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Association between body condition genomic values and feed intake, milk production, and body weight in French Holstein cows

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ABSTRACT

Body condition score (BCS) offers a good estimate of the amount of stored fat on the body, and its variations can be used as a proxy for energy balance. Many countries have implemented a genomic evaluation of BCS, including France, where estimated breeding values are based on an individual BCS determination during the first lactation. In this article, we investigate the degree to which this genomic estimated breeding value based on a single phenotype record per cow might reflect different profiles of body reserves throughout lactation and be used to predict, and perhaps limit, their mobilization during early lactation. We also investigate whether selection on BCS affects other traits. A data set including 686 lactations of 435 Holstein cows from 3 experimental farms not used in the reference population for genomic evaluation was used to estimate the effects of the BCS direct genomic value (iBCS) on BCS, body weight, feed intake, milk production, and fat and protein contents throughout the lactation period. For each trait, the model included different iBCS regressions and an effect of the direct genomic value of the trait itself when available. It thus appeared that cows with a positive iBCS always had a higher BCS than negative iBCS cows, whatever the lactation stage, and that this difference increased during the first 6 mo to reach a difference of 0.8 point. A similar effect was seen regarding body weight, but it was the opposite for milk production, with negative iBCS cows producing slightly more milk (difference of about 3% over lactation). Feed intake increased slightly faster at the beginning of lactation for cows with positive iBCS. Therefore, iBCS is a promising tool that could help to limit intense mobilization during early lactation. Should feed efficiency be included in the breeding goal, greater attention should be paid to BCS to avoid further body mobilization in early lactation.

Key words: bovine, body condition score, mobilization, estimated breeding values

INTRODUCTION

Dairy cows mobilize body fat after calving and start to recover when the energy balance returns to being positive. Indeed, during early lactation, the increase in feed intake is not sufficiently rapid to cover the energy requirements for milk production (Banos et al., 2005) and cows therefore enter a negative energy status that causes them to mobilize their body reserves (Block et al., 2001; Friggens et al., 2004). Although body fat mobilization is a physiological adaptation to a negative energy balance, if it is too intense a mobilization, it can trigger metabolic disorders (Weber et al., 2013), a weak immune system, and poor fertility. High-producing dairy cows are reported to mobilize more body reserves, and selection for milk production has generated more marked mobilization (McNamara and Hillers, 1986; Pryce et al., 2001). Conversely, later in lactation, when milk production decreases while intake remains high, the cows recover and build new body reserves. Recording BW changes is not sufficient to estimate the energy balance, as it can be confounded with growth or variations in digestive content (Faverdin et al., 2017), thus causing confusion between efficiency and mobilization. The BCS offers a good estimate of the amount of stored fat in the body (Broster and Broster, 1998), and its variations can be used as a proxy for energy balance, despite being based on the human eye, which makes it difficult to identify small changes within a short period of time. It has been shown that positive genetic correlations exist between BCS and feed efficiency components such as feed intake and BW (Manzanilla-Pech et al., 2016).

Many dairy countries have already implemented a genomic evaluation of BCS. In France, because of the large reference population used to evaluate Holstein

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cattle, a very high reliability can be achieved for any genotyped animal. In this evaluation, phenotypes are single measurements of BCS during the first lactation (Interbull, 2019). Consequently, the genomic EBV reflects the average condition throughout lactation. Days in milk is an important factor for variation included in the model, but no genetics × DIM interaction is assumed. The dynamics of body reserve mobilization and accretion vary considerably between individuals (Komaragiri and Erdman, 1997; Kessel et al., 2008). It is not known whether this BCS evaluation may also reflect within-individual variations in condition score, and particularly whether they can be a proxy for the intensity of mobilization at the start of lactation. This paper therefore investigates the degree to which this genomic evaluation based on a single phenotypic record per cow might reflect different body reserve profiles throughout lactation and could be used to predict and perhaps limit mobilization during early lactation. Based on the hypothesis that BCS direct genomic value (**iBCS**) is able to predict variations in BCS over time, we also investigated how differences in iBCS might affect the levels and trajectories of additional traits such as feed intake or milk production, which are other components of feed efficiency.

MATERIALS AND METHODS

Population Resources and Feed Intake Management

This experiment was carried out between 2014 and 2020 in Holstein cows from 3 experimental farms in France: 169 Holstein cows from the Le-Pin-Au-Haras INRAE facility (https://doi.org/10.15454/1.5483257052131956E12), 145 from the Mejusseaume INRAE facility (https://doi.org/10.15454/yk9q-pf68), and 121 from Les Trinottières experimental farm. They represented 686 lactations from 435 cows, with a parity ranging from 1 to 7. All animals were handled with care in accordance with the French Ministry of Agriculture guidelines for animal research and the applicable European Union guidelines and regulations on animal experiments.

At Le Pin, cows were part of an experiment measuring genetic divergence on body condition (**BC**) while maintaining the same milk level. It was implemented to increase trait variability by procreating 2 cow lines from sires genetically divergent for official BCS EBV (i.e., ≥1 or ≤−1 genetic standard deviation) with no genetic difference on milk yield (**MY**). The expected genetic difference between lines was 1 genetic standard deviation for BCS, corresponding to 0.5 point BCS on a 0 to 5 scale. Twenty unselected donor cows were mated with 10 bulls from each EBV group. Their embryos were collected and transferred into recipient cows. At the following generation, the daughters were mated with bulls from the same group as their sire so that divergence increased in the second generation.

The cows were fed individually using an electronic gate feeding system and ear-tag identification. They received a TMR that depended on the farm. In Mejusseaume, the TMR was based on maize silage and concentrates with an energy value of 0.93 forage unit per kilogram DM (UFL/kg DM, 1 UFL equating to 7.12 MJ of net energy for lactation; INRA, 2018). In Les Trinottières, 2 TMR were used (half of the cows received each diet): one based on maize silage and concentrates and the other also including grass silage, with energy values of 0.96 and 1.00 UFL/kg DM, respectively. The feeding data on these 2 farms had already been described in a previous study (Fischer et al., 2018). Finally, in Le Pin, the TMR was based on maize silage plus grass silage, rapeseed meal, minerals, and concentrates, with an energy value of 0.95 UFL/kg DM. The nutritional values of the TMR were all within the range of those typically recommended to support the MY level of a herd. The TMR was allocated in amounts that allow for approximately 10% orts to ensure ad libitum intake.

Phenotyping and Trait Definition

The cows were milked twice daily and MY was recorded individually at each milking. Twice a week, individual samples were collected for the determination of milk fat content (**FC**) and protein content (**PC**). Fat- and protein-corrected milk (**FPCM**) was calculated according to the formula of the Food and Agriculture Organization of the United Nations, which defines a milk with 4.0% fat and 3.3% protein as standard (FAO, 2010):

$$\text{FPCM} = \text{MY} \times (0.337 + 0.116 \times \text{FC} + 0.06 \times \text{PC}). \quad [1]$$

The cows were weighed twice daily using an automatic weighing system at milking to record BW. Individual daily feed intake was measured as the difference between distributed and next morning refusals weight (Mejusseaume and Les Trinottières) or as the sum of intakes weighed at each visit by the cow (Le Pin). Dry matter intake was calculated daily, based on the DM content of TMR. Body condition was scored on a 5-point scale with 0.25-point steps (Bazin, 1984) by the same 2 or 3 trained scorers monthly, every 2 weeks, or weekly, depending on the farm. The average BCS of the scorers was used. The study included data from 5 to 250 DIM.

Table 1. Descriptive statistics for milk yield (MY), fat- and protein-corrected milk (FPCM), fat content (FC), protein content (PC), DMI, BCS, and BW

Trait[1]	MY (kg/d)	FPCM (kg)	FC (g/kg)	PC (g/kg)	DMI (kg/d)	BCS (point)	BW (kg)
N	120,942	120,934	37,528	37,534	100,741	6,211	98,453
Mean	32.9	32.0	39.2	31.8	21.7	2.40	630.3
SD	8.2	7.8	6.2	2.9	4.5	0.60	77.9
Min	0.2	0.2	4.9	10.0	0.1	1.00	304.0
Max	85.7	96.6	76.3	58.6	48.6	4.75	1,046.0

[1]N (numbers of data), mean, SD, minimum, and maximum values.

Genotyping and Genomic Evaluation

All animals were genotyped using the Illumina SNP50k or EuroG10k chips (Illumina Inc.) from blood samples or ear punches. Genotyping was performed by LABOGENA, Jouy-en-Josas, France (www.labogena.fr). Missing 50k genotypes were imputed by FImpute (Sargolzaei et al., 2014) using the EuroGenomics Holstein bull population (n = 35,000) as a reference. The direct genomic values (**DGV**) of experimental animals were obtained by combining their genotypes with the SNP effects estimated by the French national evaluation system for about 40 traits that include BCS, milk content, FC, PC, and different proxies of BW (stature, body depth). It is worth noting that phenotypes from these experimental farms were not included in the national evaluation and therefore the index used in this study was estimated independently of any phenotypic information from the animals. Genetic standard deviations with a mean of zero are used to express iBCS. The cows were classified based on their iBCS as follows: **BC−−** if iBCS ≤ -1; **BC−** if $-1 <$ iBCS ≤ -0.5; **BC0** if $-0.5 <$ iBCS < 0.5; **BC+** if $0.5 \leq$ iBCS < 1; and **BC++** if iBCS ≥ 1. The different BC classes represented 29, 69, 184, 90, and 63 cows, respectively.

Statistical Analysis

For each trait (MY, FPCM, FC, PC, DMI, BW, and BCS), the effects of iBCS on the trait trajectory during lactation were analyzed using a model that included the following: (1) the DGV corresponding to the trait (except for DMI, as no index is yet available for this trait in France) to take account of the genetic variability of animals, (2) a lactation curve to take account of the DIM, and (3) a regression on iBCS to estimate its impact on the trait. To allow for different effects of iBCS on the trait throughout the lactation, different regression terms for the function of DIM were considered. It is important to note that iBCS and DGV for the other traits have low or moderate correlations (from −0.17 to 0.20), excluding strong confounding between effects. More precisely, at each day in milk, the following model was applied:

$$y_{it} = \mu + \mathbf{x_i} \times \mathbf{f} + WIL_t(\text{parity}) + \alpha \times \text{iBCS} + \beta \times \text{iBCS} \times st + \gamma \times \text{iBCS} \times st^2 + \delta \times \text{iBCS} \times st^3 + \varepsilon_i, \quad [2]$$

where y_{it} is the performance of animal i at day in milk t; μ is the overall mean; $\mathbf{f}$ is the vector of fixed effects of farm-date (or farm-date-diet when relevant) and the corresponding DGV (except for DMI, which is not an evaluated trait, and BCS, which EBV is already included in the regression) as a covariate; $\mathbf{x_i}$ is the incidence vector relating cow i to fixed effects; $WIL_t(\text{parity})$ is the within-parity (primiparous vs. multiparous) Wilmink model of lactation curve described as $WIL_t(\text{parity}) = a + b \times t + c \times e^{(-0.06 \times t)}$ (Wilmink, 1987); α, β, γ, and δ are the iBCS regression parameters; st is the standardized stage of lactation $[(t - 125)/250]$; and ε_i is the residual.

Analyses were performed using the GLM procedure under SAS software (SAS Institute Inc., 2008).

RESULTS

Descriptive Statistics

The descriptive statistics regarding MY, FPCM, FC, PC, DMI, BW, and BCS for overall lactations are presented in Table 1. No differences in mean DMI, BW, and milk components were observed between farms, except for a higher FC at Les Trinottières farm (41.2 g/kg vs. 38.5 and 38.9 g/kg for Le Pin and Mejusseaume, respectively). However, some differences in averaged BCS existed between farms, the highest value being seen at Les Trinottières (2.7 points), an intermediate value at Le Pin (2.3 points), and the lowest value at Mejusseaume (2.0 points).

Performance Trajectories

Wilmink parameters are presented in Table 2. The trajectories of MY, FC, PC, DMI, BW, and BCS are presented in Figure 1. Milk yield rose rapidly by 12 kg between 5 and 50 DIM, then slowly decreased. By contrast, FC and PC fell rapidly by around 8 g/kg over

Table 2. Wilmink parameters and BCS direct genomic value regression parameters for milk yield (MY), fat- and protein-corrected milk (FPCM), fat content (FC), protein content (PC), DMI, BCS, and BW[1]

Trait	MY (kg/d)	FPCM (kg)	FC (g/kg)	PC (g/kg)	DMI (kg/d)	BCS (point)	BW (kg)
R^2	0.50	0.46	0.44	0.54	0.59	0.63	0.57
Primiparous							
A	32.54	30.80	36.84	29.51	20.10	2.11	533.89
B	−0.02	−0.01	0.01	0.02	0.00	0.00	0.49
C	−17.17	−12.78	8.08	6.79	−11.97	0.64	14.21
Multiparous							
a	45.20	42.63	37.55	28.93	25.59	1.92	640.35
b	−0.06	−0.05	0.01	0.02	−0.01	0.00	0.23
c	−18.67	−11.73	9.06	8.29	−14.58	0.86	−3.86
α	−0.48 (0.04)	−0.81 (0.04)	−0.04 (0.05)	0.14 (0.02)	−0.01 (0.02)	0.29 (0.01)	21.61 (0.35)
β	−0.38 (0.21)	−1.10 (0.21)	−0.64 (0.31)	−0.66 (0.13)	−0.39 (0.11)	0.11 (0.07)	13.16 (2.03)
γ	1.50 (0.34)	1.71 (0.34)	−0.57 (0.51)	−1.36 (0.21)	1.26 (0.18)	−0.40 (0.11)	−4.91 (3.31)
δ	2.76 (1.37)	4.48 (1.36)	1.39 (2.00)	0.71 (0.84)	−0.01 (0.74)	−0.05 (0.43)	−21.63 (13.09)

[1]R^2 = percentage of variation explained by the model; A, B, C, a, b, c = Wilmink parameters defined separately for primiparous or multiparous cows; α, β, γ, δ = BCS direct genomic value regression parameters (SE in parentheses).

the same period and then slowly increased until 250 DIM (end of modeled lactation). Additionally, DMI increased by 8 kg between 5 and 50 DIM, but much more slowly than MY. Body weight fell by 14 kg during the first 2 wk of lactation and then increased consistently, with the animals gaining an average total of 80 kg. Unlike the other traits, BCS displayed high variations. The regular pattern is due to protocols used to score BC. In Le Pin and Mejusseaume, scoring occurred on a fixed weekday, leading to small groups of cows at each DIM. In Les Trinottières, scoring was performed at fixed DIM, leading to a large group every 7 DIM. In addition, this farm showed the highest BCS mean, explaining the regular peak every 7 d. The trend indicated a slight loss of condition of 0.25 point at the start of lactation, followed by a recovery of 0.4 point by the end of lactation.

Effects of iBCS on Performances

Regression parameters are presented in Table 2, and the effects of iBCS on trait trajectories are presented in Figure 2. All traits were significantly associated with iBCS, except FC. These effects were not constant throughout the lactation (Figure 2), as shown by the significant α, β, or δ estimates. In terms of the BCS trait (Figure 2a), positive BC cows always had a significantly higher score than negative BC cows, whatever the stage of lactation. This difference increased during the first 6 mo, with a 0.4 difference in score between the extremes at the start of lactation and a 0.8 difference in mid-lactation. Milk production was a bit higher among negative BC cows (Figure 2b), with almost no difference between the extremes at the start of lactation and a difference of 1.2 kg per day in mid-lactation. Exactly the same pattern was observed regarding corrected milk (not shown). No differences between cows were observed for FC during early lactation (Figure 2c). After 95 d in milk, negative BC cows displayed a slightly higher FC value than positive BC cows, the difference reaching 1 g/kg at 245 DIM. Results for PC depended on the lactation stage (Figure 2d): values tended to be higher in positive BC cows at the start of lactation, with a difference between extremes of up to 0.5 g/kg, and then much higher in negative BC cows after 165 d, the difference between extremes reaching 1.2 g/kg at the end of lactation. As for DMI (Figure 2e), positive BC cows had a higher intake at the start of lactation (+1.2 kg/d), but after 100 d, no difference was seen between the cows. Negative BC cows were lighter than positive BC cows (Figure 2f), the difference increasing during lactation from 40 to 65 kg. Comparison significance between the extreme groups, with the smallest number of data, is mentioned in Figure 2. Differences were always significant for BCS, MY, and BW. They were significant for DMI at the start and the end of lactation, for PC at the end of lactation, and for FC only in mid-lactation.

Although these effects were observed from the trajectories themselves (Figure 3), it could be seen that the shapes of the curves for BCS and BW were the same but shifted, whereas the differences in DMI appear to be limited, and very limited for MY. Regarding overall lactation (5 to 250 DIM), the cumulated difference in milk production between the extreme groups reached 232 kg of milk, which corresponded to a total difference of about 3%. In terms of DMI, the cumulative difference between the extreme groups corresponded to 14 kg of feed. This difference is concentrated in the first 2 mo of lactation but is quite low (0.25%). Almost no changes to the shapes of the curve were observed with respect to FC and PC.

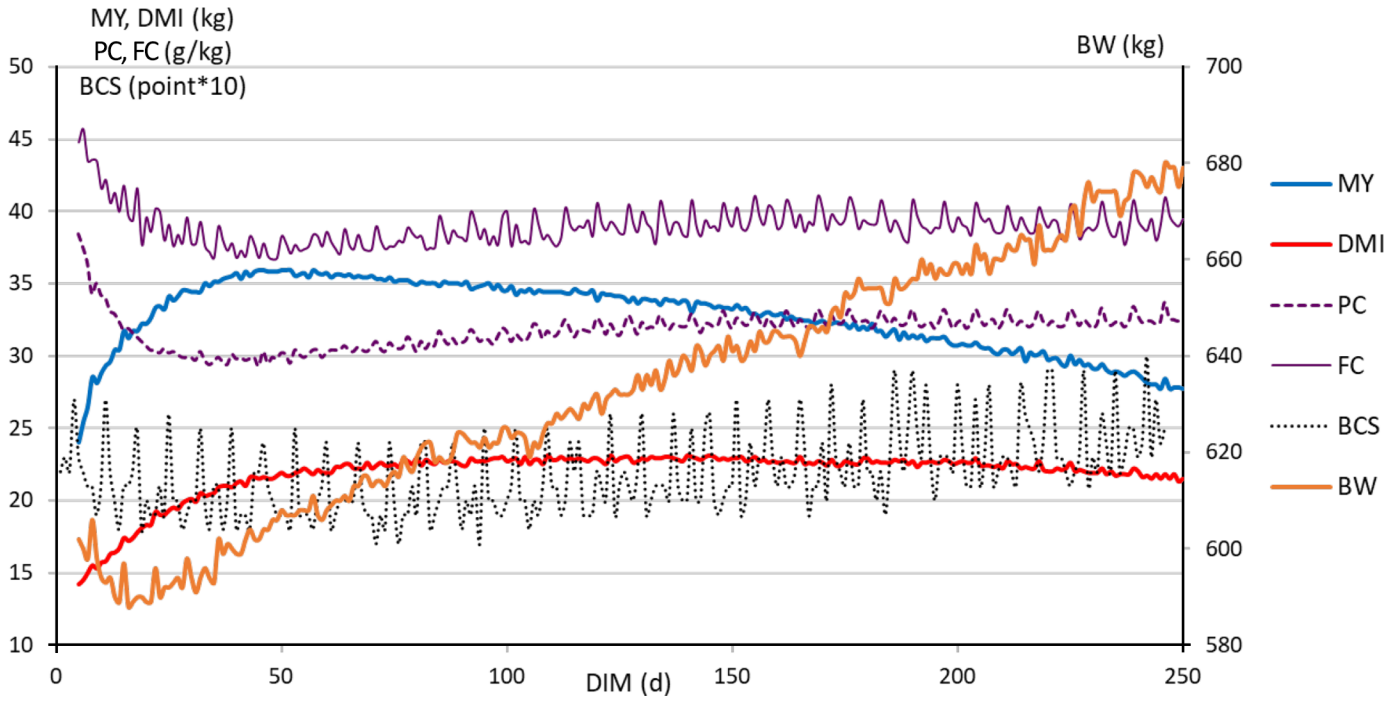


Figure 1. Mean lactation curves of milk yield (MY), fat content (FC), protein content (PC), DMI, BCS (×10), and BW.

DISCUSSION

Evolution of Phenotypic Performance During Lactation

The animals used for this study originated from 3 different experimental farms, all located in western France. Their milk production was higher than the national average (8,250 kg in 250 DIM versus 7,236 kg/yr on average; Idele, 2021) but representative of an indoor ad libitum production system with no access to pasture, which is typical for the study of feed efficiency. The difference observed in the average BCS for all the farms was more likely due to slight differences in BCS interpretations between technicians rather than real differences in body reserve, as no cross-validation was performed and no common training provided. These differences were accounted for by fixed effects in the models used for subsequent analysis and should not affect the results of this study. To overcome these technician limitations (limited number of measures and subjective appraisal), computer vision offers new opportunities to routinely and frequently record BCS over the lactation.

The evolution of the different traits over lactation followed the same pattern as that already observed in previous studies with similar levels of performance (Köck et al., 2018; Mäntysaari et al., 2019): a rapid rise in milk production during early lactation followed by an increase in intake after a short delay, whereas BW and BCS both fell slightly. This pattern reflected the energy status of the animals: during early lactation, most animals entered a state of negative energy balance with mobilization of missing nutrients from their body reserves (Collard et al., 2000; Mäntysaari et al., 2019). Our results showed that positive BC cows tend to have a smaller prioritization on milk production and less mobilization than negative BC cows. It is nevertheless worth noting that this mobilization of body reserves did not always result in a reduction in BW or this was limited, despite the negative energy balance (for an example, see Köck et al., 2018). This counterintuitive phenomenon could be explained by the nature of what is referred to as BW. Indeed, observed BW is the sum of the true BW and the digestive content weight. The increase in DMI during early lactation leads to a significant increase in digestive content that partially masks the loss of true BW linked to mobilization (Faverdin et al., 2017). With a rise in DMI from 10 to 20 kg between calving and 30 DIM, the digestive content increases by around 40 kg with a rich diet, masking an equivalent loss of weight. The additional effects of water and potential protein retention may also be seen in situations of negative

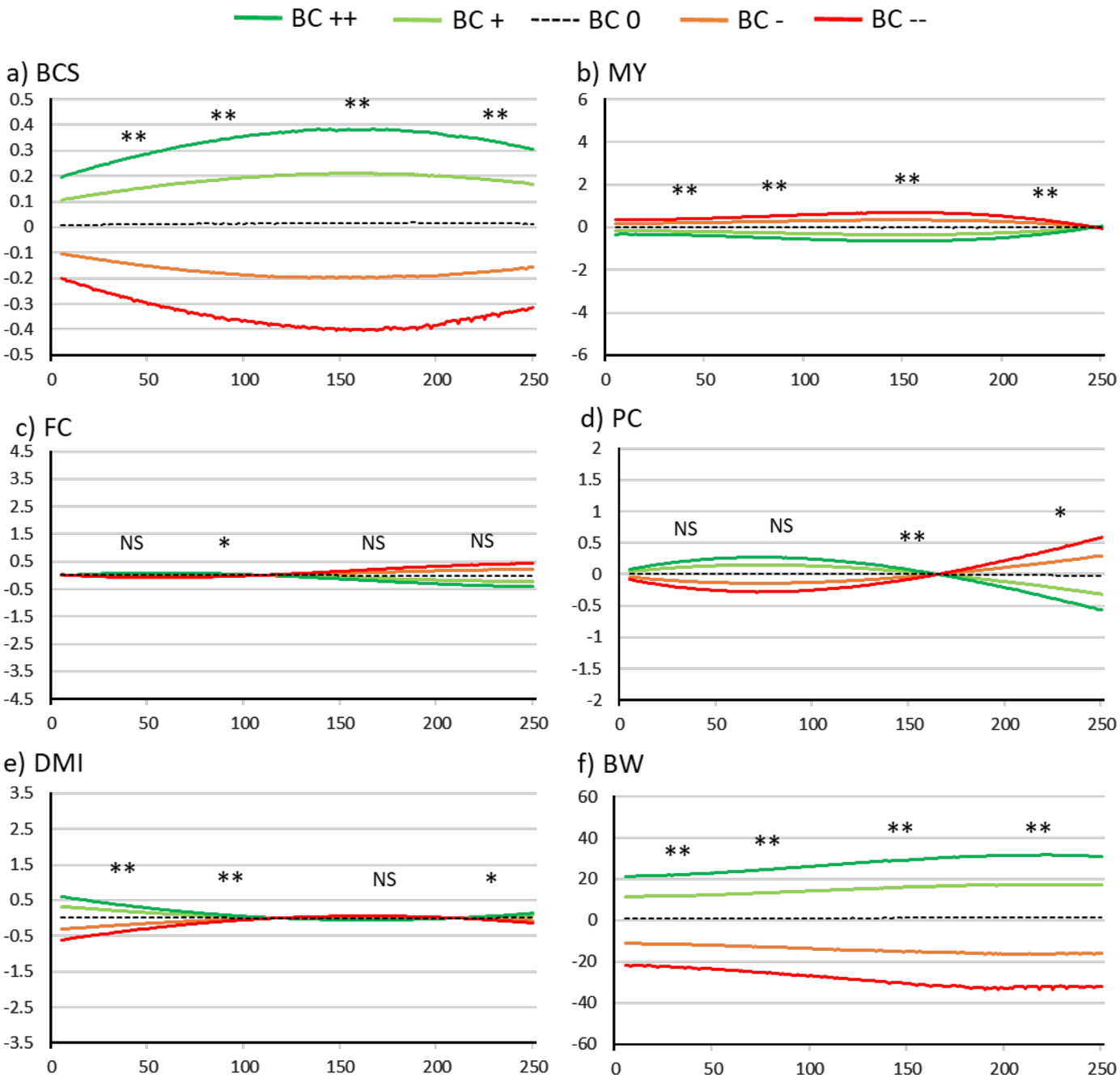


Figure 2. Effect of BCS direct genomic value on trajectories of the 5 BCS direct genomic value–based groups for BCS (point, panel a), milk yield (MY, kg, panel b), fat content (FC, g/kg, panel c), protein content (PC, g/kg, panel d), DMI (kg, panel e), and BW (kg, panel f). Milk yield and contents were adjusted for their respective direct genomic value; BW was adjusted for body capacity direct genomic value. For each trait, the Y-scale range represents 1.5 SD between minimum and maximum values. Significance symbols (NS, $^{*}P < 0.01$, $^{**}P < 0.0001$) correspond to the contrasts between BC++ and BC−− groups at 4 lactation stages (30, 90, 150, and 220 d). BC−−: iBCS ≤ -1; BC−: $-1 <$ iBCS ≤ -0.5; BC0: $-0.5 <$ iBCS < 0.5; BC+: $0.5 \leq$ iBCS < 1; and BC++: iBCS ≥ 1.

energy balance and may contribute to mitigating the observed decrease in BW (Hüttmann et al., 2009). Later in the lactation, when milk production slowly declines, intake remains constant; the animals enter a positive energy balance and start gaining new body reserves.

Effects of iBCS on Other Traits

The results observed in this study on how iBCS is associated with different types of performance are interesting for more than one reason. First, they confirmed that a single BCS determination during the first

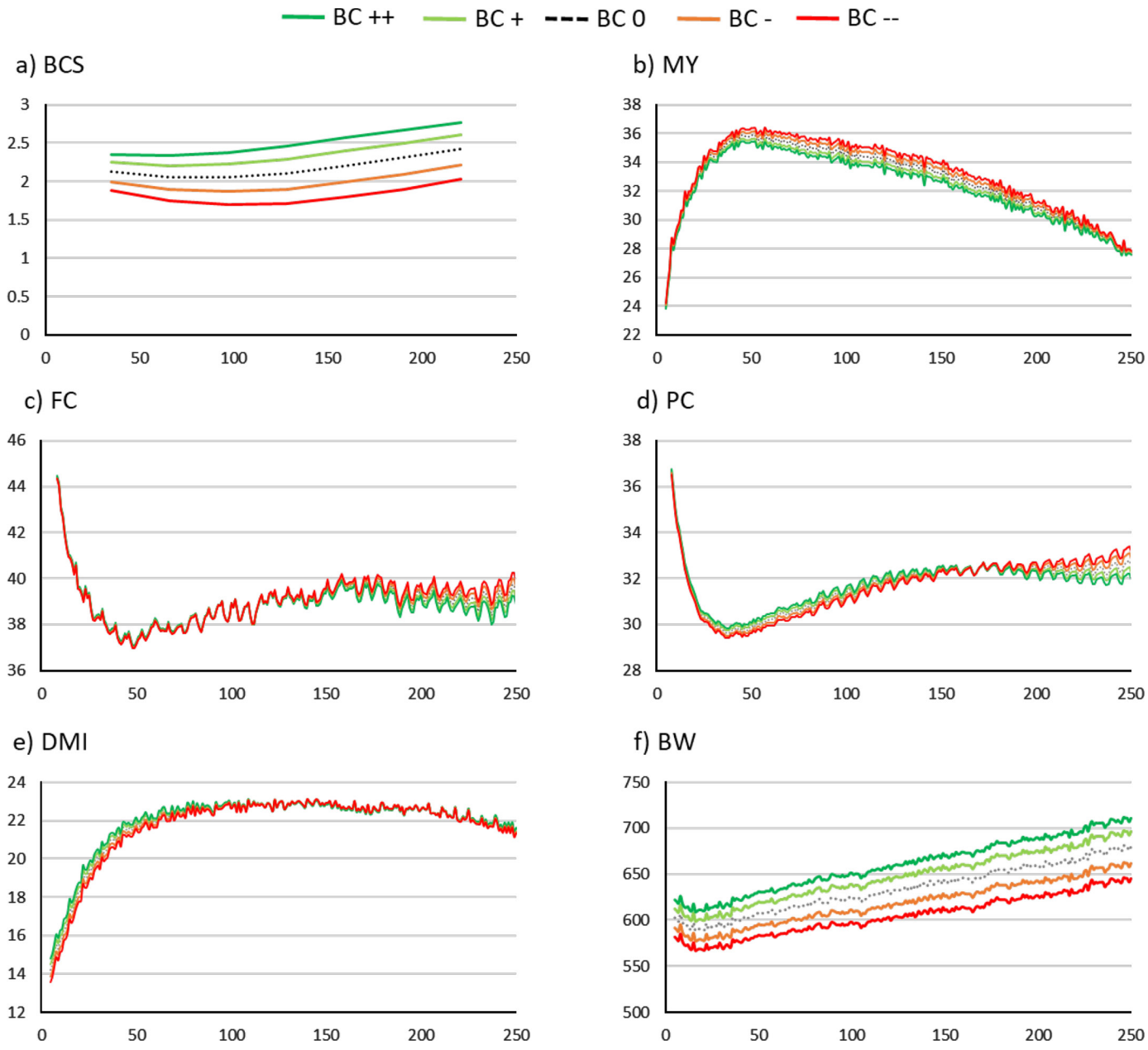


Figure 3. Trajectories of the BCS (panel a), milk yield (MY, kg, panel b), fat content (FC, g/kg, panel c), protein content (PC, g/kg, panel d), DMI (kg, panel e), and BW (kg, panel f), by BCS direct genomic value group. Milk yield and contents were adjusted for their respective direct genomic value; BW was adjusted for body capacity direct genomic value. BC−−: iBCS ≤ -1; BC−: $-1 <$ iBCS ≤ -0.5; BC0: $-0.5 <$ iBCS < 0.5; BC+: $0.5 \leq$ iBCS < 1; and BC++: iBCS ≥ 1.

lactation of the reference population was sufficient to generate a genomic prediction that discriminated cows in terms of their BCS throughout lactation and even throughout their productive life, as this study was not limited to first lactations only. Indeed, it appears that the BCS remains the same trait through the different stages of an animal's productive life, as supported by the almost complete genetic correlations between BCS measurements estimated within a lactation period or across lactations in previous studies (Berry et al., 2003; Dechow et al., 2004). Nevertheless, the effects of iBCS on BCS measurements were not constant and increased during the mobilization period at the start of lactation, showing that iBCS can also reflect mobilization. This conclusion offers some opportunities for the prediction of mobilization and solutions to limit its effects.

The second point concerns the existence of a slight effect of iBCS on milk quantity, milk content, and

BW, although these traits are adjusted for their own index included in the model. This indicates that correlations may exist between these indices. Although correlations between indices may not give the exact values of genetic correlations, given that the indices' accuracy is not equal to one, they are expected to be close for these traits and can then be compared with results in the literature concerning genetic correlations. Regarding the link between milk production and BCS, a review by Roche et al. (2009) proposed a curvilinear relationship between calving BCS and production, meaning that both extremes of the BCS are associated with lower milk production, the optimum being 3.0 to 3.25 point. This was not the case in our study. However, our findings could have been due to our low BCS animals being less skinny than the extremes studied by Roche et al. It is also worth noting that the effect was very limited regarding overall milk production. These authors also reported that calving and early lactation BCS were generally positively associated with milk FC and PC, which was also observed in our animals. However, most previous studies focused on early lactation and could find no references concerning a mid-lactation shift. The link between live weight and BCS was positive and increased slightly during lactation, similar to what had been reported by Martin et al. (2021). This stable correlation between the 2 traits is in favor of the regular use of BW changes as an indicator of body reserve mobilization in the literature (Thorup et al., 2013; Manzanilla Pech et al., 2014).

Finally, DMI had a special status among the traits studied here, as it is the only one for which an index is not available in France, which means that there is no correction for DMI differences at a genetic level between animals and there is potential for confusion with the effects of iBCS. The influence of iBCS on DMI could only be seen during early lactation in animals with a high iBCS consuming more feed than those with low indices. This result appeared to contradict the findings of a previous study that had reported a negative association between DMI and BCS (Martin et al., 2021). This study, however, did not include a genetic effect, as no data were available.

Relationships Between BCS, Mobilization, and Energy Balance

One of the key goals of our study was to determine whether selection based on the French index for BCS might help to reduce undesirable effects linked to excessive mobilization during early lactation. Such marked mobilization at this stage can indeed have a variety of detrimental health implications (Collard et al., 2000; Weber et al., 2013), as well as reducing fertility (Patton et al., 2007). In addition, a marked loss of BC during the dry to near-calving period results in an increased prevalence of postpartum metabolic and reproductive diseases (Kim and Suh, 2003; Barletta et al., 2017). The results we obtained showed that despite being based on only one phenotypic measurement during first lactation in an independent reference population, iBCS produced a good prediction of different trajectories for BCS performance and that these differences were the same throughout lactation. However, one might wonder whether these differences in BCS imply varying abilities to mobilize resources and might reduce the risk of excessive mobilization. Older studies showed that in cattle, the BCS is a reflection of subcutaneous fat, which is the primary source of energy when body reserves are mobilized (Remond et al., 1988; Petit and Agabriel, 1993), 1 point of difference in BCS corresponding to about 30 kg of lipids and 40 to 45 kg of BW. A recent review by Mann (2022) confirmed this process and reported various studies that showed that the higher the BCS, the greater might be mobilization, based on both molecular signals and the visualization of body fat. Cows with a high BCS at dry off or calving are then more prone to develop diseases such as ketosis (Vanholder et al., 2015; Rathbun et al., 2017), milk fever (Bobe et al., 2004), or displaced abomasum (Cameron et al., 1998). Based on these elements, selection in favor of a low BCS might reduce the occurrence of these detrimental effects on health. However, a low BCS has been associated with an increased risk of developing uterine disease and with a delay in resumption of postpartum cyclicity (Mann, 2022). For these reasons, selection in favor of a BCS that is too high or too low should be avoided.

All these studies only focused on early lactation, the critical period involving the most health events and the need for a resumption of cyclicity to enable future reproduction. It is interesting to note that despite the positive correlation between mobilization (studied through weight loss) and milk production during early lactation (high-producing cows being more prone to mobilize more), the same mobilization was genetically independent from milk production in mid- or late lactation after resolution of the negative energy balance (Tribout et al., 2022). This offers opportunities to disrupt any undesirable correlation.

Selection for Which BCS?

As mentioned in the introduction, BCS genomic predictions are now available in many countries, but BCS is generally not included in total merit index. Although it only represents a small proportion of the

total energy implicated in estimates of residual feed intake compared with milk production or even maintenance (Martin et al., 2021), information about BCS is highly recommended to be taken into account in dairy genomic selection when feed efficiency is the breeding goal, to avoid selection for more mobilization during early lactation. Body condition score is indeed an important trait in early lactation in terms of a genetic correlation with energy balance, feed intake, and milk production (Hüttmann et al., 2009). However, if it is necessary to consider BCS in a feed efficiency model, what should be the goal of selection on the trait itself? This study has shown that such selection would affect other traits such as milk content or BW, which needs to be taken into account. In addition, data in the literature suggest that this selection might also have effects on other traits, and that underconditioning and overconditioning, leading to rapid and excessive mobilization during early lactation, should both be avoided because of their detrimental health and reproductive consequences. A recent literature review in physiology proposed modulations of nutrition, management, and environmental factors to optimize cow BCS throughout lactation (Mann, 2022). In terms of genetics, it appears that both selection for a high BCS and selection for a low BCS would be inappropriate, so an intermediate optimum might be envisaged. Another option would be to consider that the principal issue is intense mobilization during early lactation; the best way to deal with this might be to select not for BCS itself but for a reduction in changes to the score. Selection to reduce the variability of a given trait has already been studied using canalization models that enable accommodation of both the mean and variance of a trait separately (for an example, see Garreau et al., 2008). In the case of dairy cow BCS, this would imply more than one measurement per animal, which would mean reorganization of the phenotyping system in the reference population, or an optimized use of daily BW to get rid of growth and digestive content changes.

Value of Genomic Predictions

Due to the large Holstein reference population now available, genomic breeding values are very accurate. During this study, we demonstrated that genomic EBV are an efficient tool when it comes to setting up and interpreting an experimental design. The differences anticipated from genomic EBV data were indeed observed on phenotypes. But they provided additional information by showing how they influence other traits, or how their effects can vary as a function of lactation stage.

CONCLUSIONS

Although based on single measurements during the first lactation, the BCS genomic prediction is an efficient tool to discriminate BCS profiles throughout lactation. The effects on phenotypes agreed with the predictions. The profiles differed throughout lactation, showing that the predictions are valid at any lactation stage. However, the differences increased during the first 2 mo after calving, showing that iBCS is also a good reflection of the intensity of mobilization. Cows with high iBCS also tend to have a higher feed intake, which is a favorable characteristic when trying to limit disorders during early lactation.

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