COMPARISON OF EQUATIONS AND ESTIMATION PROCEDURES OF LACTATION CURVES IN ANGUS, BROWN SWISS AND THEIR CROSSES

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SUMMARY

Milk production data (272 lactations) collected weekly by weigh-suckle-weigh techniques up to 180 d, from a diallel crossbreeding experiment at the University of Chapingo, Mexico, using Angus (A) and Brown Swiss (B) breeds were recorded. The purpose was to compare eight equations and two estimation methods of lactation curves in A, B, and reciprocal-cross cows. The following equations were evaluated for each lactation record: $Y_t = at^be^{-ct}$ (I); $Y_t = ae^{-ct}$ (II); $Y_t = t/ae^{ct}$ (III); $Y_t = ae^{(bt+ct^2)}$ (IV); $Y_t = a + bt + ct^2$ (V); $Y_t = a + bt$ (VI); $Y_t = a - bt - ae^{-ct}$ (VII); $Y_t = t/(a + bt + ct^2)$ (VIII). Parameters of the first four equations were estimated by linear (L) and nonlinear (N) least squares regression. Residual mean squares (RMS) were used as a criterion to evaluate curve fitting. Ranks for the eight equations were compared using Friedman's test. Generally the difference in RMS between L and N were not significant ($P > .1$), except for equation III, but always favored N. Equations I and VIII had the best fit to A lactation curves, whereas IV, I and V fitted better B and reciprocal-cross cows. The best equation was dependent on cow's genotype.

INTRODUCTION

Calf performance at weaning is largely influenced by the maternal ability of the cow. More than 50% of the variability in calf weaning weight is explained by the cow's milk production. Therefore, accurate predictions of lactation curves on cows of different genotypes may help in deciding appropriate breed combinations and management strategies to improve cow/calf production efficiency. Various equations have been proposed to model milk lactation curves in dairy cattle (Brody *et al.*, 1923; Sikka, 1950; Nelder, 1966; Wood, 1967; Cobby and Le Du, 1978), and some others for beef cattle (Gaskins and Anderson, 1980; Jenkins and Ferrell, 1984; Clutter and Nielsen, 1987). Scarce information on the comparison of equations and estimation methods of parameters of lactation curves in beef cattle has been reported (e.g., Hohenboken *et al.*, 1992). The purpose of this study was to compare eight equations and two estimation methods of parameters of lactation curves in Angus, Brown Swiss and their reciprocal-cross cows.

MATERIALS AND METHODS

Data came from a diallel crossbreeding experiment at the research station of the University of Chapingo, Mexico, using Angus (A) and Brown Swiss (B) breeds. Milk production data were collected weekly up to 180 d by the weigh-suckle-weigh technique. Cows were separated from the calf late in the afternoon and joined again approximately 12 h later for milk sampling. Daily milk yield was calculated doubling the 12 h milk recorded. Numbers of cows and lactation records for A, B, and reciprocal crosses were respectively, 36 and 111, 40 and 109, and 24 and 52.

The following equations (identified by roman numbers) were evaluated for each lactation record: $Y_t = at^be^{-ct}$ (Wood, 1967; I); $Y_t = ae^{-ct}$ (Brody *et al.*, 1923; II); $Y_t = t/ae^{ct}$ (Jenkins and

Ferrell, 1984; III); $Y_t = ae^{(bt+ct^2)}$ (Sikka, 1950; IV); $Y_t = a + bt + ct^2$ (V); $Y_t = a + bt$ (VI); $Y_t = a - bt - ae^{-ct}$ (Cobby and Le Du, 1978; VII); $Y_t = t/(a + bt + ct^2)$ (Nelder, 1966; VIII). Parameters of the first four equations were estimated by least squares of the linear (L; using log transformation) and nonlinear (N) regression forms (SAS, 1985). Estimation methods were evaluated using the residual mean squares (RMS), which were analyzed for each genotype and lactation number with a model including the effect of cow. Residual plots against time and predicted values were also studied. The eight equations were analyzed used Friedman's test (Conover, 1980) for rank comparisons, taking the RMS as a ranking criterion.

RESULTS

Comparison of Estimation Procedures. Table 1 shows RMS's by equation and genotype averaged across 6 lactations for A, and 5 lactations for B and reciprocal crosses. Generally the difference in RMS's between L and N for each equation were not significant ($P > .1$), except for equation III were six out of 16 comparisons were significant ($P < .1$). However, in all cases the RMS's estimated by N were smaller than those by L. Most of the residual plots, for all equations (except III) and estimation procedures, showed equally spaced residuals in time and across predicted values; all other plots, presented different unsatisfactory behaviors.

Comparison of Equations. Table 2 shows ranking of equations by genotype and lactation number and average ranks for each genotype. Significant ($P < .05$) rank differences were observed in all genotype and lactation number combinations. Except for V and VI, all equations were estimated using N. Equations I and VIII had the best fit to A lactation curves, whereas equations IV, I and V fitted better lactations of B and reciprocal-cross cows.

Table 1. Average residual mean squares across lactation numbers, for four equations estimated with linear (L) and nonlinear (N) least squares, by genotype

Genotype	I-L[a]	I-N	II-L	II-N	III-L	III-N	IV-L	IV-N
Angus	3.61	3.50	3.94	3.84	7.22	6.54	3.64	3.53
Brown Swiss	4.76	4.64	5.49	5.29	11.44	9.92	4.68	4.56
Crosses	4.29	4.10	5.23	4.93	8.70	7.27	3.91	3.76

[a] I = Wood; II = Brody; III = Jenkins and Ferrell; IV = Sikka.

DISCUSSION

Generally, estimating lactation curves by N had a small advantage over L. Cobby and Le Du (1978), using Wood's equation in dairy cattle, reported a larger advantage (50%) when parameter estimation was done with N rather than L. Thus, it is recommended whenever possible, to estimate lactation curve parameters using N (Draper and Smith, 1981). Among lactation curve equations, III and II had the worse fit. Singh and Bhat (1978) compared four equations of lactation curves in Hariana cattle and found that II did not give better fit in any of the curves. Also, Hohenboken *et al.* (1992), comparing four equations of lactation curves in beef cattle, reported that III had the poorest fit. Equation I is very flexible to fit lactation curves of different genotypes and lactation numbers. However, the best equation was dependent on the cow's genotype, possibly because of different levels of milk yield.

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Table 2. Ranks of the eight equations[1] for lactation curves by genotype and lactation number, and average ranks for each genotype

Rank	1	2	3	4	5	6	Average
				Angus			
1	Ia*	VIa	Ia	IVa	VIIIa	Ia	Ia
2	VIIa	Ia	VIIa	Ia	IIab	IVab	VIIIab
3	IVa	Va	VIIIa	Vab	Iab	Vabc	VIIb
4	VIIIa	IIa	VIa	VIIIab	VIb	VIIIabcd	Vb
5	Vab	VIIa	IIa	VIIab	VIIb	VIbcd	VIb
6	VIab	VIIIa	Va	VIbc	Vb	VIIcd	IVb
7	IIb	IVa	IVa	IIc	IVb	IId	IIb
8	IIIc	IIIb	IIIb	IIId	IIIc	IIIe	IIIc
				Brown Swiss			
1	IVa	Ia	Va	Ia	IVa		IVa
2	Ia	IVa	IVa	VIa	VIab		Ia
3	Vab	Va	VIIIab	IVa	Iab		Vab
4	VIIIb	VIIIa	VIIab	Va	Vab		VIbc
5	VIIb	VIIa	Iab	VIIIa	VIIab		VIIIbc
6	VIb	VIb	VIab	IIa	IIb		VIIc
7	IIc	IIb	IIb	VIIa	VIIIb		IIcd
8	IIIc	IIIc	IIIc	IIIb	IIIc		IIId
				Angus x Brown Swiss Reciprocal Crosses			
1	Ia	Va	IVa	IVa	Va		IVa
2	VIIa	IVa	Va	Vab	IVa		Va
3	IVa	Iab	Ia	Iabc	Iab		Ia
4	Vab	VIIabc	VIIab	VIIabc	VIIabc		VIIb
5	VIab	VIIIabc	VIab	VIbc	VIbc		VIc
6	VIIIbc	VIbc	VIIIab	VIIIbcd	VIIIbc		VIIIc
7	IIbc	IIc	IIbc	IIcd	IIc		IId
8	IIIc	IIId	IIIc	IIId	IIId		IIIe

[1] I = Wood; II = Brody; III = Jenkins and Ferrell; IV = Sikka; V = Quadratic; VI = Linear; VII = Cobby and Le Du; VIII = Nelder.

* Ranks within a column and genotype lacking a common letter differ (P < .05).