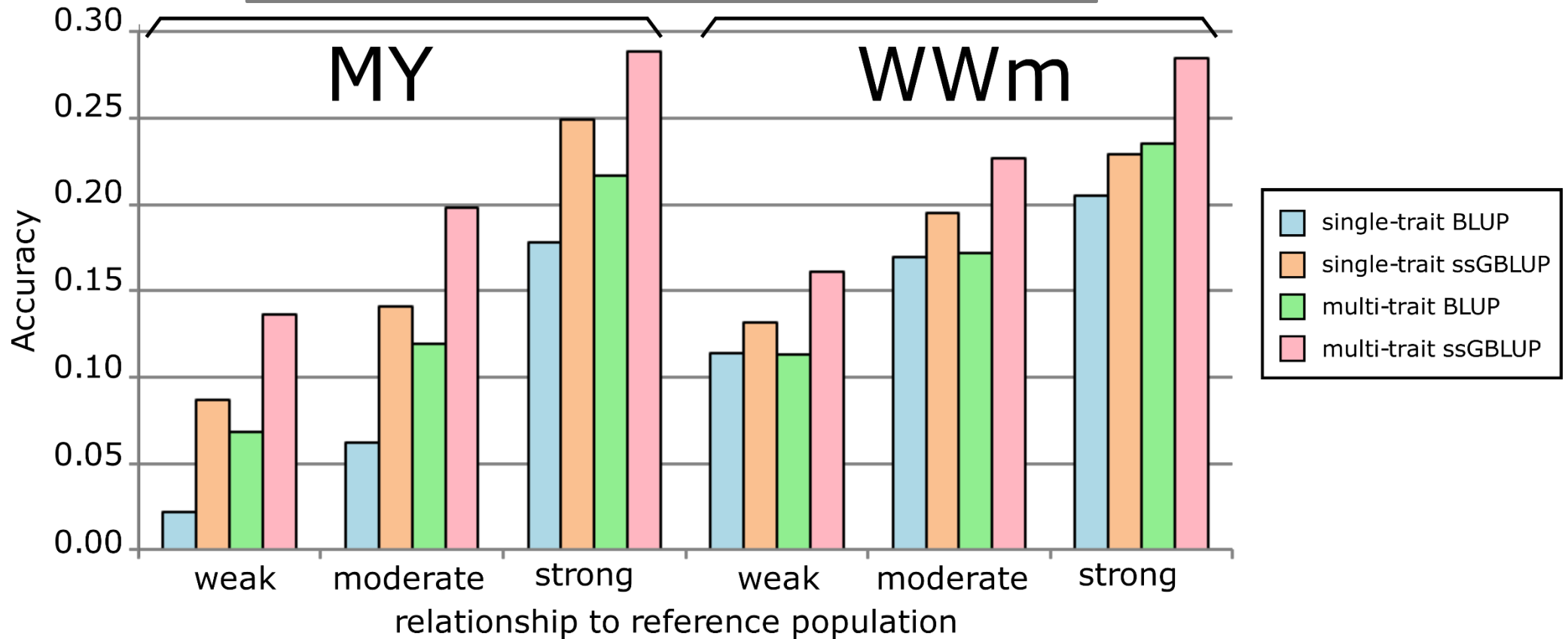
MY and WWm are strongly linked

MY and WWd are not genetically correlated



Results

Accuracy of multiple-trait EBV



ssGBLUP Vs pedigree BLUP model increases by 12 to 16% the accuracy of EBV for WWm

Multi-trait ssGBLUP Vs ssGBLUP model increases by 16 to 24% the accuracy of EBV for WWm

Conclusion

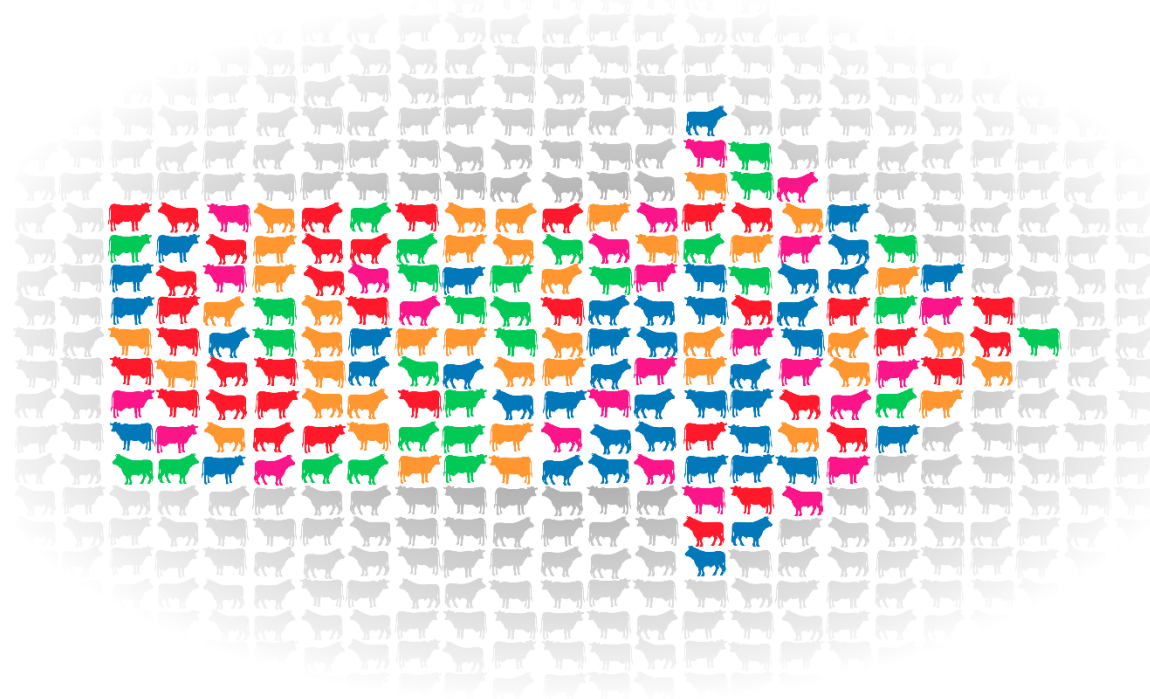
Multiple-trait single step GBLUP evaluation for WWm and MY increases by **38%** the accuracy of EBV for maternal weaning weight compared to uni-trait pedigree BLUP.



$$\Delta G = \frac{i \uparrow \times \rho \uparrow \times \sigma_a}{t \downarrow}$$

Gain in genetic value Selection intensity Accuracy Genetic variance of the trait Generation interval

These preliminary results paved the way for an efficient use of maternal EBV in beef cattle breeding programs



Thank you for your attention

