

Genetic parameters for daily milk weights in U.S. Holsteins using pen-based contemporary groups

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Abstract

The availability of daily milk weights and pen location information provides an interesting opportunity to review how contemporary groups are defined for dairy cattle genetic evaluations. In the U.S., dairy cows in larger herds are grouped into pens according to various characteristics like parity, production level, reproductive status, lactation stage, and health status. Our dataset includes pen location information for each daily milk weight, and our goal is to more accurately model contemporary groups when estimating breeding values for daily milk production. Therefore, instead of using herd-year-season, we updated our contemporary group to herd-pen-milking date, thereby capturing the differences in daily milk production more precisely by modeling the true environmental effects cows experience at the pen level. Our dataset includes 21,000,951 aggregated daily milk weights from 114,243 first parity Holstein cows in 157 herds representing 29 U.S. states. Our phenotype is 305-d milk yield or daily milk weight, and both animal and repeatability animal models were used to estimate genetic parameters and breeding values. Age at first calving (6 levels) and days in milk (10 levels) were included as fixed effects and cow (114,243 levels) was included as a random effect. Contemporary group effects included a fixed or random herd-year-season of calving effect (1,492 levels) and/or a fixed or random herd-pen-milking date effect (285,592 levels). Genetic parameters (kg^2 ; posterior SD) were estimated using GIBBSF90+ software, and we found the additive genetic variance for 305-d milk yield was 842,500 (25,093), the herd-year-season variance was 878,960 (33,617), and the residual variance was 1,442,700 (20,438). Whereas for genetic parameters estimated using daily milk weights as the phenotype, the additive genetic variance ranged from 10.48 (0.60) to 24.12 (0.66) the herd-year-season variance was 10.34 (0.40), herd-pen-milking date variance ranged from 4.91 (0.02) to 4.96 (0.02), permanent environmental variance ranged from 10.65 (0.44) to 16.94 (0.30), while the residual variance ranged from 11.81 (0.01) to 14.60 (0.01). Heritability estimates ranged from 0.21 (0.01) to 0.47 (0.01), while repeatability estimates ranged from 0.51 (0.01) to 0.71 (0.01). Although further work is required to disentangle the relationships among contemporary groups, our results suggest value in using daily milk weights and pen-based contemporary groups for genetic evaluation of production traits in dairy cattle.

Key words: daily milk weights, contemporary groups, variance components

Introduction

The dairy industry has invested significantly in modern technology such as innovative sensors that collect high-frequency data that monitors animals at the individual or group level to inform management decisions. Consequently, precision livestock farming has advanced remarkably over time, generating an extensive volume of data (Lovarelli et al., 2020). Such

high frequency data is currently predominantly used for management purposes, while production and management information collected on the test day by milk recording organizations is the gold standard data collection method used for genetic evaluations. Daily milk weights are one example of such high throughput data that are currently generated during each individual cows milking. Along with the daily milk weight, other

valuable information such as the pen location of each cow is also recorded during milking with either an automatic milking system or through in-line milk meters installed in conventional milking parlors. This information allows us to precisely identify which pen each cow belonged to on a specific date.

Currently, to estimate variance components and genetic parameters, contemporary groups are typically defined using the herd-year-season of calving. The concept is that a cow is part of a cohort within a herd that experienced similar environmental conditions based on the year and season of calving (Van Vleck, 1987). Therefore, each cow would have only one contemporary group per lactation. Given the unique nature of our novel dataset, our objective was to redefine the contemporary group definition to more precisely reflect the actual (or micro) environment each cow experiences based on the specific pen she occupies on any given day. In the U.S., cows are grouped in pens according to parity, milk production level, lactation stage, and reproductive status (Contreras-Govea et al., 2015). Managing cows at the group or pen level in the U.S. may be more labor efficient and, additionally, cows in different pens within the same farm may be fed different rations and may experience different housing or management conditions. In theory, albeit unlikely, following data edits, each cow could be part of up to 300 distinct contemporary groups throughout the lactation period, assuming a daily pen change. This indicates a substantial increase in data availability, allowing for more accurate estimation of genetic parameters and, consequently, increased reliability of sire predicted transmitting abilities (PTAs). We found that fitting the contemporary group, either herd-year-season or herd-pen-milking date as fixed or random impacts the estimates of relevant genetic parameters and also the reliabilities of sire PTAs. Additionally, we observed differences when the phenotype for milk production changed from 305-d milk yield to daily milk weights. Interestingly, when modeling herd-pen-milking date as a random

effect for daily milk weight phenotypes, we found a large increase in the additive genetic variance, and thus the heritability. However, it appears that this specific model (i.e. model 3) cannot disentangle the relationships among highly correlated daily contemporary groups, possibly due to the correlated residuals between levels of herd-pen-milking date. Consequently, we opted to model herd-year-season as a fixed effect and herd-pen-milking date as a random effect (model 4). This approach better disentangled the previous relationship and yielded estimates more consistent with the other models we evaluated. The aim of this study was to investigate genetic parameters for milk production traits using herd-pen-milking date as the contemporary group. Four models were employed to assess the impact of changing the phenotype from 305-d milk yield to daily milk weight. Additionally, these models were used to examine the effects of modeling contemporary groups using either herd-year-season or herd-pen-milking date, considering both as fixed or random, on genetic parameters and sire PTA reliabilities.

Materials and Methods

Data were provided by Dairy Records Management Systems (Raleigh, NC) and were extracted from PCDART on farm management software. Detailed descriptions of the initial data edits can be found in Guinan et al., 2024. Additional edits include a minimum of 25 cows per herd-year-season of calving and at least 25 cows per herd-pen-milking date contemporary group. After the additional edits above, our dataset contained 114,243 cows from 157 herds in 29 U.S. states with 21,000,951 daily milk weights. To investigate the differences between using 305-d milk yield and daily milk weights, along with the differences between using herd-year-season (HYS) and herd-pen-milking date (HPM) as contemporary groups and as fixed or random we estimated variance components using four different models that are described in Table 1:

Table 1. Outline of the four different models used to estimate genetic parameters for i) 305-d milk yield (kg) and ii) daily milk weights (kg).

Model	
1	305-d Milk (kg) = AFC + HYS + cow + e
2	Daily Milk Weight (kg) = AFC + DIM + HYS + cow + pe + e
3	Daily Milk Weight (kg) = AFC + DIM + HPM + cow + pe + e
4	Daily Milk Weight (kg) = AFC + DIM + HYS + HPM + cow + pe + e

AFC = Age at first calving; DIM = Days in milk; HYS = Herd-year-season; HPM = Herd-pen-milking date; pe = permanent environmental; e = residual. The contemporary group(s) for each model are in bold.

Where **AFC** is the fixed effect of age at first calving (6 levels; < = 22, 23–24, 25–26, 27–28, 29–30, 30+), **DIM** is the fixed effect of days in milk (10 levels; 30 days each), **HYS** is the fixed or random effect of herd-year-season of calving (1,492 levels), **HPM** is the fixed or random effect of herd-pen-milking date (285,592 levels), **cow** is the random additive genetic effect using up to 5 generations of pedigree data with 114,243 levels distributed as $\mathbf{a} \sim N(0, \mathbf{A}\sigma_a^2)$, **pe** is the random permanent environmental effect distributed as $\mathbf{pe} \sim N(0, \mathbf{I}\sigma_{pe}^2)$, and **e** is the random residual effect distributed as $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$.

Model 1, which utilized 305-d milk yield (kg) as the phenotype, served as a baseline for comparison with the more complex models. Models 2-4 utilized daily milk weights (kg) as the phenotype. For models 1-3, the contemporary group (HYS or HPM) was fitted as either fixed or random to estimate variance components, while for model 4, HYS was fitted as fixed and HPM was fitted as random to estimate variance components. GIBBSF90+ software was used to estimate variance components and posterior standard deviations using a Bayesian approach employing the Gibbs sampling algorithm with 50,000 samples. A total of 10,000 samples were discarded as burn in, while every 1 in 10 samples was stored to estimate posterior means and standard deviations (Misztal et al., 2024). Convergence was determined by visual inspection of the trace plots. Heritabilities (h^2) were estimated using two formulas; h^2 estimates include the

contemporary group variance (when calculated) in the denominator, whereas h^{2*} estimates do not include the contemporary group variance in the denominator. PTA reliabilities were approximated using the following formulas $PEV = (posterior\ SD)^2$; $REL = 1 - \frac{PEV}{\sigma_a^2}$, where PEV is the prediction error variance, or the squared posterior standard deviation of the PTA estimate. The reliability (REL) was estimated by subtracting the PEV divided by the additive genetic variance from 1. This serves as an estimate for the REL of the estimated PTA.

Results & Discussion

1. Milk yield phenotype - Daily Milk Weights vs 305-d milk yield

The first analysis included modeling the phenotype for milk production using the standard Council on Dairy Cattle Breeding (Bowie, MD) method to serve as a comparison for more complex models. The current phenotype typically used to estimate variance components and PTAs is 305-d milk yield where test day information is used to first fit a lactation curve for each individual cow, and milk production is projected to 305-d. Model 1 included 305-d milk production as the phenotype (1 phenotype), whereas the remaining models (2-4) used daily milk weights as the phenotype (at least 100 phenotypes). Depending on whether HYS was fitted as fixed or random, Model 1 had a h^2 ranging from 0.27 to 0.37, whereas for the remaining models with the exception of model 3 when HPM was

random, the h^2 was lower whether the contemporary group was fitted as fixed or random. The use of daily milk weights as the phenotype introduced greater environmental (residual) variance, and therefore this decreased the heritability estimates for model 2-4.

2. Updating contemporary group definition

The primary objective of this research was to update the definition of contemporary groups to estimate genetic parameters for daily milk weight phenotypes by capitalizing on high frequency data not currently utilized for genetic evaluations. The current method to capture environmental effects is HYS of calving, which was developed during a period when herd sizes were smaller, and hence all cows were experiencing similar environmental effects. As herd sizes have increased, cows are grouped according to characteristics like parity, milk production levels, and reproductive status, among others. Consequently, our novel contemporary groups are now formed based on the phenotype throughout the lactation period, for example, high producing cows may be grouped together during the late lactation period based on their milk yield production in mid lactation. The effect HYS was used as a basic model for comparison with both 305-d milk (model 1) and daily milk weights (model 2). The contemporary group currently used to estimate genetic parameters for milk production in the U.S. is HYS (Wiggans et al., 1988). Our goal was to redefine the contemporary group for daily milk weights to more accurately model the true or “micro” environment the cow is experiencing. Therefore, we utilized the pen information that is attached to each individual daily milk weight to define contemporary groups as herd-pen-milking date with at least 25 cows per level. For this section of results, we will focus primarily on model 2-4 for comparison purposes, as the variance components are in the same range. For model 2, depending on whether HYS was fitted as fixed or random, the additive genetic variance ranged

from 10.76 to 10.85, contemporary group variance (when HYS was fitted as random) was 10.34, permanent environmental variance ranged from 15.01 to 15.08, and the residual variance was 14.60. Model 3 had similar results for variance components, with the exception of when HPM was fitted as random, which will be discussed in the next section. Model 3 had a smaller residual variance than model 2, indicating that the environmental variance decreases when HPM is used as the contemporary group in comparison to HYS for daily milk weight phenotypes (Table 2). Finally, model 4 (HYS fixed; HPM random) had similar additive genetic variance (10.48) and permanent environmental variance (14.23) to models 2 and 3, with the exception of model 3 where HPM was fit as random, and comparable residual variance with model 3 (11.85).

3. Fitting contemporary group as fixed vs random

For models 1-3, we also investigated differences between fitting the contemporary group (HYS or HPM) as fixed or random. The question of fitting contemporary groups to estimate genetic parameters as fixed or random is not novel, however we were interested in understanding the differences in variance component estimates with 305-d milk yield, and more interestingly, daily milk weights. Given the size of our dataset, specifically herd size, we expect to observe minimal differences among variance component estimation methods. Additionally, as our dataset spans 5 years, we do not expect a genetic trend that we need to account for or major improvements in management practices which may indicate that contemporary group should be fit as a random effect to account for these trends. For model 1 and 2, when HYS was fit as fixed or random, we found minimal differences between variance components. Similarly, the h^2 estimates did not change, except the h^2 decreased as expected when the contemporary

Table 2. Variance components, heritability and repeatability estimates (posterior SD), and sire predicted transmitting ability reliabilities for 305-d milk yield and daily milk yield using contemporary group (herd-year-season or herd-pen-milking date) as fixed or random effects.

	305-d yield (kg)		Daily milk yield (kg)				
	Model 1	Model 1	Model 2	Model 2	Model 3	Model 3	Model 4
	Fixed	Random	Fixed	Random	Fixed	Random	Fixed & Random
σ_{cg}^2	-	878,960 (33,617)	-	10.34 (0.40)	-	4.91 (0.02)	4.96 (0.02)
σ_a^2	837,300 (27,385)	842,500 (25,093)	10.76 (0.49)	10.85 (0.47)	11.96 (0.40)	24.12 (0.66)	10.48 (0.60)
σ_{pe}^2	-	-	15.08 (0.35)	15.01 (0.33)	16.94 (0.30)	10.65 (0.44)	14.23 (0.43)
σ_e^2	1,442,700 (20,438)	1,493,200 (19,145)	14.60 (0.01)	14.60 (0.01)	11.81 (0.01)	11.86 (0.01)	11.85 (0.01)
h^2	0.37 (0.01)	0.27 (0.01)	0.27 (0.01)	0.21 (0.01)	0.29 (0.01)	0.47 (0.01)	0.25 (0.01)
h^{2*}	0.37	0.36	0.27	0.27	0.29	0.52	0.29
r^2	-	-	0.64 (0.01)	0.51 (0.01)	0.71 (0.01)	0.68 (0.01)	0.60 (0.01)
REL	0.79	0.79	0.81	0.81	0.81	0.89	0.81

cg = contemporary group. Depending on the model, this represents herd-year-season or herd-pen-milking date. σ_{cg}^2 = contemporary group variance; σ_a^2 = additive genetic variance; σ_{pe}^2 = permanent environmental variance; σ_e^2 = residual variance; h^2 = heritability; h^{2*} represents heritability calculated where cg is random without σ_{cg}^2 in the denominator of the h^2 calculation; r^2 = repeatability; REL = Predicted Transmitting Ability Reliability for sires with ≥ 10 daughters.

group variance was included in the denominator. Interestingly, we found large differences between variance components when HPM was modeled as random in model 3. The estimates for residual variance did not change, however the additive genetic variance increased from 11.96 to 24.12, while the permanent environment variance decreased from 16.94 to 10.65. Given the high number of levels in HPM, and the non-independent relationship among HPM levels, we assume that the correlations among the residuals are high, which is causing this partitioning of variance between the additive component and permanent environmental variance. Finally, in model 4, once HYS is fit as fixed along with HPM as

random, we see comparable results to model 2 and 3 (HPM fixed) in terms of variance component estimates and heritabilities (Table 2).

4. Confounding effects among variables

For model 3, we found large differences among variance components when HPM was fit as fixed vs random. Our hypothesis is that there is a relationship among residuals within the HPM variable that is creating a challenge to disentangling the relationship between repeated records in HPM levels and additive genetic variance. For example, although in theory a cow could move pens every day and have 300 unique contemporary groups throughout a

lactation, this is highly unlikely. The practice of grouping cows is to homogeneously manage groups of cows, and to avoid the management and additional labor of managing cows at the individual level. Therefore, it is likely that the same group of cows are in the same pen for multiple days or weeks and this correlation among residuals is not being captured by the permanent environmental effect. Additionally, there is a risk of confounding between the genetic effect, contemporary group effect and permanent environment effect. This is due to the fact that HPM groups are reassigned throughout the lactation depending on the phenotype expressed by the individual animal and for management purposes, whereas in the past HYS was strictly based on the calving year and season of the cow. As such, we decided to fit HYS as a fixed effect along with HPM as a random effect and we found comparable results to previous models. This is probably because HYS is capturing the additive genetic effect that HPM was not previously capturing due to the confounding effect and breaking this relationship between repeated records of the same group of cows in the same pen over longer periods of time.

5. Sire PTA Reliabilities

Sire PTA reliabilities were estimated to assess whether using large volumes of daily milk yield data and assigning contemporary groups using pen information would increase the accuracy of selection decisions. We found a 0.02 increase in mean REL of sire PTA when using daily milk weights as the phenotype in comparison to 305-d milk yield. Aside from model 3 when HPM was fit as random, we did not observe differences among reliabilities when fitting contemporary group as fixed or random (Table 2). We did not observe differences in sire PTA reliabilities when using HPM as the contemporary group instead of HYS, which could be attributed to the fact that an autoregressive structure may be more suitable for modeling the HPM variable to account for

the high correlations among residuals of each HPM levels, as discussed previously.

Conclusions

Utilizing daily milk weights generated by on-farm sensors increases the reliabilities of sire PTAs. The advent of high frequency novel data sources for use in genetic evaluation purposes may require new definitions for contemporary groups. In the specific case of milk production, the reliabilities of sire PTAs increased when using daily milk weights as opposed to 305-d milk production. Updating the definition of contemporary groups for genetic parameter estimation using herd-pen-milking date as a fixed or random effect impacts the reliabilities of sire PTAs, perhaps due to the high correlations among residuals for contemporary groups. Additional research is required to optimize genetic parameter estimation with high frequency data generated by sensors for genetic evaluation purposes. Including herd-year-season as a fixed effect along with herd-pen-milking date as a random effect may account for the non-independent relationships among residuals while also increasing sire PTA reliabilities in comparison to the current model utilized in the U.S. which uses herd-year-season along with 305-d milk yield as the phenotype.

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References

- Contreras-Govea, F.E., Cabrera, V.E., Armentano, L.E., Shaver, R.D., Crump, P.M., Beede, D.K., and VandeHaar, M.J. 2015. Constraints for nutritional grouping in Wisconsin and Michigan dairy farms. *J. Dairy Sci.* 98:1336–1344. <https://doi.org/10.3168/jds.2014-8368>.
- Guinan, F.L., Fourdraine R.H., Peñagaricano, F., and Weigel, K.A. 2024. Genetic analysis of lactation consistency in U.S. Holsteins using temporal variation in daily milk weights. *J. Dairy Sci.* 107:2194–2206. <https://doi.org/10.3168/jds.2023-24093>.
- Lovarelli, D., Bacenetti J., and Guarino, M. 2020. A review on dairy cattle farming: Is precision livestock farming the compromise for an environmental, economic and social sustainable production?. *J. Cleaner Prod.* 262:121409. <https://doi.org/10.1016/j.jclepro.2020.121409>.
- Misztal, I. Tsuruta, S. Lourenco, D. Masuda, Y. Aguilar, I., Legarra, A. and Vitezica, Z. 2024. Manual for BLUPF90 Family of Programs. Available online: http://nce.ads.uga.edu/wiki/lib/exe/fetch.php?media=blupf90_all.pdf (accessed on 21 February 2024).
- Van Vleck, L.D. 1987. Contemporary Groups for Genetic Evaluations. *J. Dairy Sci.* 70:2456–2464. [https://doi.org/10.3168/jds.S0022-0302\(87\)80309-0](https://doi.org/10.3168/jds.S0022-0302(87)80309-0).
- Wiggans, G.R., Misztal, I., and Van Vleck, L.D. 1988. Implementation of an Animal Model for Genetic Evaluation of Dairy Cattle in the United States. *J. Dairy Sci.* 71:54–69. [https://doi.org/10.1016/S0022-0302\(88\)79979-8](https://doi.org/10.1016/S0022-0302(88)79979-8).