Genetic parameter estimates in the South African Jersey breed

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Data obtained from the INTERGIS for Jersey breeders participating in the National Dairy Cattle Performance and Progeny Testing Scheme were analysed. The registered and grade records commenced in test year 1977 through 1992 (incomplete) and consisting of lactations between 240 and 300 days, were considered as normal completed records. Five production traits were evaluated, ie. milk, fat and protein yields and fat and protein percentages for first and second lactation records. Variance components and resulting heritability estimates were obtained by DFREML procedures using 45 240 first and 27 414 second lactation records. The heritability estimates for first lactation milk, fat and protein yields and fat and protein percentages were 0.35, 0.35, 0.34, 0.57 and 0.58 respectively. Corresponding estimates for second lactation traits were 0.29, 0.28, 0.28, 0.53 and 0.56. Repeatability estimates, calculated as interclass correlations when only two records per animal are available, were 0.73, 0.72, 0.74, 0.71 and 0.74, respectively, for the production traits considered. The heritability estimates were in agreement with literature results, indicating that selection for all five traits would be effective. It was suggested that an increase in environmental effects may be partly responsible for lower estimates of heritability of second lactation traits. The results indicate that selection of dairy bulls can be based on first parity records.

Data verkry vanaf die INTERGIS vir Jersey-telers wat deelneem aan die Nasionale Melkbeesprestasie- en Nageslagtoetsskema is ontleed. Geregistreerde en graadrekords tussen die jare 1977 en 1992 (onvolledig) is verwerk. Laktasierekords tussen 240 en 300 dae is beskou as normale, voltooide rekords. Vyf produksie-eienskappe naamlik melk-, bottervet- en proteïenproduksie asook bottervet- en proteïenpersentasie vir eerste en tweede laktasies, is geëvalueer. Variansie-komponente en voortvloeiende oorerflikheidsberamings is deur middel van DFREML prosedures beraam met 45 240 eerste en 27 414 tweede laktasierekords. Die oorerflikheidsberamings by eerste laktasierekords vir melk-, bottervet- en proteïenproduksie en bottervet- en proteïenpersentasie was 0.35, 0.35, 0.34, 0.57 en 0.58 onderskeidelik. By tweede laktasierekords was die beramings 0.29, 0.28, 0.28, 0.53 en 0.56 onderskeidelik. Herhaalbaarheidsberamings, bereken as interklas-korrelasies wanneer slegs twee rekords per dier beskikbaar is, was 0.73, 0.72, 0.74, 0.71 en 0.74 onderskeidelik. Die oorerflikheidsberamings is in ooreenstemming met gepubliseerde resultate, wat aandui dat seleksie vir al vyf eienskappe effektief sal wees. Die teenwoordigheid van konstante genetiese effekte en verhoogde omgewingseffekte mag gedeeltelik verantwoordelik wees vir laer oorerflikheidsberamings by tweede laktasierekords. Die resultaat is 'n aanduiding dat doeltreffende seleksie vir suiwelbulle gebaseer kan word op eerste laktasierekords.

Keywords: Jersey, production traits, variance components, heritability estimates.

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Introduction

Dairy cattle improvement depends largely on the emphasis placed on increasing production by selection. The main aim of selection is usually the improvement of production traits and this is to a large extent dependent on the effective utilisation of the additive genetic variance.

Genetic parameters are specific for a particular population. Reliable estimates of (co)variance components and resulting heritabilities of the traits for the Jersey breed in South Africa are therefore required to evaluate breeding programmes as well as to predict breeding values specific to this population. Breeding plans for dairy cattle may also have to consider repeated performance of the animal i.e., the potential for more than one lactation per cow.

Accurate estimates of these parameters are important for efficient ranking of breeding animals in the herd to choose genetically superior cows to produce sires to be progeny tested. If it is assumed that these parameters are the same for all lactations when they are in fact different, genetic improvement would be decreased by introducing errors in the selection of these cows (Butcher & Freeman, 1968).

Materials and methods

Data description

The data set consisted of 134079 grade and registered Jersey records relating to animals born from 1975 to 1990. The data was obtained from the integrated registration and genetic information system (INTERGIS) for Jersey breeders participating in the National Dairy Cattle Performance and Progeny Testing Scheme (NDCPTS). After editing, data used for the estimation of variance components and heritabilities consisted of 45240 first lactation and 27414 second lactation records. Only second lactation records of animals with completed first lactation records were included. This is in line with the recommendations of Tong et.al., (1979). It was decided to limit the study to the first two lactations as certain reports indicate that first lactation records supply a somewhat more accurate estimate of the breeding value of cows than second or third (Weller, 1986). This is supported by American results where traits based on first lactation records have a higher heritability estimate than those based on second or third lactations. Traits based on second and third lactation records are almost equally heritable as reported by Molinuevo & Lush (1965).

The initial 134 079 records were divided according to the five recognised regions in South Africa prior to April, 1994 as indicated by Hallowell (1994). Although the possibility exists that vast differences can occur among regions, this was taken into account by the inclusion of herd as an effect as reported by Rege (1991) and Hallowell (1994). During the period 1977 to 1992, a total of 1 020 herds participated in the NDCPTS. A large number (481 or 47%) of herds in the study had less than 11 daughter records, a tendency also reported by Hallowell (1994) in an evaluation of the South African Ayrshire. Furthermore, 613 (60%) of herds had less than 21 records and 926 (91%) of herds less than 131 records regarding first lactations.

Calvings were distributed throughout the year. Month of calving was therefore initially included on first parity records, but after testing for contrasts, two distinct seasons were defined: Season 1 from March to August and Season 2 from September to February of the consecutive year. These seasons were concatenated into year-season which was subsequently included as a fixed effect for both lactations (Boldman & Freeman, 1990; Sadek & Freeman, 1992). To account for the possibility of different treatments between registered and grade animals, status was included as effect in the models (Wiggans et al., 1988).

Although the animals milked three times daily are only a small proportion of the total numbers in the study, an increase was observed in the latter stage (1988–1992) of the data set. Neverthe-

less, a vast difference in milk production exists between animals milked two and three times daily, and therefore, milking frequency was included as an effect. In most studies reported, records were corrected to a twice daily milking and times milked was not included as an effect (Mirande & Van Vleck, 1985; Hermas *et al.*, 1987; Boldman & Freeman, 1990).

Age at calving in various analyses were grouped (de Jager & Kennedy, 1987; Chauhan & Hayes, 1991; Rege, 1991) and included as a fixed effect or corrected to a 305-day mature equivalent (Boldman & Freeman, 1990; Harris *et al.*, 1992). Age at calving was included as a covariate, because the data used in the present study consisted of unadjusted records. Owing to limits set for this study, the age at first freshening was between 17 to 39 months. The average age at second calving was 39 months.

Acquiring records of uniform lactation length is nearly impossible. Discarding records that do not meet a minimum lactation length results in biased genetic evaluations (Norman *et al.*, 1985), especially when the animal model is used in estimating breeding values for both male and female animals. Standard practice has been to project/extend lactations of different length to a fixed length, either 300 or 305 days (Hargrove *et al.*, 1981; Mirande & Van Vleck, 1985; Hermas *et al.*, 1987). This practice results in minimum opportunity by an animal's owner to control information that is included in genetic evaluation. Most of the projections of lactations are dependent on the milk production of the last sample-day (Wiggans & Powell, 1980). This information was not available for this study. All unadjusted lactations between 240 and 300 days were considered as normal completed records.

To enable the calculation of inter-calving period, which was included as an effect, second lactations were limited to those animals which also had a first lactation. The mean inter-calving period between first and second parities was 392 days, which is below the national mean of 401 days published in the results of the National Dairy Cattle Performance and Progeny Testing Scheme (1992/ 1993). Days dry is highly correlated with calving interval, which has not been found to be genetically correlated with yield, so correcting for calving interval will remove much of the variance due to days dry. Adjusting production records for days dry could adjust for potentially useful genetic variation and result in biased genetic evaluations (Schaeffer & Henderson, 1972; Sadek & Freeman, 1992). Animals with an inter-calving period exceeding 800 days were eliminated as recommended by Hallowell (1994).

Statistical analyses

An analysis of variance was performed on first and second parity records including the effects of year-season of calving, herd, status, times milked (fixed), age at calving, lactation length, inter-calving period (linear and quadratic regressions), sires (absorbed) as well as all two-way interactions on milk, fat and protein yields and fat and protein percentages using the SAS GLM (1988) procedure. Effects contributing significantly at a 1% level were subsequently included as fixed effects in the mixed model analyses.

A summary of the effects included in the final models on first lactation traits is presented in Table 1.

Taking the significant effects shown in Table 1 into consideration model one (the saturated model) for first lactations for milk, fat and protein yield was fitted as:

$$Y_{ijklmn} = \mu + YS_i + h_j + t_k + m_l + b_1A + b_2A^2 + b_3L + S_m + e_{ijklmn}$$

Y_{ijklmn} = an observation on the trait considered (milk, fat or protein yield),
μ = overall mean,

Table 1 Effects included in models considered for the different traits — First Lactation

Effect	Milk (kg)	Fat (kg)	Prot. (kg)	Fat (%)	Prot. (%)
			Trait		
Year-season of calving	+	+	+	+	+
Herd	+	+	+	+	+
Status	+	+	+	–	–
Times milked	+	+	+	–	–
Age at calving – linear	+	+	+	–	+
Age at calving – quadratic	+	+	+	–	–
Lactation length – linear	+	+	+	–	–
Lactation length – quadratic	–	–	—	–	–
Model	One	One	One	Two	Three

(+) Included in model; (–) Excluded from model

YS_i = the fixed effect of the i-th year-season of calving (i = 1, ... ,33),

h_j = the fixed effect of the j-th herd (j = 1, ... ,539),

t_k = the fixed effect of the k-th status (k = 1 for registered and 2 for grade),

m_l = the fixed effect of the l-th times milked pr day (1 = 2,3),

b_1A = linear regression of the appropriate deviation from the mean on age at first calving,

b_2A_2 = quadratic regression of the appropriate deviation from the mean on age at first calving,

b_3L = linear regression of the appropriate deviation from the mean on lactation length of first parity records,

S_m = random effect of the m-th sire and

e_{ijklmn} = random error associated with each record.

The model fitted for second lactation production traits was the same as that for first lactation traits, except that the linear and quadratic regressions of inter-calving period were also included. Linear regressions of age at calving and lactation length were also included for second lactation percentage traits, together with quadratic regressions of age at calving and lactation length for protein percentage.

Variance and heritability estimates were obtained by means of the derivative-free restricted maximum likelihood (DFREML) programme developed by Meyer (1989). For the analysis, considering production traits in first and second lactations, the following model was fitted:

$y = Xb + Za + e$

where:

y = a vector of observations of production traits on first or second lactation records;

b = a known vector of significant fixed effects and covariables;

a = a vector of additive genetic values of individual animals;

e = a vector of unknown residual effects and

X and Z = known incidence matrices relating observations to effects.

All available pedigree information was included in the analysis. Ignoring relationships that exist

Table 2 Variance components and estimates of heritability for first and second lactations

Parameter	Milk (kg)	Fat (kg)	Prot. (kg)	Fat (%)	Prot. (%)
First lactation					
σ_a^2	151088	293.88	191.15	0.1034	0.0269
σ_e^2	275135	534.97	373.51	0.0779	0.0199
σ_p^2	426223	828.85	564.66	0.1813	0.0468
h_2	0.3545	0.3546	0.3385	0.5706	0.5756
S.E.	0.0112	0.0108	0.0110	0.0116	0.0118
Second lactation					
σ_a^2	164898	316.28	209.44	0.1061	0.0291
σ_e^2	395545	808.26	543.80	0.0947	0.0224
σ_p^2	560443	1124.54	753.24	0.2008	0.0515
h_2	0.2942	0.2813	0.2781	0.5293	0.5647
S.E.	0.0148	0.0142	0.0146	0.0161	0.0160

σ_a^2 = additive variance; σ_e^2 = error variance; σ_p^2 = phenotypic variance; h_2 = heritability estimates; S.E. = standard error.

will result in a reduction in REML estimates of genetic (co)variance (Dong *et al.*, 1988). Repeatability estimates for the production traits were calculated as interclass correlations when only two records per animal were available (Turner & Young, 1969).

Results and discussion

The additive and residual variances as well as heritability estimates are presented in Table 2.

Additive variance was relatively constant across lactations for yield traits as well as percentage traits. Perhaps additive variance is constant for both first and later records, but environmental variation increases for later parities (Cassell & McDaniel, 1983).

The error variance increased steadily with lactation for yield traits, but in general did not change appreciably for percentage traits as reported previously by Tong *et al.*, (1979) and Hallowell (1994). These increases in error variance in later lactations may be attributed to additional sources of variation, such as dry period and days dry which do not influence first lactation (and are not included in the operational models for second lactation). Jones & Goddard (1990) assumed later lactations could have a higher error variance partly because of preferential treatment.

Heritability estimates for percentage traits were considerably higher than for yield traits with protein percentage being the highest. However, heritability estimates decreased for all yield traits and for percentage traits with succeeding lactation. These estimates were consistent with those reported by Molinuevo & Lush (1965), Wickham & Henderson (1976), Powell *et al.*, (1981) and Rege (1991). Heritability estimates of first and second lactations for protein followed trends in fat as previously reported by Tong *et al.*, (1979) and Hallowell (1994). Studies using the animal model, which considers all known relationships, indicate higher estimates of heritability compared to the sire model which neglects female relationships (Van Vleck *et al.*, 1987; Visscher & Thompson, 1990).

Generally, heritability estimates for the first lactation are higher than for the second lactation. An increase in environmental effects on second lactations would lower estimates of heritability of sec-

ond lactation traits. Environmental factors negatively influencing udder health, like mastitis, ace-
tonemia and minor injuries, add to the variation in second and later lactations (Butcher & Freeman,
1968; Cassell & McDaniel, 1983). Differences in dry period, as a source of variation on second lac-
tation, might also partially account for lower heritability estimates of later parities (Molinuevo &
Lush, 1965).

Traditional approaches to dairy sire evaluation for yield have centered on measurements of yield
on first lactation. An implicit assumption in this approach is that the genetic correlation between
first and later lactation yield is close to unity (Cassell & McDaniel, 1983). A number of studies
reported genetic correlations between first and second lactations ranging from 0.75 to 0.92 with
most estimates around 0.85 (Tong *et al.*, 1981; Powell *et al.*, 1981). Repeatability estimates in the
present study for milk, fat, and protein yields, and fat and protein percentages were 0.73, 0.72,
0.74, 0.71 and 0.74, respectively, which confirm earlier practices and indicate that selection on first
parity records is adequate for retaining animals which consistently perform well in subsequent lac-
tations.

Conclusions

Heritability estimates obtained are in agreement with results reported in the literature, indicating
that selection for all five traits would be effective. Although heritability estimates for percentage
traits are higher than for yield traits, emphasis should be placed on direct selection for yield traits,
particularly protein yield. Selection for yield could, however, lower the percentages of all compo-
nents, since other studies indicate a negative correlation between yield and percentage traits
(Welper & Freeman, 1992). An increase in environmental effects may be partly responsible for
lower estimates of heritability of second lactations. The results indicate that sufficient selection of
dairy bulls can be based on the first parity records. Owing to the long generation interval experi-
enced in dairy cattle, it would be beneficial to base selection on first parity records. This does not
mean that as later lactation records become available they should not be utilized.

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