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SINGLE–TRAIT SELECTION AS OPTIMAL SELECTION RESPONSES FOR 305 DAY MILK TRAITS BASED ON VARIOUS PARTS OF FIRST LACTATION RECORDS IN FLECKVIEH

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ABSTRACT: Data were collected in two consecutive years (1990,1991) and included 19000, 27158 and 18999 records of different data sets at 31-120, 61-150 and 31-150 day of lactation for the first lactation in Fleckvieh cows. Yields of 305-and simulated cumulative 31-120, 61-150 and 31-150-day of milk, fat, protein and fat-plus-protein and percentage of protein yield/fat yield were studied. The effects of calving year-season (CYS), age at first calving (AFC), days open (DO), the period from the first monthly test-day to next calving date (CTRDF) and sire on milk traits were investigated. Variance components, correlation coefficients and heritabilities of these traits were estimated. The indirect selection were calculated for various simulated cumulative milk traits (CMT).

Calving year-season (CYS) affected significantly most of the studied traits. Days open, age at first calving and the time from the first monthly test day to next calving date affected significantly most traits studied. The effects of sire were highly significant for all traits studied. Heritability estimates for various periods of CMT ranged from 0.32 to 0.43 at 31-120, 61-150 and 31-150 day of lactation. Genetic (r_G), phenotypic (r_p) and environmental (r_E) correlations between CMYT of either 31-120 or 61-150 or 31-150 with 305-day (MYT) yield traits were generally positive and high, the r_G estimates ranged from 0.79 to 0.97 between MYT and CMYT of 31-120, 61-150

and 31-150 day of lactation, while both the r_P and r_E estimates ranged from 0.71 to 0.89 between MYT and $CMYT_{31-120}$, 0.73 to 0.89 between MYT and $CMYT_{61-150}$ and from 0.77 to 0.89 between MYT and $CMYT_{31-150}$. It could be concluded that genetic improvement in MYT could be achieved through single trait selection for $CMYT_{61-150}$ (especially simulated cumulative fat yield at 61-150 day of lactation CFY_{61-150}) comparing to other periods of CMYT. In conclusion, this procedure would lead to a decrease in generation interval and consequently to increase gain per year.

INTRODUCTION

Increasing milk traits through selection is a main goal of dairy cattle breeders. Pricing systems of milk, in recent years, depend on yield and its contents of protein and/or fat (Mbah and Hargrove, 1982; Dommerholt and Wilmink, 1986 and de Jager and Kennedy, 1987) because of the importance of them in human nutrition and for the industrial value of the milk products. Selection for parameters such as heritability and various correlations between different cumulative and 305-day milk yield traits are useful in estimating genetic progress and in planning breeding programs.

The objective of this study is to (1) to estimating the genetic and phenotypic parameters of simulated cumulative 31-120, 61-150 and 31-150 and 305-day milk traits of the first lactation in Fleckvieh cattle. (2) investigating and compare the possibility of early selection for 305-day milk traits based on either 31-120 or 61-150 or 31-150 day of lactation.

MATERIALS AND METHODS

Data consisted of the 1st lactation of Fleckvieh cattle accumulated by the official Federation of Austrian Cattle Breeders (ZAR). Data analysis was carried out in the Department of Animal Production, Faculty of Agriculture, Zagazig University. The records were obtained for successive two years (1990-1991). Heifers were inseminated when they reached about 320 Kg body weight and were artificially inseminated using deep-frozen semen, avoiding full-sibs and sire-daughter matings. Breeding and management policies of Austrian Fleckvieh cattle are described by Hofinger *et al.* (1997).

Data were available on 19000, 27158 and 18999 records by 1424, 1748 and 1424 sires under different data sets of 31-120, 61-150 and 31-150 day at the 1^{st} lactation. Only sires with at least two daughters (paternal half-sisters) were included in the analysis. Traits analyzed were simulated cumulative milk traits (CMT_i): simulated cumulative milk (CMY_i)-, fat (CFY_i)-, protein (CPY_i)- and fat-plus-protein ($CFPY_i$) yield and protein yield/fat yield% ($CPOF\%_i$) , where i=day at 31-120 or 61-150 or 31-150 of lactation and 305-day milk traits (MT) were milk yield (MY), fat (FY)-, protein (PY) -, fat-plus-protein (FPY) yield and protein yield/fat yield% (POF%). Simulated cumulative milk traits of various periods of lactation were calculated by using the following equations :

$CMT_{31-120} = [\Sigma^3_{i=1} (TD^*_i \text{ X } 30.5)]$,

Where: i , $1=TD_2$; $2=TD_3$ and $3=TD_4$

$CMT_{61-150} = [\Sigma^3_{i=1} (TD_i \text{ X } 30.5)]$,

Where: i , $1=TD_3$; $2=TD_4$ and $3=TD_5$

$CMT_{31-150} = [\Sigma^4_{i=i} (TD_i \text{ X } 30.5)]$,

Where: i , $1=TD_2$; $2=TD_3$; $3=TD_4$ and $4=TD_5$

* TD = monthly test-day

Statistical analysis:

Traits were analyzed by using LSMLMW computer program of Harvey (1990). The linear mixed model included the random effect of sire, the fixed effects of calving year-season (CYS), age at first calving (AFC), days open (DO) and the period from the first monthly test day to next calving date (CTRDF) as partial linear and quadratic regression coefficients. Estimates of sire and remainder components of variance and covariance were computed by method III of Henderson (1953). The estimates of paternal half-sib heritability (h^2) were calculated as, $h^2_S = 4\sigma^2_S / (\sigma^2_S + \sigma^2_e)$, where: σ^2_S and σ^2_e are sire and remainder variance components, respectively. Genetic (r_G) with standard errors (SE), phenotypic (r_P) and environmental (r_E) correlations were estimated. Approximate standard errors for h^2 and r_G estimates were obtained according to Swiger *et al.* (1964).

The expected correlated response of milk traits studied were estimated according to Falconer (1981) by using the following equations:

$$CR_y = ih_x\, h_y\, r_G\, \sigma P_y$$

Where, CR_y = the correlated response of trait y; h_x and h_y are the square roots of respective heritability estimates, r_G = the genetic correlation between x and y traits, and σp_y = the phenotypic standard deviation of trait y.

The expected genetic changes per generation were calculated on cow side. The selection intensity for a trait was set to be 1.0 for the purpose of comparisons.

RESULTS AND DISCUSSION

Means:

Means ± SD, coefficients of variation (CV%), variance components, proportion of variance (V%) and heritability (h^2) of the first lactation traits for 31-120, 61-150 and 31-150 day of lactation are given in Table 1. The results showed that CV% value of CMYT ranged from 20 to 23% for 31-120, 61-150 and 31-150 day of lactation. The variation in percentage trait (CPOF%) (9.0%) was smaller than for CMYT at different periods of lactation. Similarly, Kennedy (1982) reported that yield traits showed more variability, as measured by CV% than did percentages traits. The proportion of variation (V%) due to the sire component ranged from 12 to 15% for MT under each CMT of 31-120, 61-150 and 31-150 day. Similarly the corresponding estimates for each period of CMT ranged from 7 to 11%.

Non-genetic effects:

Least squares analysis of variance for different traits studied are given in Table 2. Most traits studied were affected significantly ($P<0.001$) by calving year-season. Age at first calving had a significant effect ($P<0.05$, 0.01 or 0.001) on most traits studied (Wilmink, 1987). Most traits studied were affected significantly ($P<0.05$, 0.01 or 0.001) by days open in a linear manner, except CFY_{31-150}. The period from the first monthly test-day to next calving date had a pronounced effect ($P<0.05$, 0.01 or 0.001) on all traits studied, except $CPOF\%_{31-150}$.

Components of variance and heritability:

The effect of sire was highly significant ($P<0.001$) for all traits studied as given in Table 2. Similar findings were reported in many studies (Wilmink, 1987 and 1988). Consequently, sires

Table (1) : Unadjusted means, standard deviations (SD), coefficients of variation (CV%), variance components estimate, proportions of variations (V%) and heritability (h^2) for traits studied in Fleckvieh cattle.

Trait	CMT$_{31-120}$						CMT$_{61-150}$						CMT$_{31-150}$					
	Mean	SD	CV%	V%		h^2 ++	Mean	SD	CV%	V%		h^2	Mean	SD	CV%	V%		h^2
				Sire	error					Sire	error					Sire	error	
305 – day milk traits+++ :																		
MY	4339	796	16.5	12.2	87.8	0.49	4298	810	17.0	13.1	86.9	0.52	4339	796	16.5	12.2	87.8	0.49
FY	180	37	18.2	14.2	85.8	0.57	179	37	18.6	14.7	85.3	0.59	180	37	18.2	14.2	85.8	0.57
PY	143	27	17.3	12.1	87.9	0.48	142	28	17.7	13.0	87.0	0.52	143	27	17.3	12.1	87.9	0.48
FPY	323	62	17.3	13.4	86.6	0.53	320	63	17.8	14.0	86.0	0.56	323	62	17.3	13.4	86.6	0.53
POF%	80	7	8.0	14.2	85.8	0.57	80	7	8.0	14.6	85.4	0.58	80	7	8.0	14.3	85.7	0.57
Simulated cumulative milk traits+++ :																		
CMY	1007	236	22.2	8.1	91.9	0.32	1111	249	20.8	9.4	90.6	0.38	1426	310	20.4	8.9	91.1	0.36
CFY	45	11	22.9	9.4	90.6	0.36	48	11	22.1	10.7	89.3	0.43	63	14	21.3	10.3	89.7	0.41
CPY	36	8	22.2	7.2	92.8	0.32	39	9	21.4	9.6	90.4	0.37	50	11	20.6	8.6	91.4	0.35
CFPY	81	19	22.3	8.6	91.4	0.35	87	19	21.0	10.2	89.8	0.41	113	24	20.7	9.6	90.4	0.39
CPOF%	80	8	9.0	9.2	90.8	0.37	81	8	9.0	10.3	89.7	0.41	81	8	9.0	10.5	89.5	0.42

++ Standard errors of heritabilities are around 0.025.

+++ Yield traits in kilogram.

Table (2) : F. ratio of least squares ANOVA for simulated cumulative 31-120 (CMT_{31-120}) , 61-150 (CMT_{61-150}) and 31-150 (CMT_{31-150}) – day milk traits of the first lactation in Fleckvieh cattle.

S.O.V		D.F	F. Value				
			CMY	CFY	CPY	CFPY	CPOF%
				CMT_{31-120}			
SIRE		1423	2.16***	2.31***	2.14***	2.25***	2.33***
CYS		6	32.54***	13.97***	19.26***	15.77***	29.17***
Regressions							
Age	L	1	1.18$^{n.s}$	2.63$^{n.s}$	.11$^{n.s}$	1.18$^{n.s}$	8.43**
	Q	1	17.41***	10.79**	15.46***	13.32***	2.7$^{n.s}$
DO	L	1	49.2***	6.80**	33.74***	16.78***	55.54***
	Q	1	.42$^{n.s}$	.33$^{n.s}$	.36$^{n.s}$	.36$^{n.s}$	.06$^{n.s}$
CTR_2DF	L	1	311.89***	76.35***	95.63***	88.45***	2.75*
	Q	1	7.38**	3.03*	1.11$^{n.s}$	2.17$^{n.s}$	3.61*
Error M.S.		17564	(48614.2)	(106.3)	(64.0)	(319.4)	(.006)
				CMT_{61-150}			
SIRE		1747	2.6***	2.83***	2.58***	2.74***	2.76***
CYS		6	88.05***	31.62***	31.78***	31.44***	39.35***
Regressions							
Age	L	1	18.16***	.12$^{n.s}$	4.07*	1.22$^{n.s}$	12.13***
	Q	1	26.32***	15.11***	22.0***	10.91***	3.19*
DO	L	1	73.5***	19.87***	60.94***	36.94***	51.41***
	Q	1	.32$^{n.s}$	.34$^{n.s}$	2.67$^{n.s}$	1.14$^{n.s}$	5.69*
CTR_3DF	L	1	673.21***	213.22***	249.25***	240.63***	1.33$^{n.s}$
	Q	1	11.6***	3.58*	6.70**	5.08*	2.87*
Error M.S.		25398	(51270.0)	(108.2)	(66.0)	(326.0)	(.006)
				CMT_{31-150}			
SIRE		1423	2.30***	2.49***	2.27***	2.4***	2.56***
CYS		6	40.65***	16.88***	19.93***	17.74***	30.9***
Regressions							
Age	L	1	4.38*	.86$^{n.s}$	.16$^{n.s}$	.12$^{n.s}$	10.17**
	Q	1	17.97***	11.17***	16.39***	13.97***	2.4$^{n.s}$
DO	L	1	22.26***	2.13$^{n.s}$	16.35***	7.03**	37.04***
	Q	1	.54$^{n.s}$	.76$^{n.s}$	.84$^{n.s}$	.83$^{n.s}$	.11$^{n.s}$
CTR_2DF	L	1	263.44***	61.18***	72.34***	69.11***	.87$^{n.s}$
	Q	1	8.79**	3.64*	2.18$^{n.s}$	3.10*	1.86$^{n.s}$
Error M.S.		17563	(82172.7)	(175.3)	(106.1)	(529.0)	(.005)

ns= non-significant, *= $P<0.05$, **= $P<0.01$ and ***= $P<0.001$.

selection would lead to genetic improvement of milk yield traits. Heritability estimates (h^2) for MT as evidenced in Table 1 ranged form 0.48 to 0.59 under CMT of 31-120, 61-150 and 31-150 day. While, their corresponding h^2 estimates for each period of CMT ranged from 0.32 to 0.43. The range of h^2 estimates for $CMYT_{31-120}$ 0.32 to 0.37 were nearly similar to 0.30 to 0.35 obtained by Wilmink, (1987), however, the range for $CMYT_{61-150}$ 0.37 to 0.43 were higher than 0.33 to 0.34 recorded by the same author. In general, CMT_{61-150} had the highest h^2 estimates relative to other periods of CMT (Table 1). Moderate h^2 estimates for different periods of CMYT indicate that, selection on incomplete records can be acceptable alternative to select cows on their complete records (305-day) lactation.

Correlations:

Genetic (r_G), phenotypic (r_P) and environmental (r_E) correlations between 305-day (MT)-and different periods of simulated cumulative (CMT) milk traits are presented in Table 3. Estimates of r_G between yield traits were generally positive and higher than r_P estimates (Wilmink, 1987). Estimates of r_G between yield traits of 305-(MYT) and each CMYT of 31-120, 61-150 and 31-150 day of lactation were generally high, positive and ranged from 0.79 to 0.97. The highest r_G estimates (0.84 to 0.97) were found between MYT and $CMYT_{61-150}$ relative to other periods of CMYT (Wilmink, 1987). These mainly part-whole genetic relationships indicates that $CMYT_{61-150}$ can be used as a good indicator for MYT. The r_G estimates between MYT and CPOF% at 31-120, 61-150 and 31-150 day were generally negative, varied from low to moderate and fill in the range -0.09 to -0.46 (Table 3). The r_G estimates between POF% and each periods of CMYT were generally negative, varied in magnitude and ranged from -0.13 to -0.51 at 31-120, 61-150 and 31-150 day of lactation. While, a strong and positive r_G estimates 0.92 to 0.94 were shown between POF% and each periods of CPOF%. The highest r_G estimates were obtained with $CPOF\%_{31-150}$ (0.94).

High and positive r_P and r_E estimates were shown between MYT and each period of CMYT (Table 3). Those both estimates ranged from 0.71 to 0.84 between MYT and $CMYT_{31-120}$ and from 0.73 to 0.89 between MYT and $CMYT_{61-150}$ and from 0.77 to 0.89 between MYT and $CMYT_{31-150}$. Both the r_P and r_E estimates

Table (3): Estimates of genetic correlations (r_G) and their standard errors (SE), phenotypic (r_P) and environmental (r_E) correlations between 305- and simulated cumulative 31 – 120 (CMT_{31-120})-; 61 – 150 (CMT_{61-150}) and 31 – 150 (CMT_{31-150}) day milk traits of the first lactation in Fleckvieh cattle .

Correlated traits	CMT_{31-120}				CMT_{61-150}				CMT_{31-150}			
	r_G	SE	r_P	r_E	r_G	SE	r_P	r_E	r_G	SE	r_P	r_E
305-& simulated cumulative milk traits:												
MY & CMY	.90	.01	.83	.80	.96	.004	.88	.83	.92	.01	.88	.87
& CFY	.79	.02	.75	.73	.84	.01	.79	.75	.82	.02	.79	.78
& CPY	.85	.01	.79	.77	.90	.01	.83	.80	.87	.01	.84	.83
& CFPY	.83	.02	.78	.77	.88	.01	.83	.79	.86	.01	.83	.82
& CPOF%	-.10	.04	.03	.13	-.11	.04	.02	.13	-.13	.04	.03	.15
FY & CMY	.81	.02	.74	.72	.86	.01	.78	.74	.83	.01	.78	.77
& CFY	.94	.01	.83	.76	.97	.004	.87	.79	.96	.01	.88	.82
& CPY	.86	.01	.76	.72	.90	.01	.79	.73	.88	.01	.80	.77
& CFPY	.93	.01	.81	.76	.96	.004	.86	.79	.95	.01	.86	.82
& CPOF%	-.45	.04	-.22	-.04	-.44	.03	-.24	-.06	-.46	.04	-.25	-.05
PY & CMY	.86	.01	.79	.76	.91	.01	.83	.79	.87	.01	.84	.82
& CFY	.86	.01	.77	.71	.90	.01	.81	.74	.88	.01	.82	.77
& CPY	.93	.01	.84	.79	.97	.004	.88	.83	.95	.01	.89	.85
& CFPY	.91	.01	.82	.77	.94	.01	.86	.80	.93	.01	.87	.83
& CPOF%	-.09	.04	.08	.20	-.09	.04	.07	.21	-.10	.04	.09	.23
FPY & CMY	.85	.01	.78	.76	.90	.01	.82	.79	.87	.01	.83	.82
& CFY	.93	.01	.82	.76	.96	.004	.87	.79	.95	.01	.87	.82
& CPY	.91	.01	.81	.77	.95	.01	.85	.80	.93	.01	.86	.83
& CFPY	.94	.01	.84	.78	.97	.004	.88	.82	.96	.01	.89	.85
& CPOF%	-.31	.04	-.10	.07	-.30	.03	-.11	.07	-.32	.04	-.11	.08
POF% & CMY	-.20	.04	-.01	.15	-.15	.04	.004	.15	-.20	.04	.001	.17
& CFY	-.49	.04	-.23	-.02	-.48	.03	-.26	-.04	-.51	.04	-.25	-.02
& CPY	-.16	.04	.06	.23	-.13	.04	.07	.25	-.16	.04	.07	.27
& CFPY	-.36	.04	-.11	.10	-.34	.03	-.12	.10	-.37	.04	-.11	.11
& CPOF%	.92	.01	.70	.53	.93	.01	.75	.59	.94	.01	.77	.63

between MYT and CPOF% at 31-120, 61-150 and 31-150 day were generally varied in magnitude and signs and fill in the range –0.25 to 0.09 and –0.06 to 0.23, respectively. Estimates of r_P and r_E between POF% and each period of CMYT were generally varied in magnitude and directions and fill in the range –0.26 to 0.07 and –0.04 to 0.27, respectively. While, positive r_P and r_E estimates were found between POF% and each period of CPOF% at 31-120, 61-150 and 31-150 day and fill in range 0.70 to 0.77 and 0.53 to 0.63, respectively (Table 3). In most cases, r_P and r_E estimates were similar to the corresponding r_G estimates in direction but were lower in magnitude.

Single-trait selection:

The expected correlated responses per generation due to single-trait selection based on CMT at 31-120, 61-150 and 31-150 day for MT are summarized in Table 4. The selection intensity was set to be 1.0, just comparison for correlated response (CR_y) from different periods of CMT. In general, the CR_y for MYT were high. The reason for this is the high h^2 estimate of the former trait and the high r_G estimates between MYT and each period of CMYT.

Generally, using any CMYT as a criterion of selection would result in an increase in other yield traits (e.g. Kennedy, 1982; de Jager and Kennedy, 1987, Wilmink, 1987; Soliman *et al.*, 1990; Soliman and Khalil, 1993 and Hamed and Soliman ,1994).

Using CPOF% at 31-120, 61-150 and 31-150 day of lactation as a criterion of selection resulted in correlated loss in MYT. While, poor correlated increase was shown in POF%. Those results due to the small value of r_G between each periods of CPOF% and MYT. Generally, selection for $CMYT_{61-150}$ had the highest CR_y in MYT comparing to other periods of CMYT (Wilmink, 1987) as evidenced in Table 4.

Response per generation expressed as % of the overall means following selection for $CMYT_{61-150}$ were listed in Table 4. Selection for CMY_{61-150} results in an increase of 333, 14.7, 10.9 and 25.5 Kg of MY, FY, PY and FPY, respectively. Responses per generation as % of the overall mean were 7.8, 8.2, 7.7 and 8.0%, respectively. Selection for CFY_{61-150} compared to selection for CMY_{61-150} led to less or more changes of –0.6, 1.7, 0.4 and 1.1% of MY, FY, PY and FPY,

Table (4) : Estimates of expected correlated response (CR_Y) per generation from single trait selection for 305 – day milk traits using simulated cumulative 31 – 120 (CMT_{31-120}) , 61-150 (CMT_{61-150}) and 31-150 (CMT_{31-150}) day milk traits of the first lactation in Fleckvieh cattle.

Selection trait		Expected correlated response of 305-day milk traits (CR_Y)				
		MY	FY	PY	FPY	POF%
Simulated cumulative 31 – 120 day milk traits :						
CMY_{31-120}	a	273	12.2	8.9	21.1	-.009
	b	6.3	6.8	6.2	6.5	-1.1
CFY_{31-120}	a	254	15.1	9.4	24.5	-.022
	b	5.9	8.4	6.6	7.6	-2.8
CPY_{31-120}	a	257	13.0	9.6	22.6	-.007
	b	5.9	7.2	6.7	7.0	-.85
$CFPY_{31-120}$	a	263	14.7	9.8	24.4	-.016
	b	6.1	8.2	6.9	7.5	-2.0
$CPOF\%_{31-120}$	a	-32.6	-7.3	-1.0	-8.3	.042
	b	-.75	-4.1	-.70	-2.6	5.3
Simulated cumulative 61 –150 day milk traits :						
CMY_{61-150}	a	333	14.7	10.9	25.5	-.007
	b	7.8	8.2	7.7	8.0	-.88
CFY_{61-150}	a	310	17.6	11.5	29.0	-.024
	b	7.2	9.9	8.1	9.1	-3.0
CPY_{61-150}	a	308	15.2	11.5	26.6	-.006
	b	7.2	8.5	8.1	8.3	-.75
$CFPY_{61-150}$	a	317	17.0	11.7	28.6	-.017
	b	7.4	9.5	8.2	8.9	-2.1
$CPOF\%_{61-150}$	a	-39.6	-7.8	-1.1	-8.8	.045
	b	-.92	-4.4	-.79	-2.8	5.7
Simulated cumulative 31 – 150 day milk traits :						
CMY_{31-150}	a	295	13.3	9.5	22.9	-.009
	b	6.8	7.4	6.7	7.1	-1.1
CFY_{31-150}	a	281	16.4	10.3	26.7	-.025
	b	6.5	9.1	7.2	8.3	-3.1
CPY_{31-150}	a	276	13.9	10.2	24.1	-.007
	b	6.4	7.7	7.1	7.5	-.89
$CFPY_{31-150}$	a	287	15.8	10.6	26.3	-.017
	b	6.6	8.8	7.4	8.1	-2.2
$CPOF\%_{31-150}$	a	-45.1	-8.0	-1.2	-9.1	.046
	b	-1.0	-4.4	-.83	-2.8	5.8

a = response in actual units of measurement (Kg), except ratios.

b = response (a) per generation expressed as a percentage of the overall mean of the trait respectively, while, the corresponding, % due selection for CPY_{61-150} resulted in -.06, 0.3, 0.4 and 0.3 % for MY, FY, PY and FPY, respectively. Also, selection for $CFPY_{61-150}$ accompanied by – 0.4, 1.3, 0.5 and 0.9% compared to selection for CMY_{61-150} as calculated from Table 4. Therefore, it could be concluded that genetic improvement in MYT could be based on $CMYT_{61-150}$ (especially CMY_{61-150} and CFY_{61-150}). Such procedure will led to a decrease in generation interval and consequently increasing genetic gain per year.

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الاستجابة الأمثل للانتخاب الفردي لصفات إنتاج اللبن في ٣٠٥ يوم باستخدام أجزاء مختلفة من سجلات موسم الحليب الأول لأبقار الفلاكفيه

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استخدمت الدراسة سجلات الموسم الأول لإنتاج اللبن في عــامين متتــالين (١٩٩٠-١٩٩١) لأبقــار الفلاكفيه النمساوية ، شملت الصفات المدروسة كل من إنتاج اللبن والدهن والبروتين وإنتاج الدهــن والــبروتين معاً وكذلك نسبة إنتاج البروتين/إنتاج الدهن خلال ٣١-١٢٠ ، ٦١-١٥٠ و ٣١-١٥٠ يوم من الموسم وكذلــك ٣٠٥ يوم من الإدرار. اشتمل نموذج التحليل الاحصائى علي تأثير كل من توليفة سنه وموسم الوضــع (تــأثير ثابت) وتأثير كل من العمر عند الولادة والأيام المفتوحة والفترة من بداية يوم الاختبار الشــهري حتــى تــاريخ الولادة التالية (انحدار خطى) بالإضافة لتأثير الأب (تأثير عشوائى) علي كل الصفات المدروسة.

وتم حساب مكونات التباين والمعاملات الوراثية لهذه الصفات وحسبت معاملات الارتباط المختلفة بين السجل الكامل وكل جزء من السجل علي حدة. وفي النهاية تم حساب كمية التحسين المتوقعة باستخدام الانتخاب الفردي الغير المباشر لصفات إنتاج اللبن التراكمية للأجزاء المختلفة من السجل.

وتلخصت أهم النتائج المتحصل عليها فيما يلي:

١. معاملات الاختلاف تراوحت من ١٦,٥–١٨,٦ لصفات إنتاج اللبن عند ٣٠٥ يوم ومن ٢٠–٢٣% لصفات إنتاج اللبن التراكمية للأجزاء المختلفة من السجل بينما كان أقل من ذلك نسبة إنتاج البروتين/إنتاج الدهن حيث تراوحت من ٨–٩% للسجل الكامل والأجزاء المختلفة من السجل.
٢. تأثير كل من توليفة سنه وموسم الوضع والعمر عند الولادة معنوياً علي معظم الصفات المدروسة.
٣. تأثير الأيام المفتوحة معنوياً علي كل الصفات فيما عدا الإنتاج التراكمي للدهن عند ٣١–١٥٠ يوم من الموسم.
٤. تأثير الفترة من بداية أول يوم الاختبار حتى تاريخ الولادة التالية كان معنوياً علي كل الصفات التراكمية المدروسة لصفات إنتاج اللبن فيما عدا صفة إنتاج البروتين/إنتاج الدهن كنسبة مئوية عند ٣١–١٥٠ يوم من الموسم.
٥. تأثير الأب (الطلوقة) كان معنوياً جداً علي كل الصفات.
٦. قيم المكافئ الوراثي تراوحت من ٠,٤٨ –٠,٥٩ لصفات إنتاج اللبن في ٣٠٥ يوم ومن ٠,٣٢–٠,٣٧ ، ٠,٣٧ – ٠,٤٣ ، ٠,٣٥ – ٠,٤٢ لصفات إنتاج اللبن التراكمية عند ٣١–١٢٠ ، ٦١–١٥٠ و ٣١–١٥٠ يوم من الموسم علي الترتيب.
٧. قيم معاملات الارتباط الوراثي والمظهري بين صفات محصول إنتاج اللبن للسجل الكامل وكل جزء من السجل علي حدة كانت عالية وموجبة وبلغت معاملات الارتباط الوراثي من ٠,٧٩ –٠,٩٧ بين صفات محصول اللبن لل٣٠٥ وبين محصول ٣١–١٢٠، ٦١–١٥٠ و ٣١–١٥٠ يوم من الموسم. معاملات الارتباط المظهري قد تراوحت من ٠,٧٤–٠,٨٤ ومن ٠,٧٨–٠,٨٩ بين صفات محصول اللبن في ٣٠٥ يوم و ٣١–١٢٠ يوم وكلا من ٦١–١٥٠ و ٣١–١٥٠ يوم من الموسم علي الترتيب.
٨. قيم التحسين المتوقع باستخدام الانتخاب الفردي (٣٠٥ يوم) لصفات كميات اللبن عند ٦١–١٥٠ يوم قد حققت اعلي قيمة واعلي عائد وراثي مقارنة بالأجزاء الأخرى من السجل.
٩. أوضحت النتائج انه يمكن إجراء التحسين الوراثي المبكر في صفات كمية اللبن والدهن علي أساس الانتخاب لجزء من السجل لهذه الصفات عند ٦١–١٥٠ يوم من الإدرار خلال الموسم الأول.