



Genetic relationships between weight loss in early lactation and daily milk production until 305 days in Holstein cows

T Tribout, S Minéry, R Vallée, S Saille, D Saunier, V Ducrocq, Philippe Faverdin, D Boichard

► To cite this version:

T Tribout, S Minéry, R Vallée, S Saille, D Saunier, et al.. Genetic relationships between weight loss in early lactation and daily milk production until 305 days in Holstein cows. 12. World Congress on Genetics Applied to Livestock Production (WCGALP), Jul 2022, Rotterdam, Netherlands. pp.256-259, 10.3920/978-90-8686-940-4_52 . hal-03731285

HAL Id: hal-03731285

<https://hal.inrae.fr/hal-03731285>

Submitted on 20 Jul 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Genetic relationships between weight loss in early lactation and daily milk production until 305 days in Holstein cows

T. Tribout^{1*}, S. Minéry², R. Vallée², S. Saille³, D. Saunier⁴, V. Ducrocq¹, P. Faverdin⁵, and D. Boichard¹

¹Université Paris Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy-en-Josas, France; ²Institut de l'Elevage, 75012 Paris, France; ³INNOVAL, CS 10040, 35538 Noyal sur Vilaine, France; ⁴FCEL, France Conseil Elevage, 75009 Paris, France; ⁵INRAE, AgroCampus Ouest, PEGASE, 35590 Saint-Gilles, France; *thierry.tribout@inrae.fr

Abstract

Body mobilization of high-yielding dairy cows is intense after calving and can generate health and fertility troubles. This study aimed to estimate the genetic correlation between body weight loss during the five first weeks of lactation (BWL) and daily milk production (MY24a) in first (L1) and second (L2) lactations Holstein cows. The dataset included 859,020 MY24a and 570,651 body weight (BW) daily phenotypes from 3,989 L1 cows, and 665,361 MY24a and 449,449 BW daily phenotypes from 3,060 L2 cows, recorded in 36 French commercial farms equipped with milking robots including an automatic weighing platform. The genetic parameters of BW and MY24a in L1 and L2 were estimated using a 4-trait random regression model. Genetic correlations between BWL and MY24a ranged from -0.26 to 0.05 in L1, and varied from -0.11 to 0.10 in L2, suggesting that selecting to reduce early body mobilization while maintaining milk production is possible.

Introduction

Dairy cows experience negative energy balance after calving, and mobilize fat and protein reserves to compensate. This mechanism, if excessive, leads to health problems and low fertility and hampers cow longevity and economic profitability. In recent years, a growing proportion of French commercial dairy farms have been equipped with milking robots that record daily milk production and body weight of lactating cows. The objective of the study was to exploit these data to estimate the genetic relationship between early body weight loss, reflecting body mobilization, and daily milk yield, in order to evaluate the possibility of decoupling production and mobilization.

Materials & Methods

The data used for this study originated from 36 commercial dairy farms located in Western France. Average herd size was 92 cows [range: 46-189]. These herds are members of the *INNOVAL* DHIS network (<http://www.innoval.com>).

Data were recorded on 5,372 Holstein cows (4,464 and 3,364 cows in first (L1) and second (L2) lactation, respectively), calved from July 2014 to July 2018. Barns were equipped with Lely milking robots including an automatic weighing platform. At each visit k of a cow in the milking unit, the robot recorded the date and time of the visit, the weight of collected milk ($MILK_{elem,k}$) and the body weight of the cow. In total, more than 4.5 million visits were collected for the 5,372 cows.

For each cow i in lactation j (1 or 2) and each test day t :

- the sum of the $MILK_{elem,i,j,t,k}$ was calculated and standardized into a 24 hours milk yield (MY24) as $MY24(i,j,t) = \sum_{k=1,kt} (MILK_{elem,i,j,t,k}) * 1440 / \Delta_{time}$, where Δ_{time} is the time interval (in minutes) between the last milking of the current day and the last milking of the previous day.

Then MY24 was standardized to 4% fat (FC) and 3.3% protein (PC) contents (=MY24a). Daily FC and PC were estimated from monthly measures of each cow with Wilmink's lactation model.

- Body weight is affected by change in digestive tract content and therefore by change in feed intake. Feed intake increase in the beginning of the lactation partially hides initial body weight loss. To account for this potential bias, BW was corrected for the change in feed intake between day in milk t and calving ($t=0$), assuming a 4.5kg digestive content change per kg dry matter intake change (Faverdin, personal communication):

$$BW_{ci}(i,j,t) = BW(i,j,t) - 4.5 * (DMI(i,j,t) - DMI(i,j,0)) \quad (1)$$

where DMI at day in milk t of cow i in lactation j was predicted as:

$$DMI(i,j,t) = \mu(j,t) + \alpha(j,t) * BW(i,j,t) + \beta(j,t) * MY24(i,j,t). \quad (2)$$

The prediction equations for $\mu(j,t)$, $\alpha(j,t)$ and $\beta(j,t)$ were previously modelled as second order polynomials on a similar experimental Holstein population for which daily records of BW, MY and DMI were available (Martin et al, 2021).

For each cow and lactation, a 3rd order polynomial was fitted to the lactation MY24a and BW_{ci} data, and the outlier phenotypes deviating from prediction by more than 3 standard deviations were discarded.

Pedigree (3 generations) and dates of inseminations of the animals were extracted from the French national database. For each test date of a cow, the corresponding numbers of days in milk (DIM = test date – calving date) and of days carried calf (DCC = test date – date of conception (if necessary)) were calculated. The test dates between calving date and successful insemination date were assigned the DCC=0 specific level.

Genetic parameters estimates were obtained using WOMBAT software (Meyer, 2007). Phenotypes in L1 and L2 were considered as different traits. Due to the high number of records it was not possible to directly perform 4-trait random regressions on daily data for MY24a and BW_{ci} in L1 and L2. Therefore, a 2-step approach was applied.

Single trait analyses on daily data for BW_{ci} and MY24a in L1 and L2. Only data with DIM lower than 305 days and DCC lower than 242 days were considered. Records from animals with unknown parents, older than 3.5 years at first calving, or with less than 30 daily records available were discarded. Herd-test date contemporary groups with less than 4 records were discarded. Numbers of performances and cows after filtering are presented in Table 1.

Table 1. Numbers of daily phenotypes and cows considered in the single-trait analyses.

Trait	Lactation 1		Lactation 2	
	Daily phenotypes	cows	Daily phenotypes	cows
MY24a	859,020	3,988	665,361	3,060
BW_{ci}	570,651	3,439	449,449	2,660

The model used for single-trait analyses included the fixed effects of herd-test date (HTD), number of milkings per day (1, 2, 3, >3 – only for MY24a) (NMD), DCC as 4-node (DCC 0, 99, 174, 242 days) cubic splines, calving month x DIM interaction as 6-node (DIM 1, 15, 40, 90, 200, 305 days) cubic splines, age at calving (AaC) x DIM interaction as 6-node (DIM 1, 15, 40, 90, 200, 305 days) cubic splines. Five classes of AaC were considered: <25, 25-27, 27-30, 30-33, >33 months of age (moa) in L1, and <37, 37-39, 39-42, 42-45, >45 moa in L2. The random permanent environment effect and the additive genetic effect were modeled as second order Legendre polynomials. Finally, the residual variance was considered heterogeneous throughout the lactation period. Seven periods were defined, during which the

residual variance was supposed to be constant: DIM 1-7, 8-20, 21-50, 51-100, 101-150, 151-230, and 231-305.

Multi-trait analyses on pre-adjusted weekly means. Daily phenotypes for MY24a and BWci in L1 and L2 were adjusted for DCC, calving month and AaC, as well as NMD for MY24a, and the average performance per week in milk (WM) was calculated for each cow from WM 1 to 44 (wMY24a and wBWci). Cows with less than 9 weekly performances, as well as phenotypes of herd-test week with less than 10 cows were discarded. Numbers of performances and cows remaining after filtering are presented in Table 2.

Table 2. Numbers of weekly phenotypes and cows considered in the 4-trait analysis.

Trait	Lactation 1		Lactation 2	
	Weekly phenotypes	cows	Weekly phenotypes	cows
wMY24a	122,720	3,728	91,594	2,887
wBWci	102,582	3,253	78,137	2,553

Then, 4-trait random regression analyses were performed on the weekly averages with models including the fixed effect of herd-test week, the random effects of permanent environment and additive genetic value as second order Legendre polynomials, and a residual whose heterogeneous variance was supposed to be constant on seven periods: WM 1, 2-3, 4-7, 8-13, 14-21, 22-33, and 34-44.

Genetic correlations between early body weight loss and milk production. After adjusting BWci data for environmental effects, the maximum weight loss of cows was achieved on average 31 days after calving in L1 (-33.9 kg) and L2 (-37.3 kg), i.e. in the 5th week of lactation. The genetic variances and covariances between the random regression coefficients of wMY24a and wBWci estimated in the 4-trait analysis were therefore combined together to derive the genetic correlation in L1 and L2 between body weight loss from WM1 to WM5 ($BWL = BWci \text{ at WM5} - BWci \text{ at WM1}$) and wMY24a across lactation.

Results and discussion

The heritability for wMY24a showed similar trends in L1 and L2, increasing from 0.06 at WM1 to 0.20 at WM12, and then remaining stable. These values are in the low range of the literature for test-day milk yield of Holstein cows (e.g. Druet et al, 2005). BWL showed very small genetic standard deviations compared to BWci (e.g. 5.1 kg for BWL vs 30.2 kg for BWci at DIM 31 in L1). The resulting heritability was low (0.04 in L1 and 0.02 in L2), but consistent with the heritability estimates obtained by Berry et al (2003) for body weight changes from DIM 5 to DIM 60 (0.06) on multiparous Holstein cows.

The genetic correlations (r_g) between wMY24a at adjacent WM were very high, and decreased as the interval increased. However, r_g between early and later lactation (e.g. before WM10 vs after WM15) ranged from 0.3 and 0.8 in L1 and from 0.6 and 0.85 in L2.

The estimates of genetic correlations between BWL and wMY24a along lactations 1 and 2 are presented in Figure 1.

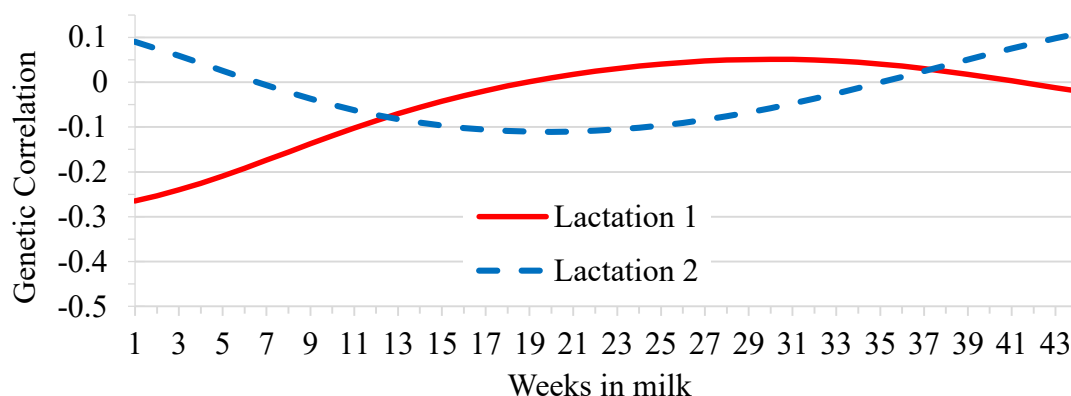


Figure 1. Genetic correlation estimates between body weight loss during the first 5 weeks after calving and adjusted daily milk yield along lactations 1 and 2.

A moderate negative genetic correlation was found on L1 cows between BWL and wMY24a before WM17, being minimum in WM1 (-0.26), and then becoming progressively closer to 0. This suggests that stronger body mobilization in early lactation is genetically associated with higher milk production. This is consistent with the results of Berry et al (2003) reporting moderate unfavourable genetic correlations between milk yield and body weight change and body condition score change during the first 2 months of lactation. After ~WM17, BWL and wMY24a appear, however, genetically independent on L1 cows. The genetic correlation between BWL and wMY24a in L2 cows was weaker, declining from 0.1 to -0.1 from WM1 to WM20, and then re-increasing up to 0.1 throughout the second half of lactation.

Milking robots are a valuable source of data. It is unfortunate that we did not have individual daily feed intake of the cows to adjust their BW, leading us to predict it under some assumptions. These predictions seem consistent, even if only approximations. However, keeping this in mind, our results suggest that it is possible to select cows with high milk yield after lactation peak while controlling body mobilization.

Acknowledgements

This work was performed in the framework of the DEFFILAIT project (ANR-15-CE20-0014), funded by the French Agence Nationale de la Recherche (ANR) and ApisGene. INNOVAL and FCEL are gratefully acknowledged for managing the data from milking robots.

References

- Berry D.P., Buckley F., Dillon P., Evans R.D., Rath M. *et al.* (2003) *J. Dairy Sci.* 86:2193-2204. [https://doi.org/10.3168/jds.S0022-0302\(03\)73809-0](https://doi.org/10.3168/jds.S0022-0302(03)73809-0)
- Druet T., Jaffrézic F., Ducrocq V. (2005) *Genet. Sel. Evol.* 37:257-271. <https://doi.org/10.1186/1297-9686-37-4-257>
- Faverdin P., Charrier A., Fischer A. (2017) Proc. of the 8th ECPLF, Nantes, France.
- Martin P., Ducrocq V., Gordo D.G.M., Friggens N.C. (2021) *Animal* 15(2):1001001. <https://doi.org/10.1016/j.animal.2020.100101>
- Meyer, K. (2007) *J. Zhejiang Uni. SCIENCE B* 8: 815-821. <https://doi:10.1631/jzus.2007.B0815>