

Various persistency measures and relationships with total, partial and peak milk yields*

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ABSTRACT

Seven persistency measures and their relationships with total, partial and peak yields were studied. Heritabilities, genetic and phenotypic correlations were estimated using mixed model equations with multiple trait restricted maximum likelihood (REML). Data were from 31,482 first lactation Belgian Holstein-Friesian cows. Differences in direction and size of the correlations between measures of persistency and total yield were found. Two types of measures were used. Persistency measures based on ratio showed positive correlations to total yield. Measures based on standard deviations of test days or partial yields were correlated negatively with total yield. Correlations with partial yields also showed a similar pattern. Genetic correlations between ratio methods and peak yield were positive. Ratio methods not only describe persistency, but are highly influenced by total yield. Methods using standard deviations of test day yields showed a similar problem, but the influence of the level of total production was negative. Heritabilities of several persistency measures were above 0.10. After considering these results, a newly defined method, based on the standard deviation of partial yields, emerged as the best choice to describe persistency and for use in genetic evaluation of persistency.

INTRODUCTION

Persistency of milk production during a lactation may become an important trait for selection. Two reasons given for studying persistency were presented by Madsen (1975) who indicated that feeding a cow with a flatter lactation curve requires less feed than one that peaks very high and then decreases rapidly. Also a flatter curve puts less stress on the cow, thereby reducing the incidence of reproductive and metabolic disorders. With the increased use of rBST (recombinant bovine somatotropin or bovine growth

hormone), the industry may need to select for increased persistency while at the same time reducing peak production. If peak production was lowered while increasing persistency, this could allow the use of rBST at an earlier period in the lactation. Many producers are reluctant to administer rBST due to the increased stress that additional production places on the udder. Selection for increased production may require changing the shape of the lactation curve thereby requiring genetic evaluation for persistency. Current selection strategies do not account for persistency. There are indications that genetic differences exist among animals for persistency, and that selection for persistency could be advantageous (Sölkner and Fuch, 1987). Two questions need to be addressed concerning selection for persistency: the choice of a parameter that gives a correct

* Published as Paper Number 10933, Journal Series, Nebraska.

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description of the shape of lactation curve, and the implementation of a correct selection strategy.

Persistency is defined in many ways in the literature. Grossman *et al.* (1986) indicated that a similar amount of milk could be produced by many different lactation curves. Their definition of persistency was related to the flatness of the curve for a given amount of production. Sölkner and Fuchs (1987) stated that persistency is equivalent to comparing shapes of the lactation. The first attempt to describe lactation curves by use of a mathematical model was made by Gaines (1927). Since then, several models have been proposed. The most widely used model was developed by Wood (1969). Mathematical models have difficulty in accounting for seasonal effects, especially during spring when cows may be pastured. Gaines (1927) and Wood (1969) were interested in modelling the curve and not necessarily in defining persistency. Ferris *et al.* (1985) reported that as many as 15% of lactation curves are atypical. Shanks *et al.* (1981) summarized the proportion of atypical curves reported in different papers. The proportion of the lactation curves that can be considered atypical ranged from 19.1% for Congleton and Everett (1980) to 45% for Schneeberger (1978) implying that it is difficult to describe persistency by this approach. For this reason models as described by Gaines (1927) and Wood (1969) will not be considered in this paper.

Ratios between partial yields have been proposed as a way to describe persistency. Sanders (1930) and Johansson and Hansson (1940) introduced the use of ratios between partial yields of the first, second and third 100 (105) days. These ratios, often called P_{2:1}, P_{3:1} and P_{3:2}, have been modified over time. Mahadevan (1951) and Danell (1982) used the same approach but modified the periods. Ericson *et al.* (1988) expressed the ratios as percentages. Keown *et al.* (1986) used the ratio between maximum yield during 300 days and yield at day 300. Sölkner and Fuchs (1987) tested ratios between maximum and mean production during 200 and 305 days. Ratios are statistically difficult functions to define (Sölkner and Fuchs, 1987). Several ratio methods will be considered in this paper because they offer an intuitively simple way to describe persistency. Ratio methods should correct for differences of mean yields among animals. Describing persistency as variation is a logical approach, but until recently was seldom considered (Sölkner and Fuchs, 1987). Sölkner and Fuchs (1987) used the variation between test day yields during the first 200 or 305 days as a measure of persistency. Unfortunately, the date sampled and number of test days during a lactation are not necessarily constant for all cows. Gengler (1990) showed that per-

sistency based on test days is influenced by the number of samples taken during a lactation and by number of test days interaction, because the time between test days differs by season in several countries (e.g., Belgium). Another problem with methods based on variation is that they do not distinguish between below or above average yields. This problem is important only when such methods are based on small differences in yields. The problem is negligible if variation of partial yields (periods) is considered. If these yields are based on partial lactations the differences can be expressed as regressions of persistency on total yield. In this paper another variation model based on fixed partial lactation yields is considered.

MATERIAL AND METHODS

Data were from the Belgian Agricultural Data Processing Centre (CTI) and comprised 31,482 first lactation records from Belgian Holstein cows having ≥ 305 days in milk, calving between 1987 and 1989, and freshening between 22 and 36 months of age. Records were eliminated for cows with unknown sires, or with a sire born and/or registered before 1978 or lacking a Belgian registration number. The sires were assigned to four genetic groups according to Holstein-Friesian inheritance (Table I).

Table I - Genetic groups assigned to the 312 sires in the dataset.

Genetic group	Holstein-Friesian (HF) inheritance	Number of sires
1	0 to 25% HF	27 sires
2	26 to 50% HF	26 sires
3	51 to 75% HF	22 sires
4	76 to 100% HF	237 sires

Partial and total yields, for the first 100, second 100 and third 105 days, as well as for the 305 day lactation were calculated. The mean yield for two consecutive test days was multiplied by the number of days in milk the tests, except for the period before the first test in which case the first test day yield was multiplied by the period from calving to the first test day. Linear extrapolation was used to calculate partial and/or total yields at 100, 200 and 305 days. Maximum yield during the lactation was retained as one possible measure to describe peak yield. Outliers were considered, but because of uncertain definition of outliers, maximum yield was regarded as peak yield.

The following persistency measures were also calculated:

$$P_{2:1} = \frac{\text{milk yield}_{\text{day 101 to 200}}}{\text{milk yield}_{\text{day 1 to 100}}} \quad (\text{I})$$

$$P_{3:1} = \frac{\text{milk yield}_{\text{day 201 to 305}}}{\text{milk yield}_{\text{day 1 to 100}}} \quad (\text{II})$$

$$P_{SD2} = - \left(\frac{1}{n-1} \sum_{i=1}^n (\text{milk yield at test day } i - \text{mean milk yield of test days during the first 200 days})^2 \right)^{0.5} \quad (\text{III})$$

$$P_{SD3} = - \left(\frac{1}{n-1} \sum_{i=1}^n (\text{milk yield at test day } i - \text{mean milk yield of test days during the first 305 days})^2 \right)^{0.5} \quad (\text{IV})$$

$$P_{YV} = - \left(\frac{1}{305} \left(\frac{(\text{total milk yield day 1 to 100})^2}{100} + \frac{(\text{total milk yield day 101 to 200})^2}{100} \right. \right. \\ \left. \left. + \frac{(\text{total milk yield day 201 to 305})^2}{105} - \frac{(\text{total milk yield day 1 to 305})^2}{305} \right) \right)^{0.5} \quad (\text{V})$$

$$P_{\text{Tomax200}} = \frac{\text{total milk yield}_{\text{day 1 to 200}}}{\text{maximum milk yield}_{\text{day 1 to 200}} \times 200} \times 100 \quad (\text{VI})$$

$$P_{\text{Tomax305}} = \frac{\text{total milk yield}_{\text{day 1 to 305}}}{\text{maximum milk yield}_{\text{day 1 to 305}} \times 305} \times 100 \quad (\text{VII})$$

The first two measures $P_{2:1}$ and $P_{3:1}$ were used by Johansson and Hansson (1940). Estimates III and IV are based on formulae of Sölkner and Fuchs (1987), which were modified by inversion in order to associate a better persistency with a higher value. Formula (V) is a new measurement based on standard deviations of partial milk yields. Measures (VI) and (VII) are also based on Sölkner and Fuchs (1987) modified by inversion. Methods V, VI and VII will be referred to as ratio measures and all other methods as variation methods.

Milk yields and persistency measures were analyzed by mixed model methods. SAS[®] PROC GLM (1989) was used to do linear adjustments for age and calving interval effects for all traits. The model consisted of a fixed herd-year-season effect (HYS), fixed

age and calving interval effects. The age effects were 14 monthly classes between 22 and 36 months of age and 13 calving interval classes (< 360, 360 to 369, 370 to 379, ..., 440 to 459, 460 to 489, 490 to 529 and > 530 days). Each record was then adjusted for age and calving interval.

The mixed model for each adjusted trait i included a fixed herd-year-season effect (HYS _{i}), and a random sire effect (s_{kl}) nested within the fixed genetic group effect (G_k):

$$Y_{ijklm} = \text{HYS}_{ij} + G_{ik} + S_{ikl} + e_{ijklm}$$

The following three multiple trait analyses were done:

- 1) milk yield (305 days) and the seven persistency measures;
- 2) milk yield (first 100 days), milk yield (days 101-200), milk yield (days 201-305) and the seven persistency measures;
- 3) maximum test day yield (during 305 days) and the seven persistency measures.

REML estimates for (co)variance components were obtained.

Different persistency measures were first analyzed together. Results indicated rather low correlations between the different measures and therefore the measures were used as different traits in the analyses.

RESULTS AND DISCUSSION

Heritability estimates are in Table II. Estimates for milk yields are also given. The estimates are pooled estimates from three multiple trait analyses. The estimates are within the range of previous literature values. Heritabilities for persistency measures ranged from 0.03 for PSD2 to 0.12 for P2:1. The newly defined measure, PYV, had a heritability of 0.10.

Table II - Estimates of heritabilities and approximate standard errors.

Trait*	Heritability	Standard error
Milk (305 days)	0.36	± 0.046
Milk (first 100 days)	0.26	± 0.039
Milk (101-200 day)	0.35	± 0.046
Milk (201-305 day)	0.32	± 0.043
Max. test day yield	0.24	± 0.037
P2:1	0.12	± 0.026
P3:1	0.11	± 0.026
PSD2	0.03	± 0.016
PSD3	0.09	± 0.024
PYV	0.10	± 0.025
P _{Tomax200}	0.04	± 0.018
P _{Tomax305}	0.08	± 0.022

*Definitions for traits are given in equations I-VII.

Table III shows genotypic and phenotypic correlations among the different persistency measures and 305 d milk yield. Phenotypic and genetic correlations are positive among all persistency measures. The phenotypic correlations ranged from 0.26 (P3:1 and P_{Tomax200}) to 0.88 (P_{Tomax200} and P_{Tomax305}). Phenotypic correlations among the persistency measures were small compared with the

anticipated correlations of near 1. The correlations are naturally high between measures that use the same formula but for different periods: P2:1 and P3:1, 0.67; PSD2 and PSD3, 0.65; and P_{Tomax200} and P_{Tomax305}, 0.88. The new persistency measure PYV had correlations above 0.50 with P3:1, PSD2, PSD3 and P_{Tomax305}. The genetic correlations between PYV and the other measures were also above 0.50, except for P_{Tomax200}. The positive correlations indicate that the ratio methods measure not only persistency, but are in fact highly related to total yield.

Table III - Estimates of genetic correlations above and phenotypic correlations below diagonal among total milk yield and persistency measures.

Trait	1	2	3	4	5	6	7	8
1 Milk (305 days)		0.65	0.51	-0.30	-0.38	-0.09	0.72	0.63
2 P2:1	0.24		0.85	0.46	0.20	0.51	0.95	0.91
3 P3:1	0.18	0.67		0.54	0.55	0.80	0.75	0.95
4 PSD2	-0.11	0.38	0.27		0.85	0.85	0.40	0.53
5 PSD3	-0.20	0.31	0.60	0.65		0.94	0.12	0.44
t PYV	-0.13	0.48	0.80	0.51	0.85		0.39	0.69
7 P _{Tomax200}	0.22	0.44	0.26	0.75	0.43	0.33		0.90
8 P _{Tomax305}	0.25	0.53	0.60	0.69	0.65	0.63	0.88	

Correlations among total yield and persistency measures are shown in Table III. The variation methods had negative correlations with total yield and the ratio methods had positive correlations. The lowest genetic correlation in absolute value for total yield was with PYV -0.09. The two methods based on variation, PSD2 and PYV, had the lowest phenotypic correlations with total yield, -0.11 and -0.13.

Traditionally, 305 day milk yield is often divided into three parts of nearly equal length, the first 100, the second 100 and the third 105 days. Table IV gives the phenotypic and genetic correlations among these three partial yields and different persistency measures. The correlations indicate how partial yields influence the different persistency measures. Phenotypic correlations indicate how the persistency measures changed with partial yields. The first partial yield had, with the exception of P_{Tomax200}, a negative phenotypic correlation with all persistency measures. The lowest correlation was -0.50 for PYV. This high negative correlation indicates that animals with low production during the first 100 days tend to have high PYV values. There were two groups of persistency measures: ratio methods with positive genetic correlations and methods based on variation with negative correlations.

Table IV - Estimates of genetic correlations above and phenotypic correlations below diagonal among partial milk yields and persistency measures.

Trait	1	2	3	4	5	6	7	8	9	10
1 Milk (1-100 d)		0.93	0.87	0.41	0.24	-0.54	-0.58	-0.36	0.49	0.38
2 Milk (101-200 d)	0.77		0.96	0.71	0.53	-0.24	-0.37	-0.07	0.74	0.65
3 Milk (201-305 d)	0.62	0.80		0.74	0.70	-0.13	-0.15	0.14	0.74	0.77
4 P _{2:1}	-0.19	0.46	0.38		0.84	0.45	0.19	0.50	0.93	0.91
5 P _{3:1}	-0.26	0.19	0.58	0.67		0.51	0.55	0.80	0.71	0.93
6 P _{SD2}	-0.31	0.01	0.00	0.38	0.27		0.84	0.84	0.42	0.53
7 P _{SD3}	-0.48	-0.20	0.14	0.31	0.60	0.65		0.93	0.11	0.43
8 P _{YV}	-0.50	-0.11	0.28	0.48	0.80	0.51	0.85		0.37	0.68
9 P _{Tmax200}	0.02	0.32	0.25	0.44	0.26	0.75	0.43	0.33		0.89
10 P _{Tmax305}	-0.06	0.30	0.45	0.53	0.60	0.069	0.65	0.63	0.88	

This difference occurs because the variation methods correct for production level. The correlations with the second period yields are more complex. Phenotypic correlations range from a low of -0.20 for P_{SD3} to a high of 0.32 for P_{Tmax200}. The correlation implies that high phenotypic values for persistency measures are related to high and low yields in the second period. The ratio methods are linked phenotypically to higher second period yields: cows with higher production have higher values for these measures. The phenotypic correlations are all positive with third period yield, except with P_{SD2}. The genetic correlations, again, show the difference between ratio methods and methods based on variation. The ratios have high positive correlations with third period yields. The methods based on variation have low to moderate negative correlations. The only positive correlation with a variation measure is with P_{YV}.

A persistency measure that measures only the shape of the curve should have no positive effect on peak yield. As peak yield is difficult to describe, the maximum test day yield during the 305 days was used as a measure for this trait. Second or third test day yields were not used as an indication of peak yield to account for atypical lactation curves. Table V shows the results. All phenotypic correlations are negative as expected, because high phenotypic values for the different persistency measures are associated with low peak yield. The genetic correlations indicate expected correlated changes by selecting on different persistency measures. Again, the ratio measures had positive correlations, and the methods based on variation had negative correlations with peak yield. These correlations are similar to the observed correlation between

Table V - Estimates of genetic correlations above and phenotypic correlations below diagonal among peak milk yield and persistency measures.

Trait	1	2	3	4	5	6	7	8
1 peak milk yield		0.50	0.32	-0.50	-0.57	-0.31	0.58	0.44
2 P _{2:1}	-0.03		0.85	0.45	0.20	0.50	0.96	0.92
3 P _{3:1}	-0.12	0.67		0.53	0.54	0.79	0.75	0.95
4 P _{SD2}	-0.51	0.38	0.27		0.86	0.86	0.39	0.53
5 P _{SD3}	-0.56	0.31	0.60	0.65		0.94	0.12	0.44
t P _{YV}	-0.47	0.48	0.80	0.51	0.85		0.39	0.69
7 P _{Tmax200}	-0.26	0.44	0.26	0.75	0.43	0.33		0.90
8 P _{Tmax305}	-0.27	0.53	0.60	0.69	0.65	0.63	0.88	

persistency and total yield (Table III). The ratios measure the shape of the curve and the mean level of the curve, with genetic correlations up to 0.72 with total yield.

A persistency measure should have a high heritability and have a positive influence on the shape of the lactation curve. P_{2:1}, P_{3:1} and P_{YV}, all have heritability estimates above or equal to 0.10.

P_{SD2} has a correlation of -0.11 and P_{YV} -0.13 with total milk yield. When the genetic correlations are compared between total yield and the different measurements, P_{YV} appears as the best choice with a correlation of -0.09. Selection on P_{YV} would lower peak yield without producing an associated reduction in total yield.

The influence of different persistency measures on the shape of the lactation curve can be examined by

using differences between the correlations of the first 100 and the third 105 days to the different persistency measures. The partial yield variation method, P_{YV} , and the $P_{3:1}$ method are the best. P_{YV} had the largest negative phenotypic correlation with first partial yield (-0.50) and a high positive correlation with the last partial yield (0.28). $P_{3:1}$ had the highest phenotypic correlation with third partial yield (0.58). $P_{2:1}$, $P_{3:1}$, $P_{T_{max}200}$ and $P_{T_{max}305}$ had positive genetic correlations with the first partial yield, second and third partial yield. P_{SD2} and P_{SD3} had negative genetic correlations. P_{YV} has the most interesting relationships with genetic correlations of -0.36, -0.07 and 0.14 with the first, second and third 100 (105) day periods.

CONCLUSIONS

Ratios of yield by period alone do not describe persistency. High genetic correlations with total yield and peak yield show that ratios measure not only the shape, but also the mean level of production. Classical methods based on variation as described by Sölkner and Fuchs (1987) have a similar problem, but the correlation with the level of production is negative. These results are similar to those reported in the literature.

The estimates of heritability are also similar to those in the literature. Only three measures had heritabilities above 0.10. This result does not necessarily prohibit consideration of persistency in dairy selection. Since January 1994, the USDA Dairy Cattle Evaluation contains predicted transmitting abilities for herd life and somatic cell scores. Both traits have a heritability below 0.10. Estimation of breeding values for persistency may be warranted, as there is interest in selecting on this trait.

When all elements are considered together the newly defined method based on partial yield variation seems most optimum. It is related to the shape of the curve without being highly influenced by total yield. Future use of this measure may require correction for the influence of total milk yield. Calculation of breeding values for P_{YV} is possible. Additional research is needed to identify the appropriate stages of the lactation because the division of the total lactation into three parts of equal length is arbitrary. Partitions should represent biological functions, such as the ascending and descending phases of lactation yield. Another approach could be to identify by multiple trait analyses of test day yield, the genetic relationships among test days in order to group them by different (genetic) stages of lactation.

ACKNOWLEDGMENTS

Thanks are given to Paul VanRaden for providing his ABSORBD and REMLD computer programs and to the Fonds National Belge de la Recherche Scientifique (FNRS) for providing partial funding of this work.

RESUMO

Foram estudadas sete medidas de persistência e seus relacionamentos com produção de leite, total, parcial e máxima. Herdabilidades, correlações genéticas e fenotípicas foram estimadas usando-se equações de modelos mistos com a REML (modelo de máxima verossimilhança restrita) de características múltiplas. Os dados foram de 31.482 vacas belgas Holstein-Friesian durante a primeira lactação.

Diferenças em direção e tamanho das correlações entre medidas de persistência e produção total foram encontradas. Dois tipos de medidas foram usadas. Medidas de persistência baseadas em taxas mostraram correlações positivas com a produção total. Medidas baseadas em desvios padrão dos dias de teste ou produções parciais foram correlacionadas negativamente com produção total. Correlações com produções parciais também mostraram um padrão similar. Correlações genéticas entre métodos de razão e produção máxima foram positivas. Métodos de razão descrevem não somente a persistência, mas são altamente influenciados pela produção total. Métodos usando desvios padrão da produção do dia de teste mostraram um problema similar, mas a influência do nível da produção total foi negativa. Herdabilidades de diversas medidas de persistência foram acima de 0,10.

Considerando-se estes resultados, um novo método, baseado em desvios padrão de produção total, emergiu como a melhor escolha para descrever persistência e para uso da avaliação genética da persistência.

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(Received November 10, 1994)