Genetic correlations between juvenile mortality traits and traits in selection in French dairy cattle breeds

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Interbull meeting

31 May – 1 June 2026, Verona, Italy

Juvenile mortality in cattle

- **The importance of reducing juvenile mortality in cattle:**
  - Animal welfare issue in livestock farming
  - Environmental issue:
    - Methane emissions from non-productive animals
  - A substantial economic issue for farmers and the sector
    - Costs: feed, veterinary expenses
    - Loss of income

- **Main causes of juvenile mortality**
  - Perinatal mortality: calving conditions
  - Digestive diseases: immune system development
  - Respiratory diseases: partial capacity of the lungs during the 1^{rst} year of life

Towards the reduction of juvenile mortality in cattle through genetic selection

- **Potential for selection**
  - Genetic parameters: Traits with **low heritability** but **high genetic variability**

- **Genomic evaluations**
  - Around the world: Several countries have developed evaluations
    - to reduce juvenile mortality in dairy cattle (e.g. the Netherlands, Nordic countries)
    - to increase resistance to the underlying causes, i.e. digestive and respiratory diseases (e.g. Canada, USA)

  - In France: No evaluation for juvenile mortality except for perinatal mortality in dairy cattle

➢ SEVITAL project

- Estimate genetic parameters for juvenile mortality traits
- Develop genomic evaluations for juvenile mortality in French cattle breeds
- **Estimate genetic correlations between juvenile mortality traits and traits in selection**

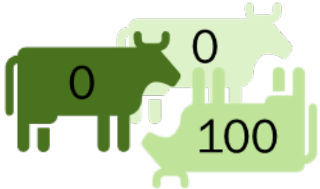
How to define mortality traits ?

- **In France: Reporting events throughout an animal's life is mandatory, including**
  - its date of birth
  - any movement between farms (sale)
  - its date of death
- **No details on the cause of death, but an indication: natural death or slaughter**

- **Three traits were defined**
  - First year of life divided into periods to reflect the principal underlying cause of mortality during the considered period
    - 3 - 30 days – mainly digestive diseases
    - 31 -365 days – mainly respiratory diseases
  - A global period : 3 - 365 days

Phenotype and dataset

- **Phenotype**
  - For each period: 3-30 days ; 31-365 days ; 3-365 days
  - Alive = alive at the end of the period or slaughtered
    Dead = natural death during the period



- **Nine dairy breeds**
- **Performances of females only**
  - Born in France between 2010 – 2025
  - With known ancestry
  - That stayed in the farm where they were born
  - No twins
  - No transfer of embryos

Methods – Pilot genomic evaluation

- **Pilot genomic evaluation run with HSSGBLUP**
  - Females only, with known ancestry, herd, date of birth, region
  - ≥ 5 animals per herd x year and per region x month x year
  - Daughters of bulls with ≥ 10 daughters from 5 different herds

- **Animal model**

$$\begin{bmatrix} y_n \\ y_g \end{bmatrix} = X\beta + \begin{bmatrix} Z_n & 0 \\ 0 & Z_g M_g \end{bmatrix} \begin{bmatrix} u_n \\ \alpha \end{bmatrix} + e$$

where *n* refers to non-genotyped animals and *g* to genotyped animals

y : vector of phenotypes
β : vector of fixed effects → herd x birth year and region x birth month x birth year
M_g: centered SNP genotypes of genotyped animals
u_n : EBVs of non-genotyped animals
α : vector of markers effects
e : vector of residual effects

- **EBV were inverted → positive EBV = better survival**

Pilot genomic evaluation

- Number of performances in the dataset for the pilot genomic evaluation

Breed	3-30 days	31-365 days	3-365 days
Abondance	60 508	49 785	53 695
Jersey	42 509	31 335	36 745
Brown Swiss	58 969	49 183	54 003
Tarentaise	23 221	18 512	20 503
Simmental	64 062	55 219	58 660
Montbéliarde	1 725 075	1 477 134	1 583 405
Normande	945 345	839 798	894 760
Vosgienne	5 423	4 498	4 750
Holstein	2 784 101	2 118 154	2 236 354

Methods – Correlations between traits

- **Approximate genetic correlations using Calo's method with the EBVs and reliabilities from the pilot genomic evaluation**

$$r_g = \frac{\sqrt{\sum_{i=1}^{n} \rho_{i,EBV1} \times \sum_{i=1}^{n} \rho_{i,EBV2}}}{\sum_{i=1}^{n} \rho_{i,EBV1} \times \rho_{i,EBV2}} \times r_{EBV1,EBV2}$$

where:

$\rho_{i,EBV1}$	is the reliability of the EBV for trait1 for the animal *i*
$\rho_{i,EBV2}$	is the reliability of the EBV for trait2 for the animal *i*
$r_{EBV1,\ EBV2}$	is the Pearson correlation between EBV1 and EBV2

- **EBV with low reliability (<0.4) were not taken into account**

Juvenile survival and milk production

- **Low to moderate favorable correlations between survival traits and milk production traits**
- **Stronger correlations in Montbéliarde than Holstein**

Holstein

	MY	FY	PY	FC	PC	SCS
3-30 days	0.122	0.145	0.190	0.038	0.099	0.121
31-365 days	0.141	0.272	0.267	0.155	0.186	0.231
3 - 365 days	0.149	0.248	0.263	0.123	0.169	0.228

Montbéliarde

	MY	FY	PY	FC	PC	SCS
3-30 days	0.494	0.484	0.599	0.023	0.257	0.363
31-365 days	0.480	0.476	0.577	0.026	0.211	0.299
3 - 365 days	0.542	0.535	0.645	0.011	0.241	0.344

MY: Milk yield ; FY: fat yield ; PY: protein yield ; FC: fat content ; PC: protein content ; SCS: somatic cell score

Juvenile survival and other survival traits


Holstein

	SURVIVAL_B	SURVIVAL_C
3-30 days	0.329	0.391
31-365 days	0.294	0.420
3 - 365 days	0.309	0.473


Montbéliarde

	SURVIVAL_B	SURVIVAL_C
3-30 days	0.514	0.327
31-365 days	0.542	0.358
3 - 365 days	0.562	0.297

SURVIVAL_B: survival at birth (48hours after birth)
SURVIVAL_C: survival at calving (maternal effect)

Juvenile survival and fertility

Holstein

	FERT_COW	FERT_HEIFER	CALV_IA1	NR_COW	NR_HEIFER
3-30 days	0.261	0.179	-0.046	0.356	0.168
31-365 days	0.424	0.339	0.032	0.436	0.213
3 - 365 days	0.355	0.260	-0.002	0.409	0.175

Montbéliarde

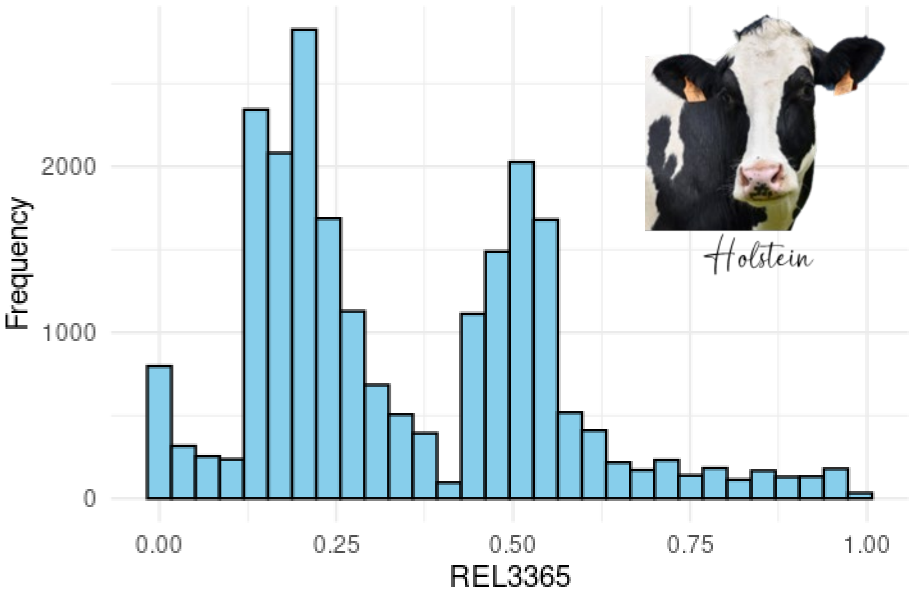
	FERT_COW	FERT_HEIFER	CALV_IA1	NR_COW	NR_HEIFER
3-30 days	0.542	0.317	0.009	0.278	0.071
31-365 days	0.577	0.288	-0.011	0.289	-0.018
3 - 365 days	0.601	0.343	-0.058	0.370	0.114

FERT_COW: cows fertility ; FERT_HEIFER: heifers fertility ; CALV_IA1: interval between calving and 1rst AI ; NR_COW: cows non return rate ; NR_HEIFER: heifers non return rate

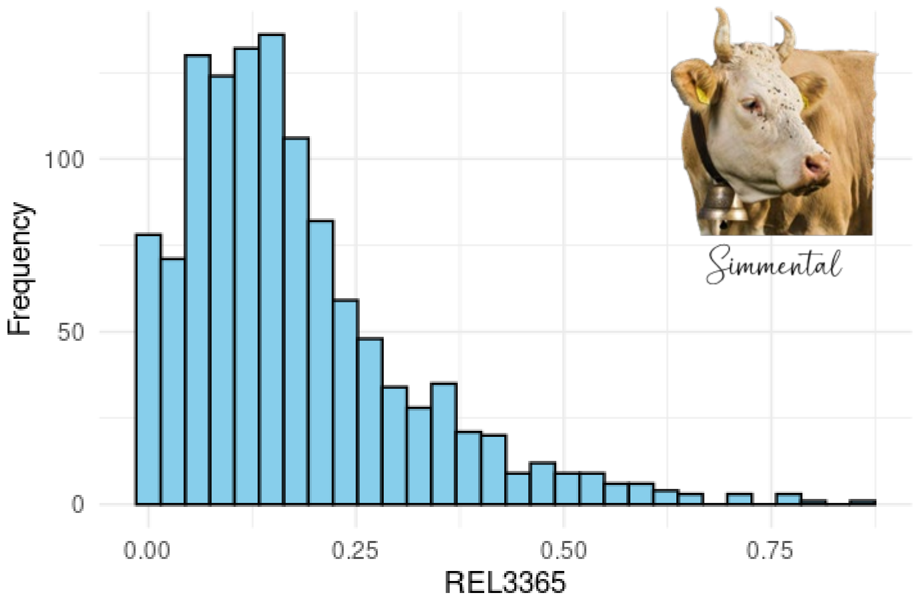
Low reliabilities for local breeds compared to national breeds

- **Low reliabilities for survival traits and some traits of interest**

National breed



Local breed



→ Difficulties to approximate genetic correlations with Calo’s method for these breeds

Conclusion

- **National breeds:**
  - Low to moderate correlations between survival traits and traits in selection in Holstein
  - Stronger correlations in Montbéliarde than in Holstein

- **Local breeds:**
  - Reasonable approximation of genetic correlations could not be achieved for local breeds
  - Low reliabilities for survival traits: combination of low h^2 and a limited number of performances

Thank you for your attention

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