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EDITORIAL

The unveiling of the complete human genome in the twenty first century marks the second major landmark in genetics research, almost 50 years after the revolutionary unveiling of the DNA structure. While a lot of attention has been focused on the impact of genetics on human health, one of the biggest beneficiaries and players in gene science is agriculture. The impact of genetics in the agricultural field is just one of the areas highlighted in this issue of the journal.

Knowledge of genetic and phenotypic parameters in the estimation of breeding values in cattle is highlighted in one of the papers in the current issue. At the same time and because of this knowledge, the paper highlights and reaffirms the importance of non-genetic environmental factors in this type of work.

The paper on the "Role of the hollow cathode cavity on the stability of multigap pseudospark discharge" is particularly interesting for a number of reasons. It represents, once more, the diversity of the journal. It is also a good example of viable collaborative work between the University of Tsinghua, in Beijing, China and the University of Zimbabwe. Lastly, while the journal focuses on applied science in Southern Africa, relevant work from other parts of the world is accepted.

The other articles in this issue cover goat production in semi-arid Zimbabwe; the effects of organic and inorganic nitrogen fertilizer on maize nitrogen uptake and nitrate leaching; water delivery in an irrigation setting in Zimbabwe and maize seed orientation in the substrate and its influence on germination, seedling structure and transmission.

The editorial team is once more thankful to all the contributors to the current issue for supporting the *Journal of Applied Science in Southern Africa*.

Professor C. F. B. NHACHI
Editor-in-Chief

Genetic and phenotypic parameters for milk protein yields in Holstein cattle

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Knowledge of genetic parameters is of paramount importance in designing sound breeding programmes. Genetic and phenotypic parameters are needed in the estimation of breeding values. The objectives of this study were to: estimate genetic parameters for milk, fat and protein yields; determine genetic and phenotypic correlations among these production traits and determine if genetic parameters are the same within lactations in Holstein cattle. A total of 17 598 Holstein 305 day milk records from the Zimbabwe Dairy Services Association were used to estimate heritabilities, variances, covariances and genetic and phenotypic correlations among 305 day yields of milk, fat and protein. The cows used were those that calved between 1994 and 1997 inclusive. This study was done in 1998. A FORTRAN iterative algorithm of REML — AIREML — (Gilmour, 1995) was used for the analyses. The animal model contained herd, year of calving, calving month, dry period, calving interval, milking frequency and animal effects. Heritability estimates for 305 day milk yield were 0.34 ± 0.04 ; 0.22 ± 0.06 ; 0.17 ± 0.05 ; 0.10 ± 0.05 and 0.09 ± 0.04 for 1st, 2nd, 3rd, 4th and 5th and later lactations respectively. For fat yield corresponding estimates were 0.34 ± 0.05 ; 0.33 ± 0.07 ; 0.17 ± 0.05 ; 0.09 ± 0.06 and 0.10 ± 0.06 respectively. Estimates for protein yield were 0.22 ± 0.04 ; 0.25 ± 0.07 ; 0.19 ± 0.06 ; 0.07 ± 0.05 and 0.12 ± 0.05 for the respective lactations. Phenotypic correlations between milk and fat, milk and protein and fat and protein in 1st parity were 0.92, 0.95 and 0.92 respectively and for 2nd, 3rd, 4th and 5th and later parities they were 0.89, 0.97 and 0.92; 0.92, 0.98 and 0.94; 0.92, 0.98 and 0.94 and 0.93, 0.98 and 0.95 respectively. Genetic correlations were 0.92, 0.92 and 0.88; 0.86, 0.93 and 0.88; 0.83, 0.93 and 0.93; 0.46, 0.88 and 0.58; and 0.68, 0.89 and 0.83 for the respective lactations.

Keywords: Protein, genetic parameters, Holstein.

Introduction

The Holstein breed is the most common dairy breed, constituting up to 85 percent of the national dairy herd. The remainder is taken up by Jerseys (13 percent) and cross breeds (Makuza, 1995). The cross breeds are primarily sired by dual-purpose breeds (Red Dane and Simmentaler) with a few sired by Holstein and Ayrshire. As

noted by Makuza (1995) in Zimbabwe there is a trend towards upgrading of native stock through cross breeding. Of late, the use of top quality semen from North America and Europe for genetic improvement of dairy breeds has also increased. Given that feed costs account for as much as 60 to 75 percent of total production costs, the feeding system hinges upon the ability to produce home-grown feeds economically. Typically only high protein concentrates (cottonseed, soyabean meals) are purchased with maize being grown for silage and grain making up the main energy source of the concentrate mix. Lucerne and soyabean hays are used as roughage sources in most zero-grazing systems.

The main purpose of milk recording is to enable performance evaluation of dairy cattle and improvement of milk production traits through a combination of prudent selection and management intervention. In order to design efficient and appropriate breeding programmes for any livestock population, genetic parameters are needed. These include heritabilities, repeatabilities, genetic and phenotypic (co)variances and correlations. Such parameters provide an indication of the potential for direct genetic or correlated response to selection. Heritability estimates are also needed to predict breeding values. It should be noted that genetic parameters such as heritabilities are population and trait specific. As such accurate values are needed in order to accurately predict the response expected from various selection schemes of various populations.

In Zimbabwe, genetic and phenotypic parameters have been estimated for the Holstein-Friesian breed (Mpofu, 1986; Makuza, 1988; Makuza, 1995; Muchenje, 1996) for milk yield, fat-corrected milk (FCM), fat yield and fat percent. However, no information is available on milk protein. This is partly attributable to the mode of payment which emphasises total milk volume delivered and fat percent. This explains why traditionally selection has focused on milk production, with type traits only coming in recently. The other reason for absence of protein parameters is that milk protein testing equipment was acquired only in 1993 and recording of protein began in earnest in 1994. The major thrust of this study was, therefore, to estimate genetic and phenotypic parameters for milk protein. For purposes of completeness and comparison, milk and fat yields were also included in the study.

Materials and Methods

Data

The data comprised 17 598 Holstein lactation milk records supplied by the Zimbabwe Dairy Services Association (ZDSA, formerly Zimbabwe Dairy Herd Improvement Association, ZDHIA) and consisted of records of Holstein cows that calved from 1994 through to 1997.

Data Edits

Those records for which the following parameters were unknown were deleted: age at calving; date of calving; herd code; lactation milk yield; fat yield; protein yield and parentage. In addition, only sires with at least three daughters were

considered. This was done to improve estimation of the sires' breeding values. The edits were described in detail by Mandizha (1998).

Analyses

After the preliminary analyses in SAS (SAS, 1994), the Average Information Restricted Maximum Likelihood (AIREML) FORTRAN iterative algorithm of Gilmour (1995) was used to estimate variances, repeatabilities, correlations and heritabilities. This method employs sparse matrix techniques to calculate those elements of the inverse of the coefficient matrix required for the first derivatives of the likelihood function. It has become the preferred method of analysis for animal breeding data because it accounts for the loss in degrees of freedom due to fixed effects in the model and is effective in reducing selection bias.

Residuals and fitted values for random effects can be used to derive additional right-hand sides for which the mixed model equations can be repeatedly solved in turn to yield an average of the observed and expected second derivatives of the likelihood function. Convergence with this method generally occurs within less than 10 iterations. In this study the number of iterations for each evaluation ranged from 3 to 7. The convergence criterion, which is the difference between estimates at each successive iteration, was 0.001.

The Animal Model

The following model was used for analysis:

$$Y_{ijklmno} = \mu + H_i + YR_j + MO_k + Cl_l + DD_m + Animal_n + \epsilon_{ijklmno}$$

where: $Y_{ijklmno}$ = performance observation on the trait considered for each cow;

μ = overall mean (constant);

H_i = fixed effect of the i^{th} herd; $i = 1, 2, \dots, 71$;

YR_j = fixed effect of the j^{th} year of calving; $j = 1994, 1995, 1996, 1997$;

MO_k = fixed effect of the k^{th} month of calving; $k = \text{January}, \dots, \text{December}$;

Cl_l = fixed effect of the l^{th} calving interval; $l = 0, 250, 300, \dots, 600$;

DD_m = fixed effect of n^{th} days dry; $m = 0, 15, \dots, 135$;

$Animal_n$ = n^{th} random additive genetic effects pertaining to cows, sires and * dams;

$\epsilon_{ijklmno}$ = random residual error associated with the observation, $ijklmno$
 $\sim N(0, I\sigma^2_e)$.

For first parity, calving interval and days dry were excluded because these values were just the same (zero) since the cows had calved for the first time. Parity was also excluded from the animal model because the analyses were done within parity. For the same reason, permanent environmental effects were not included since there were no repeat records within parity.

The inverse of the matrix of additive genetic relationships was added to improve linkage between sires and improve the accuracy and precision of the estimates. The factors that affect milk, fat and protein yields were assumed to be the same. In matrix notation, the model was as follows:

$$Y = Xb + Zu + e$$

where: **Y** is the vector of observations for the trait (milk, protein or fat yield);
b is a known vector ($n \times p$) of fixed effects of herd, year of calving, month of calving, calving interval, dry period and milking frequency;
u is a known vector ($n \times q$) of random additive effects pertaining to animals, $u \sim N(0, A\sigma_a^2)$;
X and **Z** are known incidence matrices of order $n \times p$ and $n \times q$ respectively. They are for fixed and random effects and relate the elements in **b**, **u** to **Y** and **Z** respectively.
e is a vector of random residuals, $e \sim N(0, I\sigma_e^2)$.

Assumptions

The following assumptions were made:

$$E \begin{matrix} Y \\ \mu \\ e \end{matrix} = \begin{matrix} Xb \\ 0 \\ 0 \end{matrix}$$

and

$$V \begin{matrix} Y \\ \mu \\ e \end{matrix} = \begin{matrix} ZGZ' & 0 & 0 \\ 0 & A\sigma_a^2 & 0 \\ 0 & 0 & R \end{matrix}$$

The Mixed Model Equations (MME) for the BLUE estimable functions of **b** and for BLUP of **u** are:

$$\begin{matrix} X'R^{-1}X & X'R^{-1}Z & b & X'R^{-1}Y \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} & u & Z'R^{-1}Y \end{matrix}$$

Matrix **G** is $A * G_0$ where **A** is a matrix of additive genetic relationships; and G_0 is a square matrix with genetic covariances between traits.

First and later lactation models

Days dry and calving interval were excluded in the **Xb** component for first lactation cows. This is because these animals have not yet had any previous dry period nor calving interval, hence corresponding values for these would be zero for all first lactation cows.

Number of lactations

It has been established that precision of estimates is increased by including more than first lactation but the extent of improvement diminishes with each additional record (Dommerholt *et al.*, 1980). In addition, Dommerholt, *et al.*, (1980) found that there was a computational advantage in restricting cow records to the first three. Hill and Swanson (1983) have reported the use of five lactations in cow evaluations in Zimbabwe. The use of all lactations compared with that of first lactations only was found to increase genetic progress per year due to selection (Ufford, *et al.*, 1979). In addition, because first lactations are a subset of all lactations, prediction error variances will be smaller when all records are used. Nonetheless, incorrect age factors could cause bias when records from all lactations are used because young sires could have a disadvantage in the proportion of first lactation heifers included in their evaluation. Culling of cows based on their records will cause bias if variance components are incorrect (Henderson, 1975).

In this study 1st, 2nd, 3rd, 4th and 5th and later lactation records were studied to establish any possible trends.

First lactation records have no repeatability estimate hence lead to reduced accuracy. First lactation cows are not yet exposed to a lot of environmental forces with the result that environmental variation in these cows tends to be smaller than the same variation in multiparous cows (Muchenje, 1996). On the same score, total phenotypic variation also tends to be smaller in first lactation cows than cows in other lactation groups.

Results

Heritability estimates are shown in Table 1. For the first two lactations heritabilities are highest for fat yield. Lactation 4 has the lowest heritability for fat yield. Milk is slightly more heritable than protein for lactation 1. However, for lactations 3 and above there seems to be no differences in heritabilities for milk, fat and protein yields. Table 2 shows the estimated breeding values for protein yield for the top and bottom 10 sires. The estimation of breeding values ranged from -150.9 to 48.6 whilst the sire with the highest number of progeny had 201 offspring. Genetic and phenotypic correlations between milk and fat, milk and protein and fat and protein yields are shown in Table 3. Milk and protein are positively strongly correlated genetically and phenotypically. The lowest genetic correlations were between milk and fat at 0.46.

Table 1: Lactation heritabilities for the production.

Traits	Lactation				
	1	2	3	4	5+
Milk	0.34 ± 0.04	0.22 ± 0.06	0.17 ± 0.05	0.10 ± 0.05	0.09 ± 0.040
Fat	0.34 ± 0.05	0.33 ± 0.07	0.17 ± 0.05	0.09 ± 0.06	0.10 ± 0.060
Protein	0.22 ± 0.04	0.25 ± 0.07	0.19 ± 0.06	0.07 ± 0.05	0.12 ± 0.002

Table 2: Estimated breeding values (EBVs) for the top 10 and bottom 10 sires for protein yield in first lactation.

Sire ID	EBV	No. of progeny	Sire ID	EBV	No. of progeny
713073	48.6	15	718056	-41.6	48
701092	48.2	46	707066	-45.1	80
719094	46.6	43	720046	-45.6	4
702072	46.6	40	716058	-50.3	3
710028	46.4	43	715017	-53.7	32
705037	45.0	10	702098	-54.6	27
702080	43.8	143	708049	-71.6	6
701072	42.6	201	708052	-80.3	7
708045	42.6	28	719073	-103.2	19
718075	42.4	74	704060	-150.9	22

Table 3: Genetic (below diagonal) and phenotypic correlations (above diagonal) for production traits in Holstein cattle.

Parity		Traits		
		Milk	Fat	Protein
1	Milk		0.92	0.95
	Fat	0.92		0.92
	Protein	0.92	0.88	
2	Milk		0.89	0.97
	Fat	0.86		0.92
	Protein	0.93	0.88	
3	Milk		0.92	0.98
	Fat	0.83		0.94
	Protein	0.93	0.93	
4	Milk		0.92	0.98
	Fat	0.46		0.94
	Protein	0.88	0.58	
5 +	Milk		0.93	0.98
	Fat	0.68		0.95
	Protein	0.89	0.83	

Discussion

Heritabilities

Heritabilities for milk yield traits in the tropics have been reported to range from 0.03 to 0.64 (McDowell, 1972). Mao (1984) reported heritabilities for milk production in the range 0.15 to 0.40. The heritability estimates obtained in this study were

within the ranges found elsewhere in literature albeit somewhat lower. The most probable explanation for this is that local bulls are found mostly in non-recorded herds. Most semen sold by AI companies is from imported sires which have for a long time been subjected to intense selection for milk, fat and protein yields. Consequently, the low genetic variation and the resultant low heritabilities for these traits in Zimbabwe. Inclusion of local sires in the genetic evaluations might increase the genetic variation (hence heritabilities) for these production traits. Differences in heritabilities among authors may be due to differences in measurements, samples, population structures, data edits, models and/or estimation procedures. For instance, daughter-dam regression analysis are not as accurate as REML analyses since they tend to inflate parameter estimates due to maternal effects and the environmental covariance between daughter and dam. Estimates from this method have been found to increase with herd production level. Hence, estimates from countries with low production would be lower than those from countries with higher production levels (Makuza, 1995).

Literature genetic parameter estimates of different breeds also differ due to differences in population structures among breeds. Heritability estimates from first lactation records tend to be higher when compared to later lactations. This is because in first parity environmental factors like calving interval, previous dry period, days open and production level in previous lactation have not yet come into play. This results in reduced phenotypic variance thus leading to a higher proportion of additive to phenotypic variance. Lower heritability estimates for subsequent lactations could be due to the effect of numerous environmental factors or an increase in error variances. Powell, *et al.*, (1981) noted that heritabilities will decrease as an animal gets older. This could be due to senescence or the cumulative effects of injury and susceptibility to diseases like mastitis, ketosis, udder oedema and others (Cassell, *et al.*, 1983; Tong, *et al.*, 1979).

Van Vleck, *et al.*, (1988) using first lactation yields of New York Holstein cows, found heritabilities of 0.36, 0.35 and 0.33 for milk, fat and protein yields respectively. This is in close agreement to what was obtained for the same lactation group in the present study (Table 1).

Hallowell, *et al.*, (1998b) suggested that first lactation heritability estimates were higher than second lactation because not all of the non-genetic effects in second lactation are accounted for by the model (eg. management prior to calving). In addition, the lower subsequent heritabilities could be explained by production-based selection (Schutz, *et al.*, 1990b). This is a situation whereby animals are selected for production, and this results in a reduction in additive genetic variance, hence reducing heritability estimates in later parities.

Another possible explanation for the decrease in heritabilities is that yields in later lactations are caused partly by different genes from those affecting first lactations. The proportion of genetic control of first and later records differs or perhaps additive variance is constant for both first and later records, but environmental variation increases for later parities. Hence the most rapid genetic

progress should be made by selecting on the first two records, since heritabilities were largest. Selecting earlier will also lead to a shorter generation interval. A reduction in generation interval should increase genetic progress.

It has also been reported (Carabano, *et al.*, 1989) that inaccuracy of pedigree recording and management conditions may limit expression of genetic potential of superior cows.

Heritabilities of 0.54 (Banga, 1992); 0.25 (Ngwerume, 1994; Musani, *et al.*, 1997); 0.21 (Makamba, 1997) have been reported for milk yield in Zimbabwe and elsewhere. That obtained by Banga (1992) was slightly high possibly due to the estimation method used; namely Harvey's Least Squares Mixed Models. In addition, this was in Jersey cattle, and low selection pressure may also explain this higher value.

Low heritabilities (<0.10) imply that very little genetic gain would be made regardless of genetic evaluations and selection methods used, whereas medium to high heritabilities (0.25-0.50) and large additive genetic variances imply that high gains/progress can be achieved through direct selection. This is particularly true of production traits as opposed to reproductive traits (calving interval, age at calving, days dry) which have to be improved through better management. The estimates obtained in this study suggest the production traits would be amenable to improvement through selection.

Estimated breeding values

The EBVs show considerable variation which suggests that the Zimbabwean dairy industry could utilise local dams and sires with high genetic potential. The large variations in EBVs also entail a high scope for response to selection. There is thus adequate genetic variance to practise effective conventional selection programmes in the Zimbabwean dairy herd. Table 2 also indicates underutilisation of some superior quality sires. The probable explanation for this could be limited knowledge of the genetic make-up of some of the sires used.

Genetic and phenotypic correlations

The average phenotypic correlations for milk/fat, milk/protein and fat/protein were 0.75, 0.91 and 0.82 and the corresponding average genetic correlations were 0.92, 0.97 and 0.93. These correlations were generally high, especially in the first three lactations. Because of low heritability in later parities, the genetic correlations were found to be correspondingly lower. The positive correlations mean that an improvement in one of these traits will lead to an improvement in the other. This has been supported by the increase in all yield traits in the Zimbabwean milk-recorded population (MRS, 1991) primarily due to selection on milk yield. Working with Zimbabwean Jerseys, Banga (1992) also found a positive correlation between milk yield and fat yield. As has been widely observed elsewhere, Banga (1992) found negative genetic and phenotypic correlations between milk yield and fat percent. Selection for one of these traits therefore leads to a decline in the other. In Zimbabwe producers are paid for the total volume of milk delivered as well as on

fat percent but very little regard has been given to the latter trait. This has seen an increase in milk yield at the expense of fat percent, which has actually declined in milk-recorded herds (MRS, 1991).

Van Vleck and Dong (1988) reported that correlations between milk and protein tend to be more similar from study to study than between milk and fat. Using Holstein cows in New York, they found genetic correlations of 0.72 for milk and fat; 0.88 for milk and protein and 0.77 for fat and protein. Their corresponding phenotypic correlations were 0.81, 0.91 and 0.82, respectively. Schmidt, *et al.*, (1988) found genetic correlations between milk/fat, milk/protein and fat/protein to be 0.65, 0.80 and 0.75 respectively. Phenotypic correlations were 0.85, 0.95 and 0.90 respectively in that study.

Conclusions

The estimated genetic parameters were consistent with published estimates in the tropics. The heritability estimates were somewhat lower and correlations were higher than those generally found in the literature. Estimates of heritabilities are similar for fat and protein yield. Heritabilities decrease with age from first lactation onwards. This study, reaffirms the importance of non-genetic environmental factors. As such there must be a correction for systematic environmental effects. The various sources of information for breeding value estimation should be addressed with the appropriate genetic-economic weights. On-farm selection should continue and can be supplemented by use of imported semen from proven bulls and artificial insemination.

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