



# A stayability approach for the longevity evaluation of Italian Holstein cattle

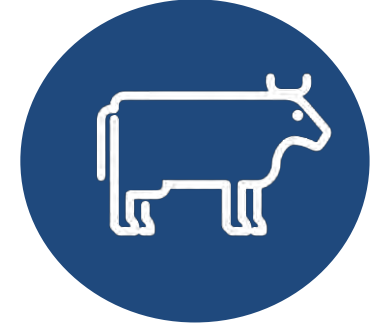
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## Introduction

**Longevity** plays a relevant role in the **profit** of a dairy herd, but also on **animal welfare**.

**Aim:** to compare 4 different genetic models applied to stay-ability in Italian Holstein population.

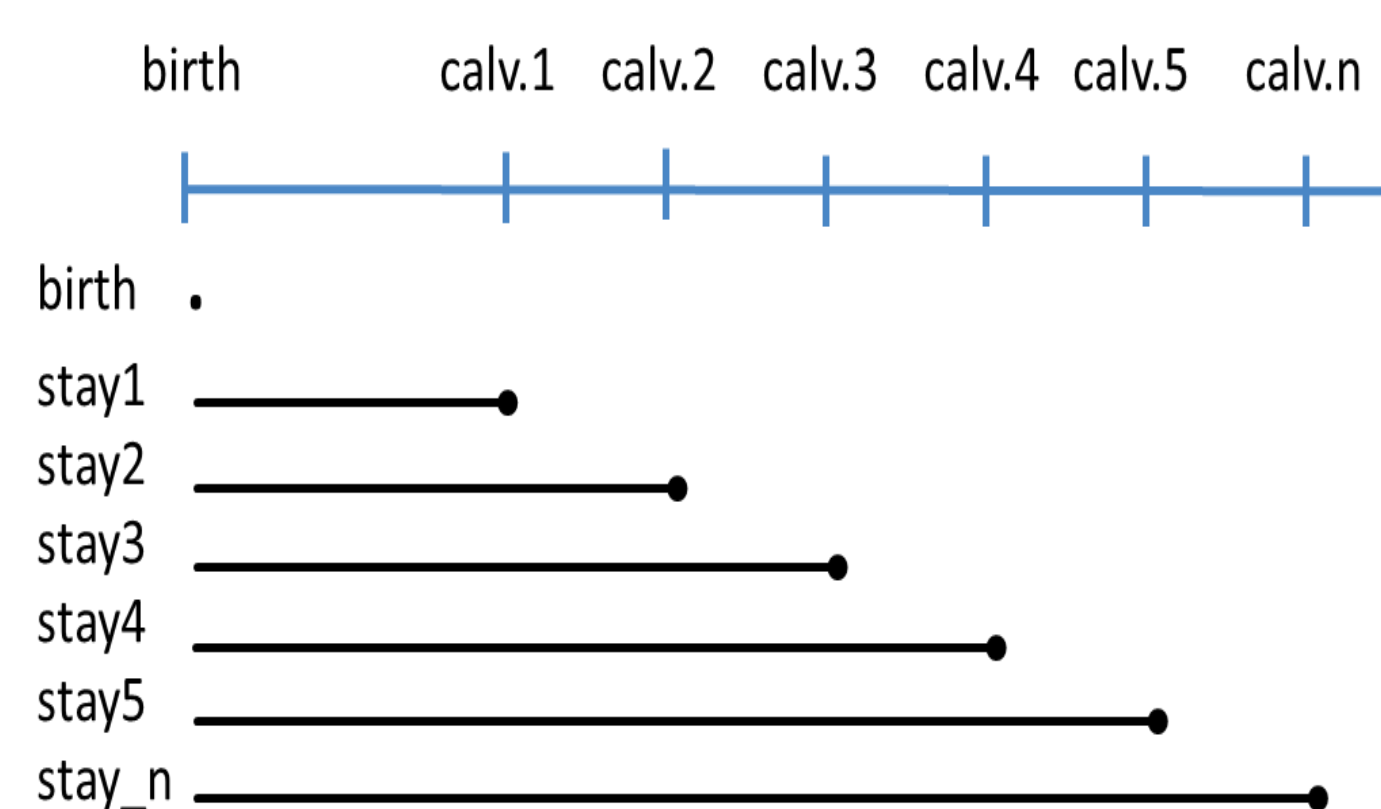
## Material and methods

**Dataset:** 307,812 Italian Holstein cows

### Data editing:

- Birth year from 1984
- Calving intervals: 240d to 700d
- Parity: 1 to 4
- Sires with at least 228 daughters, herds with at least 500 cows and at least 228 sires
- Age at first calving: 18 to 36 months
- 1 as survived cow, 0 not survived cow

**Approach:** stay-ability, which is a binary trait for success or failure to remain in the herd until a given time point.



STAY was analysed comparing different animal model

$$\mathbf{M1}: STAY = HY + hsc + dm + a + e$$

$$\mathbf{M2}: STAY = HY + hsc + dm + lac + a + pe + e$$

**HY** = random, effect of herd-year of calving;

**hsc** = fixed, classes of herd size changes (7 classes within calving year);

**dm** = fixed, classes of milk production difference from herd's average (10 classes within calving year);

**lac** = fixed, parity order;

**pe** = random, permanent environment;

**a** = random, additive genetic effect;

**e** = random error.

**M1:** single trait animal model, Gaussian (**M1g**) and Liability-Threshold (**M1t**)

**M2:** repeatability animal model, Gaussian (**M2g**) and Liability-Threshold (**M2t**)

Genetic parameters estimation → THRGIBBS1F90

Post-Gibbs analysis → POSTGIBBSF90

## Results

**Table 1.** Estimates for model M1.

	M1g		M1t	
	gen	herd_year	gen	herd_year
stay2	2.459 (1.927; 3.085)	1.827 (1.693; 1.964)	0.070 (0.057; 0.083)	0.047 (0.043; 0.051)
stay23	4.740 (3.994; 5.374)	4.194 (3.925; 4.498)	0.084 (0.068; 0.100)	0.077 (0.072; 0.082)
stay34	5.801 (4.797; 6.746)	4.534 (4.167; 4.865)	0.114 (0.090; 0.142)	0.084 (0.077; 0.091)

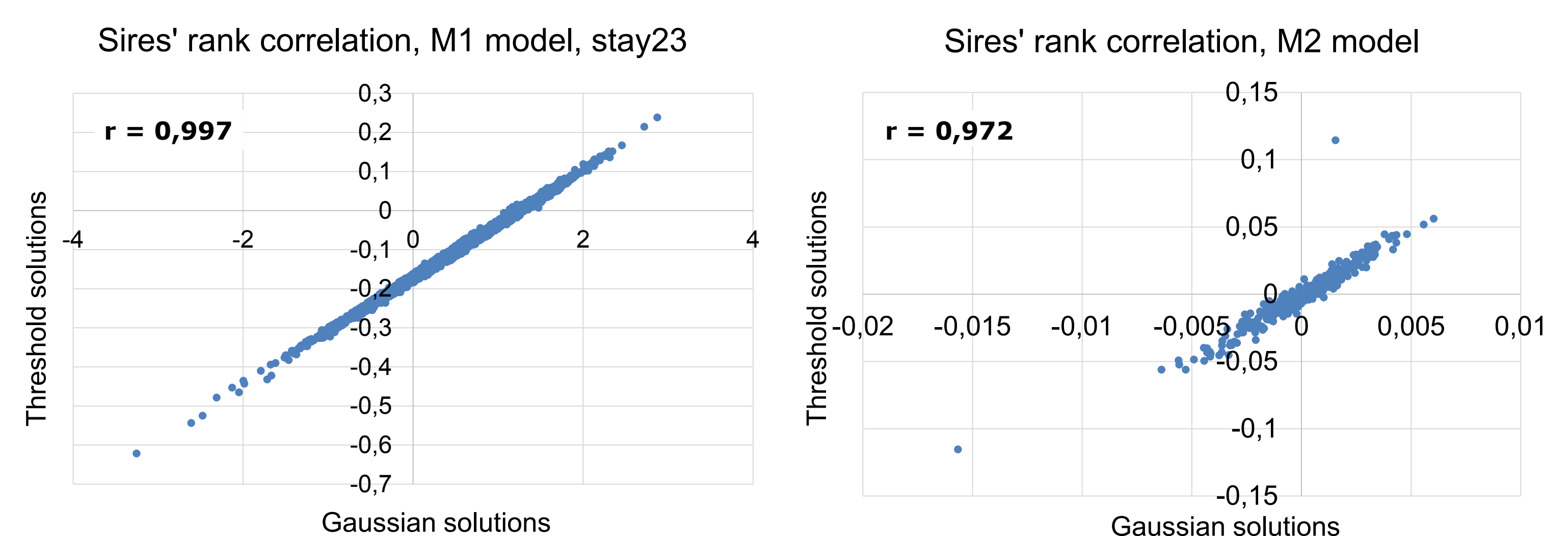
**Table 2.** Estimates for model M2.

	gen	pe	herd_year	h <sup>2</sup>
M2g	0.192 (0.124; 0.274)	2.180 (2.019; 2.340)	0.989 (0.965; 1.013)	0.003 (0.002; 0.004)
M2t	0.679 (0.603; 0.755)	0.293 (0.262; 0.324)	0.667 (0.653; 0.682)	0.257 (0.235; 0.278)

**Table 3.** Heritability estimates for M1g and M1t.

	M1g	M1t
stay2	0.029 (0.023; 0.036)	0.063 (0.051; 0.073)
stay23	0.041 (0.035; 0.046)	0.072 (0.060; 0.086)
stay34	0.047 (0.039; 0.054)	0.095 (0.076; 0.115)

**Graphs 1-2.** Sires Spearman rank correlation within M1 and M2 models.



## Discussion

- In Threshold models, genetic variances are higher compared to other random effects variances
- Higher h<sup>2</sup> for Mt vs Mg (even when transformed in the observed scale - Dempster and Lerner, 1950)
- High sires rank correlations: Gaussian and Liability-Threshold models are comparable

## Conclusion

- Threshold models give higher heritability and genetic variances; however, sires rank correlations are very close to 1 suggesting that the models are comparable.
- M1 compared to M2 allows to estimate more precise single traits.