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COMPARISON AMONG DIFFERENT MATHEMATICAL MODELS OF LACTATION CURVES TO DESCRIBE THE SOMATIC CELL COUNTS IN FLECKVIEH MILK

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ABSTRACT: Comparison was carried out between seven fitting functions of somatic cell curves. Somatic cell counts were analyzed in 29550 Fleckvieh cows included 317992 test-day somatic cell count (SCC), in five regions in Switzerland. Least square means of average and log natural scales somatic cell counts were estimated during the first parity by using mixed model.

The results show that, generally, the animals which have cell counts excess of 17000 cells/ml are only 14 %. Original and log somatic cells were the highest shortly after calving, declined rapidly, and then rose slowly throughout the remainder of the lactation. Milk, fat and protein yield decreased as somatic cell score increased from score 3 to 5. Regression model (RM) was the best in predicting average and log SCC, but inverse quadratic polynomial (IQP) and parabolic-exponential (PEF) were the poorest in predicting average and log daily SCC, respectively. Bias was the greatest in the second week of lactation for all model functions and in first week of lactation for mixed log model (MLM). The MLM had residuals with a very narrow range, while the IQP had residuals with a very large range. The estimated residuals by the most functions were negative in weeks 1, 4-15 and 17-18 and positive in weeks 2-3, 15-16 and 19-30, which suggest a serial correlation between the residual of average and stages of lactation. Most functions were, generally, under predicted log SCC in weeks 1-2 and 14-30 and over predicted log SCC in weeks 3-13 and 41-46. This was because most of the curves tend to flatten before the observed peak log SCC resulting in high

positive residuals between the 1st and 2nd weeks and 14th and 30th weeks of lactation and negative residuals between the 3rd and 13th weeks of lactation. The gamma function (GF) had a very narrow range of residuals, while the parabolic-exponential fitted by log-linear regression (PEF_L) had a very large range of residuals. The estimated residuals by the most functions were negative in weeks 1-2 and 14-30 and negative in weeks 3-13 and 41-46 which suggest a serial correlation between the residual and stages of lactation. In this study, all lactation curve models may be useful to describe the original and log transformed scale of somatic cells, but the regression model (RM) is the most accurate method when used to predict original and log scale somatic cell.

Key words: Somatic cell count, lactation curve models, lactation stage, milk traits, Fleckvieh breed.

INTRODUCTION

Somatic cells are simply white blood cells and epithelial cells present in normal milk. High levels of these cells in milk indicate abnormal, reduced-quality milk that is caused by an intramammary bacterial infection (mastitis). Somatic cell counts (SCC) have been considered as an accurate indicator of mastitis and a useful criterion for selection decisions (Rupp and Boichard, 2000). Genetic correlations between somatic cell counts and measures of mastitis have been estimated in several studies (Emanuelson *et al*., 1988 and Weller *et al*., 1992). Shook (1986) claimed that consideration of SCC in selection programs could improve the genetic gain of mastitis (i.e. decreasing mastitis incidence). Selection could be carried out indirectly for reduced incidence of mastitis by selection for lowered SCC and including somatic cells in genetic improvement programs, decrease susceptibility to mastitis, despite low to moderate heritability values of somatic cells and its apparent antagonism with yield traits (Schutz *et al*., 1990 and Gere *et al*., 1998).

An appropriate mathematical model may be used to predict future SCC for lactation currently in progress. Before somatic cells are endorsed as a tool for selection, fitting the SCC curve by using different lactation curve model functions must be clarified. This study aimed to compare between existing fitting function models of somatic cell curve and to define which of them could provide the best fit for prediction.

MATERIAL AND METHODS

Data used in this study were supplied by Swiss Simmental and Red & White Cattle Breeding Association, Switzerland. Cows calved between 1987 and 1992 distributed over five regions (Jura, lower land, hills, Prealps and Alps), were included in the study. The data set used for estimation least square means of the traits studied consisted of 29550 cows and 317992 tests in the first lactation. Data analysis was carried out in the Department of Animal Production, Faculty of Agriculture, Zagazig University, Egypt. Data consisted of monthly test -day records on Fleckvieh cows (Simmental, Red Holstein and cross products among these two breeds). Daily milk yield with fat, protein and somatic cell contents were available. The interval between consecutive tests was 30 days in average. The weekly least square means were calculated after transferring monthly test to daily test and the daily test for all test records were classified into weekly test by making categorical classes by lactation week. Adjustment of weekly test to genetic and environmental factors was made to obtain weekly least squares means. The minimal numbers of test-day records per lactation was set to nine.

Somatic cell counts on sample day were estimated to the nearest thousand cells per millilitre (ml) of milk by a fossomatic cell counter. Test-day cell counts were processed under two scales: the first was original, unadjusted cell count (1000 cells/ml) and the second was transformed to log natural scales. An alternative linear score from 0 to 6 digits, was calculated. Linear scores of unadjusted cell count and log natural scales are shown in Table 1. The test-day records were also validated in the range of 10-60 kg milk yield/day, 2.0-7.0% fat and 2.0-5.5 % protein contents.

Least square means of original and log natural scales somatic cell counts were estimated by using mixed model including herd, sire within herd as random effects, region, year, month of calving as fixed effects, age at calving, calving interval and level of milk yield as partial linear and quadratic regression coefficients of average and log somatic cell count on those factors (as covariatis).

Mathematical models of lactation curve

In models described, Y_t denotes daily SCC, t denotes time from parturition, a, b, c and d denote model parameters and e is the base of the natural logarithm. The mathematical models used to describe the curve of original and log somatic cell counts were:

1.The parabolic-exponential function (PEF) fitted directly (Sikka, 1950):

$$Y_t=ae^{bt+ct2}$$

2. The parabolic-exponential function (PEF_L) fitted by log-linear regression (Sikka, 1950). Model [1] was fitted in log linear:

$$Ln(Y_t)=Ln(a)+bt+ct^2$$

3. The incomplete gamma function (GF) fitted directly (Wood, 1967):

$$Y_t=at^be^{-ct}$$

Where: a, b and c were the curve parameters associated with overall scale of SCC production, pre-peak rate of increase and the post-rate peak rate of decrease in SCC, respectively.

4. The gamma function (GF_L) fitted by log-linear regression (Wood, 1967), to estimate the parameters of model [3]. Natural logarithms are taken of both sides of equation [3]:

$$Ln(Y_t)=Ln(a)+b\ Ln(t)-ct$$

5. The inverse quadratic polynomial (IQP) function (Yadav *et al.*, 1977):

$$Y_t^{-1}=a+bt^{-1}+ct$$

Where: Y_t^{-1}=Inverse of the SCC on day t.

6. The regression model (RM) function (Ali and Schaeffer, 1987):

$$Y_t=a+bt+ct^2+d\ Ln(t^{-1})+e\ (Ln(t)^{-1})^2$$

Where: t is the day in SCC divided by the maximum in SCC for the standard lactation (305) and a, b, c, d and e are the curve parameters.

7. The mixed log model (MLM) function (Guo and Swalve, 1995):

$$Y_t = a + b\sqrt{t} + c\ In(t)$$

Each model was fitted to the same data using non-linear regression (Sherrod, 1998) to each of two data presentations (original and log scale of SCC).

Accuracy evaluation of the models was based on:

1.The coefficient of determination (R^2), Where: R^2=1-(Residual sum of squares / total sum of squares).

2.The adjusted coefficient of determination (R^2_a) which adjusts the R^2 for the number of parameters in the equation and the number of data observations; $(R^2_a)=1-((n-1)/(n-p))*(1-R^2)$, Where: n is the number of observations, p is the number of parameters and R^2 is the unadjusted coefficient of determination. 3.The correlation between observed and predicted SCC or log (SCC). 4.Durbin-Watson statistic (D-W): the Durbin-Watson statistic (Durbin and Watson, 1951) was used as measures of first-order positive autocorrelation to test whether the residuals were randomly distributed (Grossman and Koops, 1988). Small values of "D-W" indicate the presence of autocorrelation. Standardized residuals from each analysis were obtained for comparison and to give an indication of how well individual daily SCC or log SCC, were predicted. The residuals were plotted against lactation stage to show, by visual inspection, how each function was biased in prediction SCC or log SCC in different phases of lactation and to determine if the bias was random or dependent on lactation stage.

RESULTS AND DISCUSSION

Linear score of SCC and milk traits

Table 1 shows day-test numbers, mean and range of somatic cell count, log natural scale and mean±S.E. of daily milk, fat and protein yield of different linear scores (SCS). The linear score divides the somatic cell count into seven categories from 0 through 6, to provide more uniform SCC reporting. The animals that have cell counts excess of 17000 cells/ml are 14 %. The normal SCC in milk is, generally, below 100000 cells /ml in the first lactation animals. A SCC above 250000-300000 is considered abnormal and is considered as an indication of bacterial infection causing inflammation of the udder (Duane and Gerald, 1997). Original and log somatic cell counts were the highest shortly after calving, declined rapidly to a nadir between weeks 8 and 12, then rose slowly throughout the remainder of lactation (Figures 1 and 2). The rate of ascending in original and log SCC increased as lactation progressed. The period of the lowest SCC was coincided closely with peak lactation. similar to results of pervious studies (Reents *et al.*, 1995 and Choi *et al.*, 1999). Temporary increase in original and log SCC may occur just after calving as the udder adapts from non-lactating to lactating status. Schalm *et al.* (1971) attributed high cell counts early in lactation to excessive shedding of epithelial cells in a small volume of milk as mammary gland resumes function after a dormant period and in late

Table 1. Linear score of somatic cell counts (SCC) and milk traits during the first lactation in Fleckvieh breed.

Linear cell count score	Day-test numbers	Score %	Somatic cell counts 1000 s / millilitre		Log natural scales		Daily yield ±S.E. (kg) of		
			Means	Ranges	Means	Ranges	Milk	Fat	Protein
0	273620	86.0	0.28	0-17	2.51	1.61-2.83	16.72±0.01a	0.69±0.001a	0.54±0.001a
1	12388	3.9	25.73	18-34	3.23	2.89-3.53	18.00±0.04b	0.74±0.002b	0.58±0.001b
2	14806	4.7	49.91	35-70	3.89	3.56-4.25	17.11±0.04c	0.72±0.001c	0.56±0.001c
3	9714	3.1	98.05	71-140	4.57	4.26-4.94	16.49±0.04d	0.70±0.002d	0.55±0.001d
4	4527	1.4	192.42	141-282	5.24	4.95-5.64	16.11±0.07e	0.69±0.003a	0.54±0.002a
5	1794	0.6	387.45	283-565	5.94	5.65-6.34	16.18±0.10e	0.69±0.004a	0.54±0.003ad
6	1143	0.4	852.01	566-1000	6.73	6.35-6.91	16.59±0.13ad	0.72±0.005c	0.56±0.004c
Mean	317992	100	14.55	0-1000	3.95	1.61-6.91	16.77±0.03	0.71±0.001	0.55±0.001

Means in the same column having different letters, differ significantly ($P<0.01$).

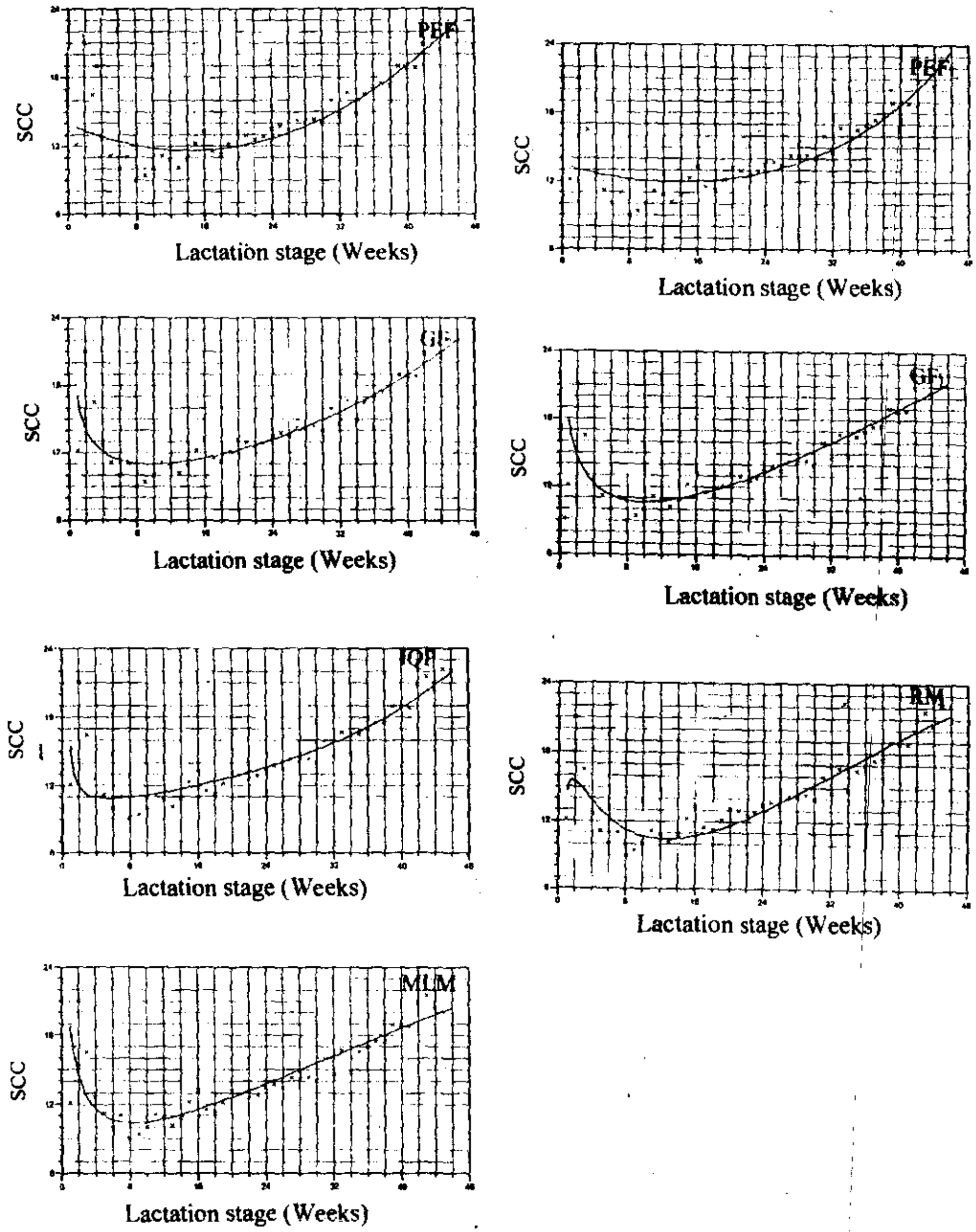

Figure 1. Prediction of somatic cell count (SCC) by different functions.

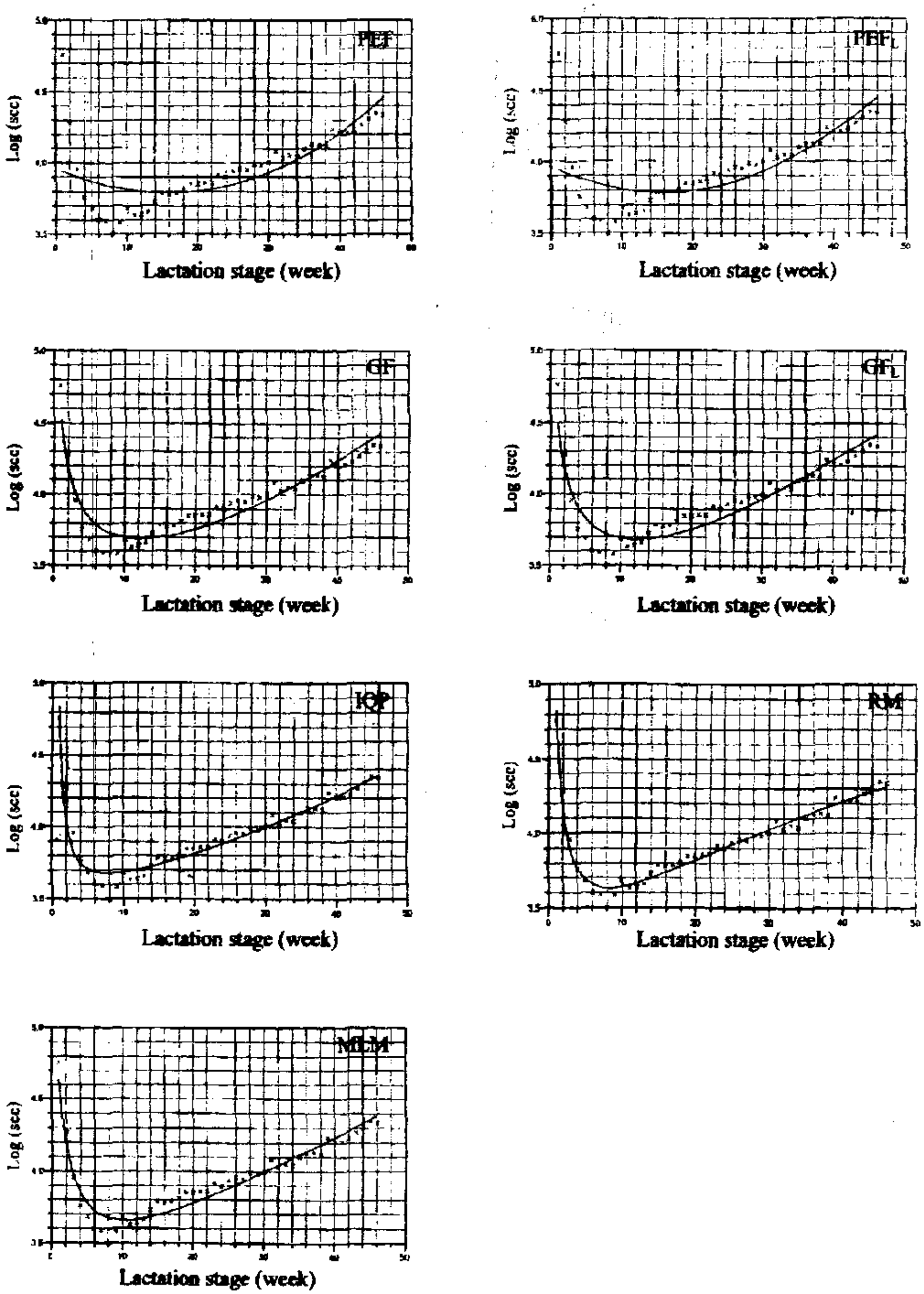

Figure 2. Prediction of log (SCC) by different function

lactation to a mere concentration of cells in a smaller volume of milk as milk yield declines. In general, high SCC occurs in milk in late gestation and two months following calving. Duane and Gerald (1997) reported that SCC elevation appears to be part of a cow's natural immune system response in preparation for calving, to enhance the mammary gland defense mechanisms at this critical parturition time. Increased somatic cell count have been associated with decreased daily milk, fat and protein production from score 3 to 5. This result is in agreement with those of pervious studies (Jeffrey, 1997 and Koldeweij *et al.*, 1999).

Fitting the somatic cell count curve

Parameters of SCC curve obtained by the various models are presented in Table 2. Table 3 contains coefficient of determination (R^2), adjusted coefficient of determination (R^2a), correlation between observed and predicted SCC (r_p) and Durbin-Watson statistic (D-W), which reflect the accuracy of each function in predicting daily SCC. Generally, the RM was the best and IQP was the poorest of the functions in predicting daily SCC. Olori (1997) reported that, the models could be ranked from best to worst as RM > PEF > IQP > MLM > GF in terms of accuracy of predicting the lactation curve of milk, fat and protein.

Figure 1 and Table 4 show a comparison between the seven functions of original SCC tested. Most models generally under predicted SCC in weeks 1 and 4-14 and over predicted SCC in weeks 2-3 and 15-16. This was because most curves tend to flatten out before the observed peak of SCC resulting in high positive residuals between 2 and 3 weeks and 15 -16 weeks of lactation and negative residuals in weeks 1, 4 and 14 of lactation, thereafter, the curve ran close to the average observed SCC curve.

Figure 3 shows plots of the residuals SCC estimated by the different models. The residual ranged between –3.2 and +8.0 for PEF; –3.1 and +7.7 for PEF_L; –4.9 and +6.9 for GF; –4.9 and +6.9 for GFL; –3.3 and +9.1 for IQP; –2.4 and +5.5 for RM and –6.6 and +6.5 for MLM.The greatest bias was observed in the second week of lactation for all model functions, except MLM in the first week of lactation. The MLM had a very narrow range of residuals, while the IQP had a very large range of residuals. The estimated residuals by most functions were negative in weeks

Table 2. Estimates of the parameters a, b, c, d and e of original and log SCC scale curve fitted by various functions during the first lactation, in Fleckvieh breed.

Items #	Parameters of somatic cell curve				
	a	b	c	d	e
Original SCC curve					
PEF	13.45	-64.542	2.383		1.00
PEF_L	1145598	-0.3239	0.01127		
GF	16.49	-0.3179	3.360		0.99
GF_L	31594861	-5.098	-0.51167		
IQP	0.1066	-0.04049	-0.00131		
RM	12.546	2.0329	-0.01022	-1.80	-4.77
MLM	11.68	7.0865	-10.2622		
Log SCC curve					
PEF	3.962	-31.598	1.004		1.00
PEF_L	52.79	-0.02291	0.0007		
GF	4.476	-0.1281	2.3438		
GF_L	85.44	-0.5100	-0.0419		
IQP	0.293	-0.0542	-0.00135		
RM	4.832	-0.00957	3.2110	1.14	0.29
MLM	4.009	0.6285	-1.0156		

Table 3. Suitability functions of original and log SCC scale curves, during the first lactation of Fleckvieh breed.

Measures of fit #	Curve models						
	PEF	PEF_L	GF	GF_L	IQP	RM	MLM
SCC curve							
R^2	0.78	0.80	0.82	0.82	0.75	0.86	0.77
R^2a	0.77	0.79	0.80	0.81	0.74	0.84	0.76
R_p	0.87	0.89	0.87	0.89	0.82	0.95	0.89
D-W	1.22	1.31	1.82	1.82	1.49	1.48	1.66
Log (SCC) curve							
R^2	0.54	0.55	0.87	0.87	0.94	0.97	0.93
R^2a	0.51	0.53	0.86	0.86	0.94	0.97	0.93
R_p	0.88	0.88	0.98	0.98	0.94	0.98	0.99
D-W	0.31	0.31	0.31	0.34	1.13	1.26	0.45

Abbreviations of curve models:

(PEF) Parabolic-exponential function, (PEF_L) Parabolic-exponential function fitted by log-linear regression, (GF) Gamma function, (GF_L) Gamma function fitted by log-linear regression, (IQP) Inverse quadratic polynomial, (RM) Regression model and (MLM) Mixed log model.

Abbreviations of measures of accuracy:

(R^2) Coefficient of determination, (R^2_a) adjusted coefficient of determination, (R_p) Correlation between observed and predicted and Durbin-Watson statistic (D-W).

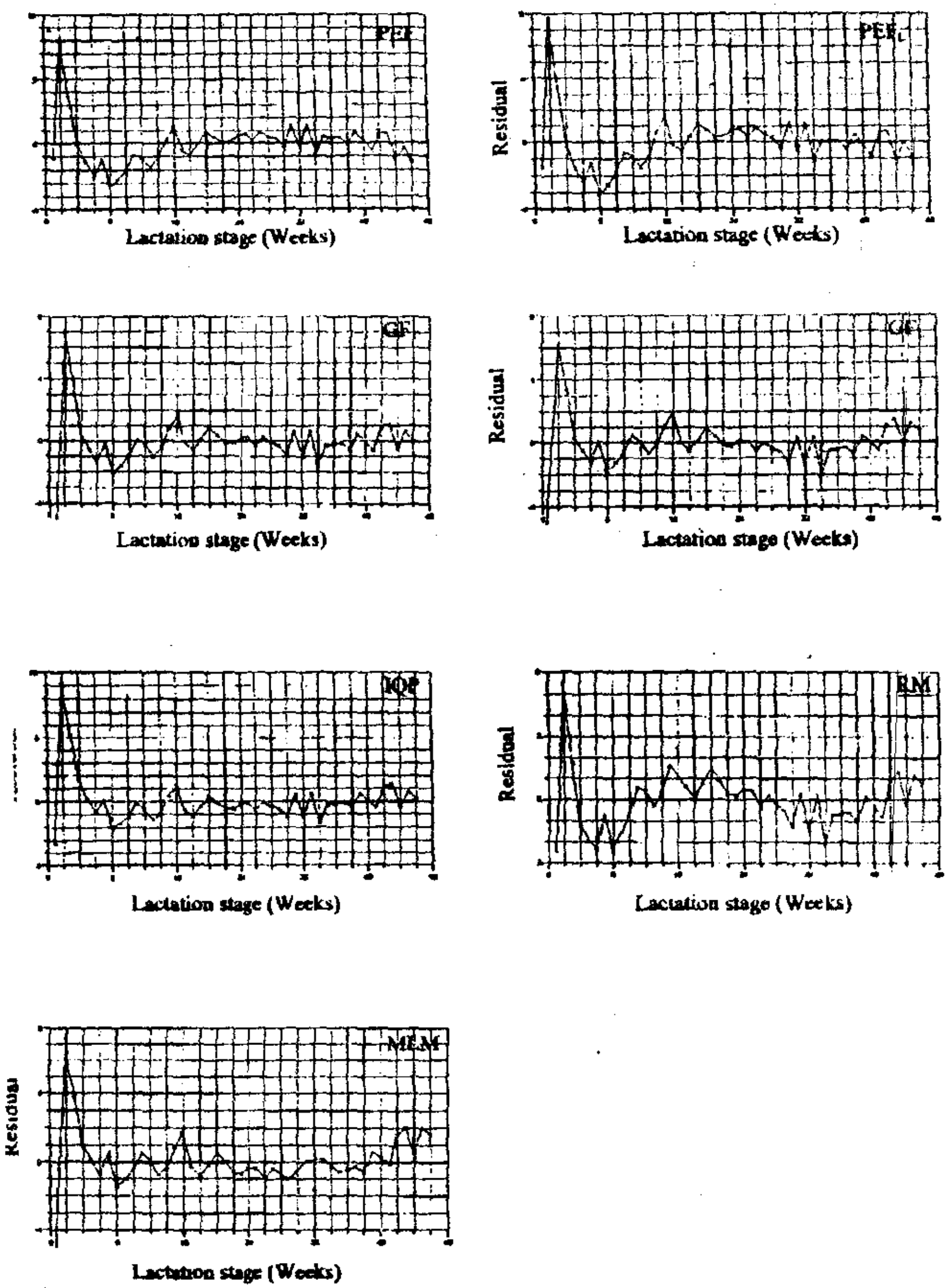

Figure 3. Effect of lactation stage on residual SCC estimated by different functions.

Table 4. Predicted original scale daily SCC during the first lactation of Fleckvieh breed by fitting various functions.

Weeks	Observed SCC (1000/ml)	Predicted SCC by different models (1000/ml)						
		PEF	PEF_1	GF	GF_1	IQP	RM	MLM
1	27.13	13.22	13.64	17.03	17.78	15.44	14.57	18.76
2	21.04	13.02	13.35	14.12	14.76	11.94	15.52	14.59
3	16.50	12.84	13.08	12.82	13.20	11.21	14.77	12.68
4	12.61	12.67	12.83	12.09	12.25	10.96	13.83	11.62
5	11.16	12.53	12.61	11.64	11.62	10.88	12.99	11.01
6	9.99	12.40	12.41	11.35	11.20	10.87	12.27	10.65
7	11.02	12.29	12.23	11.17	10.93	10.91	11.70	10.46
8	8.97	12.19	12.08	11.06	10.76	10.98	11.25	10.38
9	9.39	12.11	11.95	11.01	10.67	11.07	10.92	10.39
10	10.02	12.05	11.84	11.00	10.64	11.18	10.69	10.46
11	11.04	12.00	11.75	11.03	10.67	11.29	10.54	10.57
12	10.85	11.97	11.68	11.09	10.74	11.43	10.46	10.73
13	10.17	11.96	11.64	11.17	10.84	11.56	10.45	10.91
14	10.80	11.96	11.62	11.27	10.97	11.71	10.51	11.11
15	12.26	11.97	11.63	11.39	11.13	11.86	10.60	11.33
16	13.28	12.00	11.65	11.53	11.31	12.03	10.75	11.57
17	11.54	12.05	11.70	11.69	11.51	12.20	10.93	11.82
18	11.25	12.11	11.70	11.86	11.74	12.38	11.15	12.08
19	12.19	12.19	11.86	12.05	11.97	12.56	11.39	12.35
20	13.17	12.28	11.98	12.25	12.22	12.75	11.66	12.63
21	12.91	12.39	12.12	12.46	12.49	12.96	11.96	12.91
22	12.59	12.52	12.28	12.69	12.76	13.16	12.27	13.19
23	12.83	12.66	12.83	12.93	13.05	13.38	12.61	13.49
24	13.44	12.82	12.67	13.18	13.34	13.60	12.95	13.78
25	13.74	13.00	12.90	13.44	13.64	13.84	13.31	14.08
26	13.43	13.21	13.50	13.72	13.96	14.08	13.68	14.38
27	14.29	13.42	13.42	14.01	14.28	14.33	14.06	14.68
28	14.24	13.67	13.72	14.31	14.60	14.59	14.44	14.98
29	14.32	13.93	14.04	14.62	14.93	14.87	14.82	15.28
30	14.01	14.22	14.38	14.95	15.27	15.15	15.23	15.59
31	15.95	14.53	14.74	15.28	15.61	15.45	15.63	15.89
32	14.61	14.87	15.13	15.63	15.97	15.76	16.03	16.20
33	16.70	12.23	15.54	16.00	16.32	16.08	16.43	16.51
34	14.78	15.63	15.97	16.38	16.68	16.42	16.83	16.81
35	16.53	16.05	16.42	16.77	17.05	16.77	17.23	17.12
36	16.96	16.51	16.90	17.17	17.41	17.13	17.63	17.42
37	17.44	17.00	17.40	17.59	17.79	17.52	18.02	17.73
38	17.47	17.53	17.92	18.02	18.16	17.92	18.42	18.03
39	18.96	18.10	18.46	18.47	18.54	18.34	18.80	18.34
40	18.87	18.71	19.03	18.93	18.92	18.78	19.19	18.64
41	18.80	19.37	19.62	19.41	19.31	19.24	19.56	18.94
42	20.82	20.07	20.23	19.90	19.70	19.73	19.93	19.25
43	21.60	20.83	20.87	20.42	20.09	20.25	20.30	19.55
44	20.41	21.64	21.53	20.94	20.48	20.79	20.65	19.85
45	22.18	22.52	22.20	21.49	20.88	21.36	21.00	20.15
46	22.07	23.64	22.91	22.05	21.28	21.96	21.34	20.45

The abbreviations of curve models are given in Tables 1, 2 and Material and methods.

, 4-15 and 17-18 and positive in weeks 2-3, 15-16 and 19-30 which suggest a serial correlation between the residual and stage of lactation.

Fitting the log somatic cell count curve

Parameters of log SCC curve obtained by the various functions are presented in Table 2. Table 3 contains coefficient of determination (R^2), adjusted coefficient of determination (R^2a), correlation between observed and predicted SCC (r_p) and Durbin-Watson statistic (D-W), which reflect the accuracy of each function in predicting daily log SCC. Generally, the RM was the best and REF was the poorest of the function in predicting daily log SCC. The RM was superior to REF, GF and IQP to accurate prediction of daily milk yield (Ali and Schaeffer, 1987).

Figure 2 and Table 5 show a comparison between the fit of the seven functions tested. Most functions were generally under predicted log SCC in weeks 1-2 and 14-30 and over predicted log SCC in weeks 3-13 and 41-46. This was because most of the curves tend to flatten out before the observed peak log SCC resulting in high positive residuals between weeks 1 and 2 and 14 and 30 of lactation and negative residuals between weeks 3 and 13 of lactation.

Figure 4 shows plots of the residual log SCC estimated by the different functions. The residual ranged between –0.33 and 0.82 for PEF; –0.33 and 0.82 for PEF_L; –0.23 and 0.24 for GF; –0.22 and 0.27 for GFL; –0.18 and 0.25 for IQP; –0.13 and 0.12 for RM and -0.17 and 0.12 for MLM. The greatest bias was observed in week 1 for PEF, PEFL, GF and GFL and in week 2 for IQP and in week 8 for RM and MLM functions. The GF had a very narrow range of residuals, while the PEF_L had a very large range of residuals. The estimated residuals by the most functions were negative in weeks 1-2 and 14-30 and negative in weeks, 3-13 and 41-46 which suggest a serial correlation between the residual and stage of lactation.

CONCLUSIONS

Key factors for choosing optimal mathematical model to describe the somatic cell curve are fit's accuracy, interpretation of the curve's parameters and possibility for calculating characteristics of the curve. In this study, all lactation curve models may be useful to

Table 5. Predicted daily log SCC scale during the first lactation of Fleckvieh breed by fitting **various functions.**

Weeks	Observed log SCC	Predicted log (SCC) by different models						
		PEF	PEF$_L$	GF	GF$_L$	IQP	R.M	MLM
1	4.76	3.94	3.94	4.52	4.48	4.84	4.82	4.63
2	4.28	3.92	3.92	4.18	4.18	4.03	4.16	4.19
3	3.96	3.90	3.90	4.01	4.01	3.83	3.89	3.98
4	3.76	3.88	3.88	3.91	3.91	3.75	3.76	3.86
5	3.68	3.87	3.87	3.84	3.83	3.71	3.69	3.78
6	3.60	3.85	3.85	3.79	3.78	3.69	3.65	3.73
7	3.59	3.84	3.84	3.75	3.75	3.68	3.63	3.69
8	3.50	3.83	3.83	3.73	3.72	3.68	3.63	3.67
9	3.58	3.82	3.82	3.71	3.70	3.68	3.63	3.66
10	3.68	3.81	3.81	3.70	3.69	3.68	3.64	3.66
11	3.63	3.80	3.80	3.69	3.68	3.69	3.65	3.66
12	3.64	3.81	3.79	3.69	3.68	3.70	3.66	3.66
13	3.66	3.79	3.79	3.69	3.68	3.71	3.68	3.67
14	3.73	3.79	3.78	3.69	3.69	3.72	3.70	3.68
15	3.79	3.79	3.78	3.70	3.69	3.74	3.72	3.69
16	3.78	3.79	3.78	3.71	3.70	3.75	3.73	3.71
17	3.79	3.79	3.79	3.72	3.71	3.76	3.75	3.72
18	3.81	3.79	3.79	3.73	3.73	3.78	3.78	3.74
19	3.85	3.80	3.79	3.74	3.74	3.80	3.80	3.76
20	3.85	3.80	3.80	3.76	3.76	3.81	3.82	3.78
21	3.86	3.81	3.80	3.77	3.77	3.83	3.84	3.80
22	3.86	3.82	3.81	3.79	3.79	3.85	3.86	3.82
23	3.82	3.83	3.82	3.81	3.81	3.86	3.88	3.84
24	3.90	3.84	3.83	3.83	3.83	3.88	3.90	3.86
25	3.94	3.85	3.85	3.85	3.85	3.90	3.92	3.88
26	3.96	3.86	3.86	3.87	3.87	3.92	3.94	3.90
27	3.95	3.88	3.88	3.89	3.90	3.94	3.96	3.93
28	3.99	3.89	3.89	391	3.92	3.95	3.98	3.95
29	3.98	3.91	3.91	394	3.94	3.97	4.00	3.97
30	4.00	3.93	3.93	396	3.97	3.99	4.02	3.99
31	4.08	3.95	3.95	398	3.99	4.01	4.04	4.02
32	4.03	3.97	3.98	4.01	4.02	4.04	4.06	4.04
33	4.05	3.99	4.00	4.04	4.05	4.06	4.08	4.07
34	4.04	4.02	4.03	4.06	4.07	4.08	4.10	4.09
35	4.10	4.05	4.06	4.09	4.10	4.10	4.12	4.11
36	4.13	4.07	4.08	4.12	4.12	4.12	4.14	4.14
37	4.13	4.11	4.11	4.15	4.15	4.14	4.16	4.16
38	4.12	4.14	4.15	4.15	4.18	4.17	4.17	4.19
39	4.24	4.17	4.18	4.20	4.21	4.19	4.19	4.21
40	4.21	4.21	4.21	4.23	4.24	4.21	4.21	4.23
41	4.21	4.24	4.25	4.27	4.27	4.24	4.23	4.26
42	4.23	4.28	4.29	4.30	4.30	4.26	4.24	4.28
43	4.27	4.32	4.33	4.33	4.33	4.28	4.26	4.31
44	4.31	4.37	4.37	4.36	4.36	4.30	4.28	4.33
45	4.35	4.41	4.41	4.40	4.39	4.33	4.30	4.36
46	4.34	4.46	4.45	4.43	4.42	4.36	4.31	4.38

The abbreviations of curve models are given in Tables 1, 2 and Material and methods.

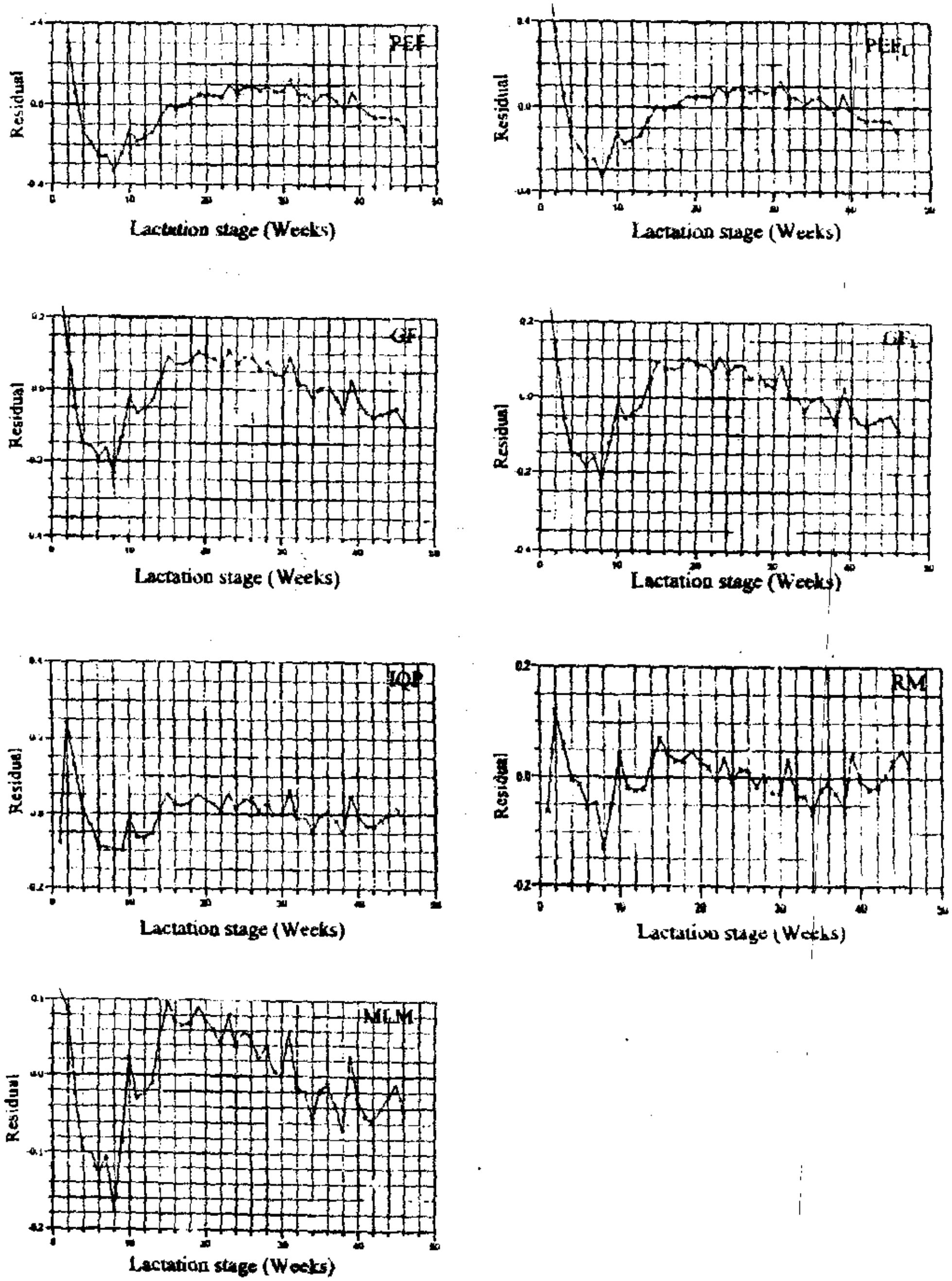

Figure 4. Effect of lactation stage on residual log SCC estimated by different functions.

describe the original and log transformed scale of somatic cell in Fleckveih cows. The regression model (RM) is the most accurate model when used to predict original and log scale somatic cell.

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مقارنة نماذج رياضية لمنحنى الحليب لوصف تعداد الخلايا الجسمية في ألبان الفلكفيى

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يهدف البحث دراسة مدى ملائمة الدالات الرياضية المستخدمة في وصف منحنى الحليب لوصف والتنبؤ بعدد الخلايا الجسمية في اللبن خلال مرحلة الحليب. تمت المقارنة بين سبع دالات رياضية لعدد ٢٩٥٥٠ بقرة فلكفيى متضمنة ٣٧١٩٩٢ اختبار يومي لتقدير الخلايا الجسمية في اللبن خلال موسم الحليب الأول لسلالة الفلكفيي السويسرية. تم تطبيق الدالات على صورتين ، الأولى المتوسط اليومي لعدد الخلايا الجسمية في اللبن مقدرة بألف/ مليليتر والثانية بالتحويل إلى اللوغاريتم الطبيعي – هذا بالإضافة إلى تحويل الصورة الأولى إلى Scores (٧ أقسام من ٠ إلى ٦). وتتلخص أهم نتائج الدراسة في النقاط التالية: ١. ١٤% فقط من مجموع الحيوانات يزيد عدد الخلايا الجسمية بها عن ١٧٠٠٠٠ خلية/مل. ٢. متوسط ولوغاريتم الخلايا الجسمية أعلى بعد الولادة ثم ينخفض سريعا ثم يبداء في الزيادة تدريجيا مع تقدم مرحلة الحليب. ٣. إنتاج اللبن، الدهن و البروتين اليومي يقل مع زيادة ال Score من (٣ إلى ٥) ٤. وجد أن دالة أل Regression Model (RM) الأفضل في التنبؤ بمتوسط ولوغاريتم عدد الخلايا الجسمية في اللبن ، بينما كل من الدالة Inverse Quadratic Polynomial (IQP) و الدالة Parabolic-exponential (PEF) كانتا اقل تنبؤ ودقة. ٥. الدالة Mixed Log Model (MLM) كانت اقل الدالات مدى للمتبقي Residuals لمتوسط عدد الخلايا الجسمية بينما الدالة (IQP) كانت الأعلى مدى للمتبقي. ٦. الدالة Gamma Function (GF) كانت اقل الدالات مدى للمتبقي للوغاريتم الخلايا الجسمية ، بينما الدالة Parabolic-exponential (GF) باستخدام لوغاريتم الانحدار الخطى كانت الأعلى مدى للمتبقي. من أهم نتائج المقارنة يتضح إمكانية تطبيق كل الدالات الرياضية المدروسة والخاصة بمحنى اللبن لوصف والتنبؤ بمتوسط عدد والصورة اللوغاريتمية للخلايا الجسمية خلال مرحلة الحليب ، وتعتبر الدالة (RM) افضل الدالات لوصف والتنبؤ بمتوسط ولوغاريتم الخلايا الجسمية في اللبن بدقة عالية واقل انحراف.