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INFLUENCE OF IMPORTED SIRES ON PRODUCTION
OF DAIRY HERDS IN ZIMBABWE

By
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ABSTRACT

INFLUENCE OF IMPORTED SIRES ON PRODUCTION OF DAIRY HERDS IN ZIMBABWE

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Records were obtained on 18,000 Zimbabwean Holstein cows that are registered with the Milk Recording Scheme. The Zimbabwean Holstein cows can be divided into two groups according to the source of sire, daughters of imported sires or of local sires. The imported sires originate either from North America or Britain. There are also three classes of cows: pedigree, appendix and grade.

SAS's GLM and an EM-REML programmes were used. Daughters of imported sires gave higher yields in milk, dollars and fat yield and higher heritabilities, genetic correlations, sire, residual and phenotypic variances throughout all the lactations.

Daughters of local sires had higher fat percentages and phenotypic correlations in all the four lactations.

Source x area interaction was not significant but class x area interaction was significant for yield traits in lactations one and four ($P < .05$).

To my mom Estina Ndakaziva and dad Jonisai Muvingi and my brothers Tarirai Vitalis and Jacob Chinonyiwabodo.

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INTRODUCTION

Animal breeding and genetics are major tools for improving performance in cattle and thus can contribute to increased income per animal. This is done by mating genetically superior sires to superior females. Therefore the main goal of a dairy producer's genetic improvement program should be to produce replacement females with the greatest possible genetic capability for making a profit. Fulfilling this goal requires strong, healthy cows that produce high levels of milk of desirable composition. Also, these cows must be able to stand the stress of high production through many lactations with a minimum of special treatment. This goal can be attained by combining the best of the genetic material presently in the herd, for economically important traits, with the best available germ plasm from outside the herd. For Zimbabwean herds this means purchasing genetically superior semen from bulls currently in artificial insemination units. In Zimbabwe, the goal of genetic improvement, at present, is focussing on increase milk yield and butterfat yield because dairymen are paid on the volume of milk and fat content, these being the most economically important traits. At present, pricing of milk to producers is based on yield of milk and percentage of milk fat. Thus, breeding goals in sire selection based on these two traits are consistent with the pricing system. In recent years emphasis on selection has been based on first lactation yield. Another interest was to look at

various aspects of yield in the subsequent lactations and the desire to assess imported versus native genetics. In practical animal breeding, information on more than one trait is often combined into an index to estimate aggregate breeding value. This is called multiple trait selection, which was used in this study to obtain better estimates of the fixed factors such as source, class, area and season and Best Linear Unbiased Predictors (BLUP) solutions. It should be noted, however, that BLUP can yield solutions for single or multiple-traits.

Milk Pricing in Zimbabwe

In Zimbabwe, in addition to the basic price which is based on the volume of milk produced, farmers are also paid according to the quality of their milk. This is known as the quality premium scheme, which is based on keeping quality, butterfat content, cell count, and presence of antibiotics or water. These tests are carried out and administered by Dairy Services and also the Dairy Marketing Board (D.M.B) (bulk tank samples) in the Ministry of Lands Agriculture and Rural Resettlement, while payment is made by the D.M.B also in the same Ministry. The D.M.B is required, by the Dairy Act, to buy milk from all licensed dairy producers provided it is of acceptable quality. Marketing, manufacturing and distribution of dairy products is the responsibility of the D.M.B , a statutory board within the Agricultural Marketing Authority (A.M.A), the government marketing agency. Basically the milk quality premium scheme is based on the following: bonus for good quality milk, deduction for poor quality milk and penalty for substandard milk. The payment for

butterfat percentage is a premium based on a differential payment for each .1 percent above or below the base price for 3.2 percent butterfat. The payment for Methylene Blue Test (clean milk production) is a premium or deduction of 1 percent of the basic price for every half hour deviation from the standard of 3 hours from October to April and 4 hours from May to September. The payment for the level of subclinical mastitis in a herd is 1 percent of the basic price for a geometric mean cell count less than 500,000 ml and 1 percent deduction for a geometric mean count greater than 1 million cells per ml. The antibiotics in milk and water in milk, which are the TTC test and Freezing point (F.P) tests respectively, their penalty is on a day's consignment. For these 2 tests there is a 20 percent basic price deduction for TTC or freezing point below standard and rejection of milk if its the first time or a 50 percent basic price deduction for TTC or freezing point below standard for second and subsequent times within a 90 day interval.

Gene Importation into Zimbabwe

Much of the genetic progress that has been made in the dairy industry has been due to the dissemination of superior genetic material by the A.I industry. McDowell (1972) stated that a majority of the cows and a major portion of semen exported from the U.S. and Canada goes to warm climatic regions of the world like Zimbabwe. About 90% of cows and 80% of semen exported from the U.S. and Canada have been Holstein due to their high production (Abubakar et al., 1986).

The United States Agency for International Development (U.S. A.I.D.) and Canadian International Development Agency (C.I.D.A.) have provided funds for the purchase of semen from proven artificial insemination (A.I.) sires. Semen has also been imported under a loan agreement from the United Kingdom.

The importance of the importation of semen (germ plasm) from top ranking sires throughout the world to improve the local genetic pool cannot be over-emphasised. The availability of proven imported semen has had a very marked effect on the overall genetic pool within the country and is clearly reflected in improved production trends. Milk deliveries by farmers to the Dairy Marketing Board (D.M.B.) have grown from 98 million litres in 1968 to 224,0 million litres in 1986/87 season. In 1987/88 season 236.8 million litres were delivered to the D.M.B. and in 1988/89 season they are projecting to deliver 263.8 million litres.

One need to note however that, production was relatively static during the 1970s with an average annual production of about 150 million litres. All the increase per cow can be attributable to improved management and genetics (use of superior sires and cows via frozen semen and and daughters of bull studs of frozen embryos are not yet in production).

A Brief History of A.I. in Zimbabwe

Artificial Insemination has catapulted genetic improvement to the extent where it is possible to improve milk production in any country drastically in a 10-15 year period, provided management is improved to meet the potential. Artificial Insemination (A.I.) began in Zimbabwe in

about 1959, using mainly local bulls with some from Britain, Canada and the United States of America. It was used mainly by pedigree breeders. It increased significantly in about 1982 when commercial dairymen became proficient in A.I. and American semen became very popular (John Tiffin, personal communication). Lately, however, with the acute shortage of foreign currency, importation of American semen has been severely curtailed. Fortunately, semen from the embryo transfer bulls (from frozen embryos imported a few years ago) has started to become available.

The Zimbabwe Herd Book(ZHB)

The Zimbabwe Herd Book (ZHB) is the sole registering agency in the country for pedigree and appendix livestock. It serves all recognised livestock breed societies, clubs, etc, which include 15 beef breeds and 4 major dairy breeds mainly Holsteins, Jerseys, Guernsey and Ayrshire. The ZHB plays an important role in that it ensures the maintenance of breed standards and provide pedigree information and thereby guarantees a supply of high quality bulls into the commercial sector. The average farm size of commercial farms is about 5, 000 acres and are highly mechanized and therefore their contribution to the gross domestic product is significant (Bourdillon, 1987).

The Milk Recording Scheme (M.R.S.)

The objectives of the Zimbabwe M.R.S. are a) To encourage and assist milk producers to record accurately the quantity and quality of milk

produced by their cows, together with such other information as will assist in the breeding and management of dairy cattle and in the production of milk, and b) To make proper use of milk records in investigating problems affecting milk production (Milk Recording Handbook, 1980). There are about 530 registered dairy producers who are members of the M.R.S.

The main purpose of keeping records in a dairy enterprise is to serve as an aid in culling of females and, to provide a basis for progeny testing for selection of sires. Milk recording schemes therefore enable the genetically superior bulls with good conformation scores to be selected. Accuracy in selection depends upon how well the phenotype reflects the genotype and this can be improved by keeping as many records as is economically practical. The M.R.S provides valuable information in evaluating milk production trends and dairy systems. The production of herds in M.R.S have tended to be much higher than the national average (Commercial Agriculture in Zimbabwe 1986/87 annual report). The average yield per cow per 300-day lactation on the milk recording scheme is about 4, 601 kgs. However, individual herds have averaged over 7, 000 kgs indicating a potential for genetic improvement in lactation yields. Data is not available on the national average of milk production of all cows in Zimbabwe.

Dairying in the Communal Areas

Since independence in 1980, the Government policy has encouraged the small-scale farm sector to play a more meaningful role in the production of milk. The small-scale farm sector consist of farms of national average

of about 200 acres and are partially mechanized compared to communal areas where arable land may be limited to as little as 5 acres per family, which must be used in perpetuity and are not mechanized and grazing is shared among many families (Bourdillon, 1987). In the communal areas, there are virtually no registered dairy or beef producers, but cooperatives are being started. In the small scale sector, the first cooperative is the Marirangwe scheme near Harare where about 25 farmers have started dairying on a commercial basis. Each member is milking his own cattle and delivering milk to a central collection depot which markets milk to the local community and sells the surplus to D.M.B. A similar project on a much bigger scale involving about 600 settler farmers is presently being set up in the Rusitu Valley near Chipinge. In the communal areas the first one is in Chikwaka near Harare.

Justification for the Study

Milk is one of the largest single sources of food from animals. Milk and milk products contribute protein, energy, vitamins, and minerals for humans. In terms of contribution to the agricultural industry in Zimbabwe, dairying contributes 6% of the total value of agricultural production compared to 19% by beef.

The overall genetic value of a cow is primarily determined by her lifetime performance. This includes both a high lactation yield and the ability to maintain this level of production over lactations. Semen importation by developing countries creates a major demand for foreign currency which is a major constraint to developing countries. Therefore

a study to assess the impact of gene importation through A.I would be appropriate for a country such as Zimbabwe which has been importing semen since about 1959 and has severe foreign currency constraints. This will give an insight and determine whether it is worthwhile or beneficial or not to continue importing genes.

The null hypothesis to be tested in this study is that the source of sire does not make a difference in production of their daughters.

Objectives

- 1) To measure genetic differences among sires that are domestic (locally-bred) and imported. Such measures of differences between sources of germ plasm include of milk yield, butterfat yield, fat percentage. And which group of sires is contributes to the generation of additional money to the country i.e., contributes to higher average daily production; more profit to the farmer; increase forex and be self-sufficient in milk and its products.
- 2) To determine whether there are any genotype by environment interactions i.e., which genotype is best suited for each environment/area. The two genotype categories are source of sire (North American and British versus Zimbabwean) and class of cow (Zimbabwean). The environments considered are the 4 regions/ areas. Do these sources of sires and classes of cows give different results in different areas, i.e., are the differences between source of germ plasm and class of cow (i.e., pedigree, appendix and grade) the same

across all areas/regions of the country or does it tend to differ in different areas.

- 3) To compute heritabilities, genetic and phenotypic and residual correlations between the traits.
- 4) To compare these genetic parameters from different sources of sires and for different lactations.

LITERATURE REVIEW

Research has shown that 75% of the variation in herd production is determined by animal health, feeding and management practices and 25% is due to genetics (Brackett et al., 1981). Through selection and improved management the milk production per cow corrected to 305 days on Michigan D.H.I.A test has increased from 14, 977 in 1977 to 17, 083 pounds in 1987. Similarly, butterfat yield increased from 558 kg to 630 kg in the same period. (Michigan D.H.I.A. 1987 annual report). Not all this improvement is due to selection but the selection practiced has caused a major improvement.

On a national level the annual increase in sire breeding values from 1970-1983 were 75 kg for Holsteins, 42 kg for Ayrshire, 84 kg for Brown Swiss, 58 kg for Guernseys, 78 kg for Jerseys and 76 kg for Milking Shorthorns. Annual trends of cow breeding values were 68-78 % of the sire trend (about 54 kg per year). Breeding values of Holstein sires for milk yield increased by 55 kg per year from 1970-1977 and 98 kg per year from 1977-1983 (Powell et al., 1985). Milk production increased from 6, 966 kg in an unselected group of cows at South Dakota State University to 7, 865 kg after three generations of selection, and milk fat increased from 238 kg to 270 kg for the respective groups (Volker and Ludens, 1982). Hollon et al. (1983) in a selection experiment reported that daughters of

selected A.I sires gave 502 kg of PDM (predicted difference milk) while the control group gave 49 kg.

Environmental variations in production traits vary from year to year depending on conditions such as the feed resources, climatic factors and the management ability of the dairy manager or farmer but genetic improvement is normally permanent and additive from year to year when it is due to selection. Therefore the area of genetics is the area we should emphasis in herd improvement. However, phenotypic variations due to environment are important because (1) they are not transmitted from parents to offspring, (2) they mask variations due to heredity, (3) the proper environment is necessary for an individual to reach its genetic potential, and (4) rapid improvements can be made in the efficiency of livestock production by supplying uniform and superior environmental conditions to breeding animals and those used for commercial production (Lasley, 1978).

Non-genetic (or environmental) factors that influence production

Herd effects

Herd environment is a major source of the variation in milk and butterfat yield between herds of the same breed due to the differences in the level of nutrition and management. Approximately 20-40 % of the total variance in lactation yield within the same breeding population is due to differences in the average yield of the herds over the years (Hancock, 1953). Baker and Robertson (1966) in the U.K found that herd component

is an important part of the total variation, being 20-30 % of the variance for British and 15-20 % for imported animals. The genetic variance between herds is 7 % of the total genetic variance (Robertson and Asker , 1951). Robertson and Mcarthur (1955) indicated that 12 % of the total variance between individual sires arose from differences between herds in which the bulls were born and raised. In first lactation records, herds accounted for 35-40 % of the variation in both age at calving and milk yield (Lee and Hickman, 1972). Lee (1976) found that herds accounted for 32.1 % of the variance in milk yield, 26.7 % of the variance in age at calving and 6.3 % of the covariance between them.

Year effects

Year and season contribute about 15% of the variation in herd production (U.S sire summaries, 1982). In India, Pakistan and Jamaica, year effects accounted for 30-38% of the total variance in milk yield (McDowell, 1983). The year-season effect contributes about 2% of the variation in first and second lactation milk yield as reported by Van Vleck et al., 1961, or less than 5% (Baker and Robertson, 1966).

Season (month of calving)

Climate influences the animal both directly and indirectly (through availability of feed supplies) in expressing its genetic ability for growth, production, and reproduction. Optimum milk yield and efficiency usually are obtained within the comfort zone of 5 C to 22 C (Sharma et

al., 1988). Below 5 C no appreciable declines in milk yield are noticed unless temperatures drop to - 15 C. Temperatures above 25 C result in declines in milk production due partially to heat-induced depression in feed intake (Sharma et al., 1988). Variance in lactation milk yield associated with temperature effects range from 3-10% (Nelson et al., 1969). Month of calving accounted for about 10% of the variation in first lactation yield within herds within years (Baker and Robertson, 1966). Cows calving in hot seasons (summer) produced less milk (due to summer stress) than those calving in the cool season (winter) (Miller, 1971). McDowell (1985) found that season of calving, days dry, days open and calving interval individually accounted for less than 5% of the variance in milk yield.

Age at first calving

The relationship between age at first calving and yield is curvilinear. Highest milk yield during the first lactation is obtained when the heifers freshen a little above 3 years of age, and decreases as the age at first calving increases beyond that age (Johansson, 1961). Age at first calving increases milk and fat yield: 992 kg and 36 kg at 21 versus 35 months of age respectively (Cue et al. 1987). Other work reports the optimum age at first calving is 25 months (Dadati et al., 1986). Simerl et al. (1980) reported that the optimum age at first parturition for total performance is 22.5 to 23.5 months. Age at first calving can have an influence on total performance. Generally, the differences in average yield between first and second lactation cows are

due to age, parity and culling. In the first lactation the effect of age at calving on milk yield is similar across herds, seasons, years and regions (Lee, 1974, Miller et al., 1970). Harville and Henderson (1966) found that on a within herd-year, sires account for 18% of the variance in age at first calving and from 5-9% of the variance in milk yield.

Age at calving

One of the major non-genetic sources of variation in lactation yield is age at calving, and thus adjustments of milk records for age differences have been widely practiced. Mature cows produce more milk than either younger or older cows. This is because the capacity of milk yield increases at a decreasing rate until body maturity is reached, and thereafter it decreases at an increasing rate with advancing age (Johansson and Hansson, 1940). The production ability of young cows is influenced not only by body development (age at calving) but also by the development of the udder, which does not reach its maximum productive capacity in the first but rather in the third or fourth lactation (Kruger, 1934, Johannsson and Hansson, 1940). The increase in milk and fat production over the first three or four lactations may also result from a cow's physiological development in general. Wada and Turner (1959) found that the content of DNA in the mammary glands of mice increases considerably from the first to the second lactation and that there is a slight increase from second to third lactation, indicating a corresponding increase in the number of secretory cells. The rate of increase in milk yield with age is dependent on the level of nutrition and management

(Johannson, 1961), but for second and later lactations, age effects differ between years and months of calving (Lee, 1973 and 1974). Wunder and McGilliard (1971) showed that three-year olds produced more milk than two-year olds, age being a more important source of variation than season. Lactation milk yield increased only 13- 15% with age, of which 80% of the change occurred from first to second lactation (McDowell, 1985). Miller, 1973 found variations in age account for somewhat less than 10% of the variation in milk records, while Smith and Legates (1962) found that 17% of the variance for milk and fat was attributable to age in 305-day milk and fat records. The age at which maximum production is reached is slightly different among breeds.

Days dry

Dias and Allaire (1982) reported that optimum number of days dry decreases as a cow ages and is dependent upon peak yield and total production during the previous lactation. The milk yield in the second and later lactations is influenced by the length of the preceeding dry period. Age and month of calving have been implicated to influence the length of the dry period. Later lactations are less affected by the dry period than the second lactation (Shaeffer and Henderson, 1972). High producing dairy cows tend to receive shorter dry periods than low producing cows and cows which survive for another lactation are those with shorter dry periods (Shaeffer and Henderson, 1972). For an individual cow the lactation yield increases with increasing length of the previous dry period up to 7 or 8 weeks, but further increase in length of the dry

period has has a decreasing effect on the yield in the following lactation (Johannson, 1961). This implies that the relationship between milk yield and days dry is non-linear. In practice it means that cows, which have long dry periods tend to have low persistency in milk production and are poor producers (Johannson, 1961). The optimum length of the dry period is 35-40 days (Johannson, 1961). For all lactations, 51-60 days is the point at which the rate of increase in subsequent lactation begins to decline for additional days dry (Dias and Allaire, 1982). Coppock et al. (1974) reported 31-60 days as the optimum number of days dry to maximize subsequent lactation production. Klein and Woodward (1943) showed that a dry period of 1-2 months was enough to allow maximum production. A dry period shorter than one month lowered production whereas a dry period longer than three months is not beneficial. Short dry periods significantly diminished milk production in the following lactation (Whilton et al., 1967). However, per lactation, older cows tended to have a longer previous dry period than younger cows (Shaeffer and Henderson, 1972). The genetic correlations of days dry with 305-day milk yield were estimated to be $-.18$, $-.41$ and $-.31$ for second, third and later lactations (Shaeffer and Henderson, 1972). Therefore the dry period does appear to contain a very small amount of genetic variation. There is a distinct negative correlation between the length of the dry period and the length of the interval between the next 2 calvings. A long dry period is generally followed by a short calving interval and vice versa. This is due to the fact that cows with long dry periods may have had breeding problems and did not calve at the season desired. Then they are bred earlier the next time in order to regain the lost time (Klein and

Woodward, 1943). Wilton, Burnside, and Rennie (1967) concluded that the effect of the previous dry period on subsequent milk production is largely environmental. The effects of days dry are largely environmental because heritability estimates for previous days dry were less than 7% which suggests that days dry are primarily a result of management and other environmental influences rather than due to large genetic component. Cows dry 60 to 69 days gave the most milk the following lactation whereas cows dry less than 40 days produced much less milk the next lactation (Funk et al., 1987)

Calving interval

Calving interval, the period between calvings, is one measure of breeding efficiency, although it cannot be used alone to describe a herd's breeding efficiency because it does not account for cows culled after failure to conceive (Bozworth et al., 1972). The milk yield is influenced by the length of the current and by the length of the preceding calving interval or service period (Johannson, 1961). Variations in the preceding calving interval exert the greatest influence, because maximum daily yield is influenced more than persistency. The magnitude of this effect depends on the age of the cow and the level of nutrition and management (Johannson, 1961). The average length of the calving interval is approximately 13 months. In Zimbabwe the average calving interval is about 12-13 months (Titterton, personal communication). The optimum length of the calving interval is between 12-14 months. Factors such as conception rate, high milk production, seasonal and environmental factors,

incidence of disease, age of the cow and service sire have been implicated in lengthened calving intervals (Slama et al., 1976). The primary factor affecting calving interval is longer intervals from parturition to first service (Bozworth et al., 1972). Touchberry et al. (1959) reported that interval to first service alone accounted for 16.8% of the variance of the interval from parturition to conception. In a study by Olds and Cooper (1970) where cows were bred 82+ 33 days after calving, reported that each day earlier, up to 35 days post-partum, shortened the calving interval by .9 day.

Length of a Lactation

Lactation is the period from calving to when a cow dries off. Total yield for ten months has been found to be approximately 87% as much as for 12 months (Gilmore, 1952). The effect is primarily one of number of days milked out but with decreased persistency in advancing lactation. The average daily yield is higher in short than in long lactations (Gilmore, 1952). However, some lactations are terminated/truncated before the desired time because of low persistency (Gilmore, 1952). The length of lactation has a fairly high correlation with lactation yield of about .50 for Holsteins (McDowell, 1972). Heritability for lactation length was .06 (Abubakar et al., 1986).

Genotype x Environment Interaction

Planning of breeding programmes in the tropics depends as much on the magnitude of G x E interactions as it does on the genetic parameters (Falconer, 1981). Interaction of genotype and environment hampers selection to the extent that it reduces accuracy in predicting from the phenotypic ranking of a series of genotypes in one environment what their ranking would be in other environments. When there is no genotype x environment interaction the phenotype can be partitioned into a genetic and environmental components, i.e., $P = G + E$. In the case where genotype x environment interaction occurs it becomes $P = G + E + I_{ge}$ where I_{ge} is the interaction between genotype and environment. Similarly, the variance components when interaction between genotypes and environments is present are $V_p = V_g + V_e + V_{ge}$. Any variance due to genotype X environment interaction according to Falconer (1981) should be regarded as being part of the environmental variance included in any estimate of V_e . The interaction between heredity and environment means that animals of a certain genotype may perform more satisfactorily in one environment than in another. If there is no interaction, then there is no change in rank of the genotypes in different environments. But, if there is significant interaction particular genotypes must be sought for particular environments (Falconer, 1981). For example the breed of cattle with the highest milk yield in temperate climates is unlikely also to have the highest yield in tropical climates (Falconer, 1981). Such interactions may cause decreased performance when a population selected under one environment enters a new environment, a regression that Dickerson in 1962

termed "genetic slippage". Genotype x environment interaction becomes very important if individuals of a particular population are to be reared under different conditions, e.g., a breed of livestock may be used by different farmers who treat it differently (Falconer, 1981).

Since 1950 genetic improvement has been the major reason for importing livestock from the temperate zone to the tropics (McDowell, 1972). If genotype x environment interactions are important, prospective parents should be evaluated and selected under the same conditions in which their offspring will be produced (Lasley, 1978). If these Genotype x environment interactions are very significant, tropical producers might better concentrate on selective breeding of native or indigenous stock. But on the other hand, if these interactions are small or non-existent, they would do well by gene importation to improve the genetic potential of their stock (McDowell, 1972). Economic variation will be the primary underlying factor in determining which type of animals will be most appropriate. There is not much experimental evidence of genotype x environment interaction for dairy cattle. This is because where environmental control is feasible, such as milk production or poultry production, G X E interactions are of minor importance (Pirchner, 1983). Evidence from the subtropical portion of Louisiana has shown that progeny of sires proven in the Northern U.S ranked in the same order in Louisiana herds as in the more temperate areas (McDowell, 1972). The ranking of sire progeny of U.S Holstein sires in Puerto Rico and Venezuela further confirm that sire x location effects are not important for Holsteins (McDowell, 1972).

Forces That Change Gene Frequency

The way a breed can be improved in performance using genetic tools is by changing the gene frequency. The four forces that can change gene frequency are: genetic drift (chance), mutation, migration and selection. Breeders will use mainly selection and migration to improve productivity in the next 10-15 years.

Chance or random genetic drift

Random drift is chance change in gene frequency and the rate of change depends on the size of the population. This is a major force in changing gene frequency in a small population, but is unimportant in most livestock breeds (Lush, 1948).

Recurrent mutation

Recurrent mutation is a very feeble (weak) force in changing gene frequency. Its major role is to present new genetic material (mainly desirable and undesirable genes) into the population. Selection will then increase the frequency of desirable mutation.

Migration

Migration is bringing in material from outside a base population. The factors that determine the amount of change in gene frequency per

generation due to immigration are: 1) The difference in gene frequency of the immigrant population and the native population. 2) The number of immigrants that come into the native population. In commercial herds most males are brought in from purebred herds and females are produced within the herd. In upgrading a population however, the trend is to bring in some males and use local males as well, e. g., in the U.S they used their own males and also bring in males from Europe (Magee, 1971). In Zimbabwe, local males/sires are used along with imported semen from sires originating in North America and Britain.

The frequency of the gene in the base population today will be:

$$q_1 = mq_m + (1-m)q_o = m(q_m - q_o) + q_o$$

where m = the fraction of the genes coming from outside the herd, $1-m$ is the fraction of the genes from within the herd, q_m is the frequency of the gene in the immigrant population and q_o is the frequency of the gene in the native population last generation (Falconer, 1981). The change in gene frequency after one generation of immigration is the difference in gene frequency before and after immigration:

$$q = q_1 - q_o = m(q_m - q_o) \text{ (Falconer, 1981).}$$

In almost all countries of the world the breeding structure can be represented by a pyramid, which comprises leaders or the elite breeders, the Multiplier herds and the Commercial producers (Figure 1 below). The commercial producers get the males either from leaders or multipliers

(migration) and produce a product to sale (milk, meat, wool, hides etc). The leaders usually improve by selection within the population of leader herds. This whole concept is based on the assumption that "Leaders" are making progress for traits that are important for improvement in the whole country herd and is constantly released. The Elite group therefore controls the genetic makeup of the whole population because the direction in which multipliers and commercial producers must depend on selection and migration of males from Leaders. If North American and British sires were not better than Zimbabwean sires there would not be any basis for gene importation from these countries (Magee, 1971).

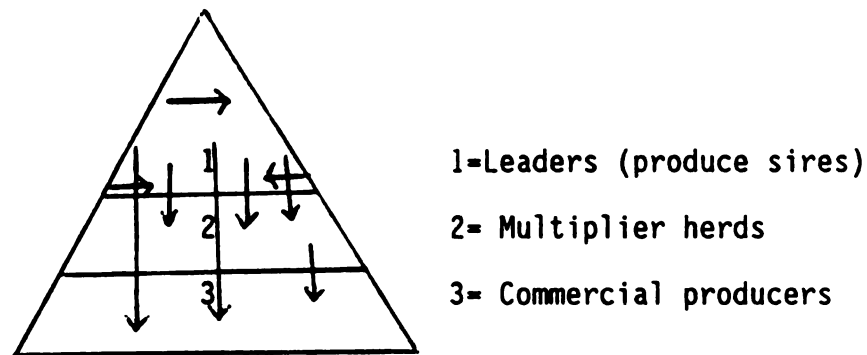


Figure 1. An Improved Breed Structure

Selection

Selection allows selected individuals to contribute more genes to the next generation than other individuals in the same population. Selection is usually Man's major way to change gene frequency for a breed. Heritabilities provide an index of the probable efficiency of selection. Where heritabilities are high, the most effective program for genetic

improvement of the trait would be mass selection of those individuals exhibiting the desirable trait. Little attention would be given to ancestry, sibs and other collateral relatives and to progeny tests. On the other hand, where heritabilities are low, selection should include some form of progeny test and be based on ancestry and the performance of close relatives.

The rate of genetic progress per generation depends on the selection intensity, accuracy of selection, generation interval and genetic variation or genetic standard deviation (Pearson, 1984).

"Selection intensity"

Selection intensity is the selection differential expressed in phenotypic standard deviations. Selection differential is the difference between the average phenotype of those selected to be parents and the average of the whole generation from which they were chosen. The fewer animals needed as parents the higher their average merit can be. The intensity of selection is in large part determined by the number of animals available for culling. Selection intensities are decreased when the animals culled are not the worst animals for the trait which is being improved. This decreased intensity usually results from involuntary losses like injury, non-breeders, mastitis etc, plus breeders selecting for other traits and one sire can produce thousands of daughters versus a cow producing only a few daughters even with superovulation and embryo transfer. In most dairy herds of fixed size, very few females can be culled for voluntary reasons (Ferris, 1985). Generally for dairymen, the

selection intensity for sires is much higher than for cows. A farmer must keep most of his cows to maintain his herd size but he can choose to use just a few of the superior sires from the A.I sire population.

"Accuracy of selection"

Accuracy of selection is the correlation between the estimated breeding value (BV) and the true breeding value (TBV). Breeders never know the true breeding value of an animal. The accuracy of selection is determined by how well the breeding value is predicted by the phenotypic measures used for selection. Accuracy depends on heritability, number of records available and relationship of animals with the records to the animal being evaluated. For individual or own performance accuracy is the square root of heritability and for correlated traits accuracy will be the square root of heritability x genetic correlation between the two traits.

Improvement per year = accuracy x selection intensity x genetic standard deviation / generation interval.

"Generation interval"

Generation interval is the average age of the parents when their first offspring are born. The length of the generation interval varies with different species of animals and with the breeding and management systems followed to produce a generation of breeding animals. In dairy

cattle the average length of the generation interval for dams of cows is 4.5 to 5 years and for sires of cows is 6.0 years, for dams of bulls is 5.5 years and sires of bulls is about 9.0 years (Pearson, 1984). This gives an average generation interval of about 6.25- 6.4 years. The generation interval is lengthened if progeny-testing is practised or if performance records of cows determine whether or not their offspring are kept for breeding purposes (Lasley, 1978). The longer the generation interval with the other factors held constant, the slower the rate of genetic progress.

"Sire selection"

Genetic progress is dependent on identification and extensive use of superior sires (Powell and Shainline, 1979). The improvement in sire merit can be thought of as consisting of five phases (Powell and Shainline, 1979) which are: 1) Making matings to produce bulls with high pedigree index (PI); 2) Selecting on pedigree only the most promising bulls for sampling; 3) Conducting an unbiased, multi-herd progeny test; 4) Retaining only the best bulls after the progeny test; and 5) Making maximum use of the best proven bulls. The goal of sire selection is herd improvement. To improve the next generation, parents must be genetically superior to the current population. This means that genetic improvement, or the increase in merit depends on the superiority of parents to the population from which they are chosen. The superiority of selected sires is much higher than for dams, resulting in a higher average merit for sires relative to those available. This, according to Ferris (1985), is

because we can be very picky in selecting sires available from A.I i.e we may only need the top 2 to 10%, whereas we must keep most of the cows in our herds as parents in order to maintain herd size. About 93% of the genetic progress in a herd comes from the outside sire selected, whereas 7% is from cows selected as dams; Ferris (1985). McDowell (1972) gave figures as 94% and 6% respectively. This is because selection is more intense on sires than dams. Also the accuracy of estimating genetic merit of a sire is much greater than for a cow as reflected by the maximum repeatabilities for PD's (99%) and CI's (55%) (U.S sire summaries, 1988). Blake (1983a) reported that 75% of the possible genetic gain is from sire selection. In the U.S annual genetic trends in milk yield from 1968 through 1975 were estimated at 21 kg for Holsteins and 16 to 45 kg for five other breeds (Powell et al., 1977). Trends in breeding values of sires were generally larger, 38 kg for Holsteins and 7 to 80 kg for the other breeds. The 'genetic trends' in the breeding values of producing females are predominantly the result of trends in sire merit. Therefore, the trend in sire merit often is used to describe genetic changes in the entire population (Powell and Shainline, 1979). The genetic or estimated transmitting ability (ETA) of the offspring is equal to the average merit of the parents, (i.e average of the BV of dam and BV of sire). This is illustrated by the equation:

$$BV_{\text{offspring}} = BV_{\text{sire}} + BV_{\text{dam}} + \text{mendelian sampling.}$$

2

and assume mendelian samplings sum to 0 with a large number of offspring.

Population Parameters

Genetic parameters have very important animal breeding applications. Development and realization of animal breeding plans require knowledge of the heritabilities and phenotypic and genetic correlations of the traits considered. These parameters are needed to evaluate the breeding plan itself as well as to predict breeding values. They are also used in the following ways:

- 1) Estimating sire and dam breeding values and accuracies of these predictions e.g., heritabilities and phenotypic and genetic correlations are used in the construction of selection indices.
- 2) To predict genetic progress per year or per generation.

Improvement per generation = accuracy x selection intensity x
genotypic standard deviation.

- 3) To design and implement progeny testing schemes having determined the effectiveness and the optimum number of offspring required.

$$\text{Accuracy of a progeny test} = \sqrt{\frac{n}{n + \frac{(4-h^2)}{h^2}}}$$

where h^2 is the heritability of a trait and n is the number of progeny per sire. Therefore the accuracy of a progeny test depends on the heritability of a trait and the number of records used.

- 4) To design and establish selection experiments. If the traits are positively correlated genetically, selection for one leads to

improvement of the other (indirect selection).

5) In multiple trait evaluations. If correctly accommodating the genetic and phenotypic relationship between traits, this can improve accuracy as well as account for some forms of selection bias (Cue et al., 1987). Assessing the value of later records for both sire and cow evaluations, requires knowledge of the genetic parameters, i.e., heritabilities and genetic correlations concerned (Meyer, 1984). Genetic values from other countries are not necessarily applicable to Zimbabwe because of genetic differences and differences in environment (feeding and management).

The genetic parameters of particular importance to animal breeding applications are heritabilities, genetic, phenotypic and residual correlations and phenotypic and genetic standard deviations.

Phenotypic variance/standard deviation

Phenotypic standard deviation measures how different animals are in production traits or the average spread of a population. The larger the phenotypic variance/standard deviation the greater the progress through selection. There is a high phenotypic standard deviation for milk yield. Abubakar et al.(1986) reported total variance for milk yield of 1, 385, 436 kg² whereas Van Vleck et al. (1961) reported a variance in milk of 1, 405, 711 kg. Phenotypic standard deviations between all cows were 961 kg and 35.2 kg for milk yield and fat yield, respectively (Lawlor and Pollack, 1983).

Genetic variation

The genetic variation is a measure of the variation of breeding values for the trait being considered. The genetic variation tends to be nearly constant for a given population and trait and, thus, breeders can influence it very little. The genetic standard deviation is determined by the frequency and effect of the alleles which control the trait. The genetic variation for a trait in a population is important because it relates to the difference between the average individual and the top individual animals. The more superior the top individuals are above the average, the greater the potential to make genetic progress.

Heritabilities

The heritability of a trait refers to the relative degree or proportion of superiority or inferiority in the parents that will be transmitted to the progeny. That is a ratio of the portion of variation in a trait due to the genetic effects to the total variation. Heritability values range from 0.0 to 1.0 by definition. Selected parents are usually above average in a trait because they are genetically better than average, and because they have enjoyed a better than average environmental opportunity. The higher the degree of genetic control, the more indicative an animal's outward appearance (phenotype) is of the genetic makeup (genotype) of that animal. Heritabilities of less than 15% are usually too low to yield significant progress from selection if selection depends entirely on the phenotype. The coefficient of

heritability is not constant but indicates the proportion of variance caused by differences in additive gene effects in a particular population at a particular time.

Powell et al.(1981) reported that heritabilities are higher for first lactation than later lactations. Tong et al.(1979) reported heritabilities for the first 3 lactations for Holsteins of .26, .19, .17 for milk yield and .26, .17 .15 for fat yield and .35, .43 and .51 for fat percentage. Powell et al. (1981) reported heritabilities of the first five lactations of about .36 ,.36, .36, .20, .22 for milk yield and .23, .27,.28, .20 and .16 for fat yield. Powell et al.(1981) also showed that heritabilities for milk and fat production of Holstein cows were highest at .35 and .33 for first lactation and decreased to .21 and .20 for the fifth lactation respectively. Heritabilities decreased for all yield traits but increased for percentage traits with succeeding lactations (Powell et al., 1981). Maijala and Hanna (1974) have surveyed the general literature and reported weighted average heritabilities for the first three lactations of about .26, .20 and .17 for milk yield, .25 , .16 , and .17 for fat yield and .45 , .39 and .34 for fat percent. Heritabilities of .33, .33, and .34 for the first, second and third lactation milk yield were found by Swalve and Van Vleck (1987). Milk yield and fat yield had heritabilities of .36 and .38 respectively (Cue et al., 1987). Heritabilities for milk yield and fat percent were found to be .41 and .23 for first lactation Zimbabwean dairy cows (Mpofu, 1986). Hoque and Hodges (1980) reported heritabilities of milk yield and fat yield of .22 and .25 respectively. D de Jager and Kennedy (1987) reported heritabilities for milk yield, fat yield and fat percentage of .28,

.31, and .61 respectively. Lawlor and Pollack (1983) found heritabilities of .19 for milk yield and .30 for fat yield.

Heritability range for milk yield in the temperate areas is .12 to .59 (Maijala and Hanna, 1974). McDowell (1972) found heritability range to be .03 to .64 in the tropics. Only one study that of Fimland et al. (1972) indicated higher heritabilities for second lactation records than for first lactation (.24 versus .21) for milk yield. A summary of the Estimates of heritabilities for milk, fat percentage and fat yield is given by (Maijala and Hanna, 1974 and Mao 1984).

Correlations

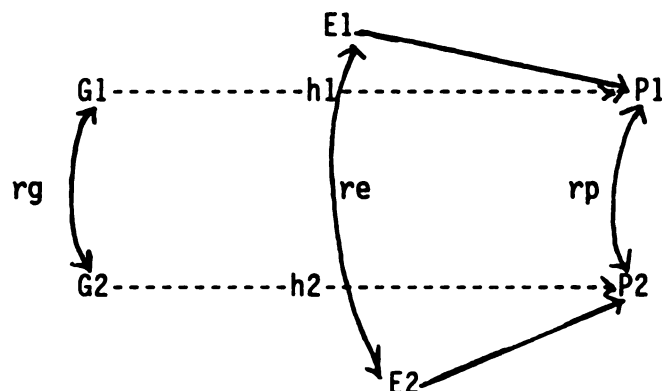
Many genes are responsible for the breeding value of a quantitative trait. The correlations range from -1.0 to 1.0. The direction and extent of correlated response depend on the sign and size of genetic correlation. Genetic correlation is the correlation of the breeding values.

The causes of genetic correlations are twofold (Pirchner, 1983):

1. Permanent genetic correlations are caused by pleiotropy. The same genes may be responsible for the breeding values of several traits. These traits therefore become related because of sharing of these common genes.
2. Second, genetic correlations may be caused by linkage disequilibrium and such a correlation will be transient and will disappear when equilibrium proportions are attained. Linkage will tend to retard the dissolution of the disequilibrium.

An example of linkage disequilibrium causing genetic correlations is when one has different breeding goals within a population. For

example, if in one segment of the population breeders select for dairy merit and against fleshiness of cows, while in another segment selection favours muscularity and is directed against too great a milk yield, e.g., cows used as beef dams, then the two traits will become negatively correlated. The genetic and environmental correlations (common environment) are the main causes of the overall relationship between two traits which is measured by a phenotypic correlation. Environmental correlation is the correlation of environmental deviations with non-additive genetic deviations. Good examples of genetic correlations are genes that increase growth rate increase both stature and weight, so that they tend to cause correlation between these two characters. Some genes may increase both characteristics, while others increase one and reduce the other; the former tend to cause a positive correlation and the latter a negative one (Falconer, 1981). Because of the genetic correlation, the deliberate change in one trait would inadvertently cause changes in other traits. Such changes are called correlated responses. Genetic correlations indicate the expected change in other traits occurring concurrently with change in a trait under selection. Genetic correlations are therefore useful in obtaining estimates of genetic change in a trait of interest such as fat yield or fat percentage when selection pressure is placed on another trait, such as milk yield.



E = non-genetic effects (contains the effects of environment, dominance and epistasis.)
 G = genic value of an animal
 P = observed phenotype or the record of the animal we are using.

Figure 2: The relationship between Genetic, Environmental and Phenotypic correlations between the traits for Hoslteins.

Generally, correlations can be interpreted as follows (Cassel 1984).

- 1) (.4 to 1.0) traits will progress strongly in the same direction.
- 2) (.4 to -.4) traits will progress almost independent of each other.
- 3) (-.4 to -1.0) traits will progress strongly in opposite directions.

Mpofu (1986), working with Zimbabwean data found genetic and phenotypic correlations for milk yield and fat percent of -.65 and -.26 respectively. The genetic correlation between fat yield and fat percentage was positive and relatively high at .48 (D de Jager and Kennedy, 1987). Maijala and Hanna (1974) and Wilcox et al.(1971), respectively, reported the genetic correlation between fat yield and fat percentage to be .26 and .30. The average genetic correlation between fat yield and fat percent is .14 and ranges from -.03 to .26 (Lasley, 1978). This means that very few of the same genes affect these two

traits, and selection for one should not cause a significant genetic change in the other.

Table 1. General literature Estimates of genetic and phenotypic correlations between the traits for Holsteins.

Traits	rg	rp	source
Milk & Fat(kg)	.70-.95	.70 - .95	Mao 1984
	.85-.95		Mcdowell 1972
Milk & fat(%)	-.20- -.60	-.10- -.40	Mao 1984
	-.07- -.67		Pirchner 1969
	-.01- -.66	-.03- -.29	Maijala and Hanna 1974
	-.20- -.50		Mcdowell 1972

Multiple Records

In contrast to animal breeding plans for meat production, breeding plans for dairy cattle have to consider repetitive performance of the animal, i. e., the potential for more than one lactation per cow (Swalve and Van Vleck, 1987). The general increase in lactation average in later lactations is partly due to selection. Often performance in later lactations is assumed genetically to be due to the same genes that influence performance in first lactation (Swalve and Van Vleck, 1987; Tong et al., 1979). Generally, the first lactation is about as or more accurate in evaluating breeding values of sires and dams than all

lactations weighted equally. Butcher and Freeman (1968) reported that individual lactation weightings would increase accuracy of a cow evaluation by 1.5% for two lactations and by 3% for three lactations. Many studies showed more additive control in first lactations than in later lactations (Tong et al., 1979). Cows reaching a second or later lactation have normally been subject to culling decisions based, at least partly, on their performance (Meyer, 1984). Therefore, later lactations are potentially subject to selection, and much of the controversy on the value of later lactations is concerned with effects of selection. Maximum profit per day of herd life would be expected from cows with 4.5 lactations (Silva et al., 1986). The majority of procedures for prediction of breeding values, either consider only first lactations or imply a genetic correlation of 1.0 between all lactations (Swalve and Van Vleck, 1987).

Artificial Insemination (A.I.)

A.I. is a practical means of obtaining improvement in farm animals by using the sperm of potentially genetically superior sires in many herds. The key to success in A.I. is the use of superior bulls and a high conception rate. Its main purpose is to promote herd improvement by obtaining semen from genetically superior bulls to be used on cows within the herd. Generally the more traits in which a sire excels, the more expensive his semen. Semen price is a determining factor in sire selection, but purchase of semen from A.I. bulls pays excellent returns. A.I. provides two primary benefits:

- 1) A mechanism to widely distribute semen from superior sires and
- 2) A mechanism to sample sires across herds.

In the world today the percentage of dairy cows inseminated artificially has increased as the total number of dairy cows has decreased steadily. A.I. has contributed to higher production in the entire dairy cattle population because of greater selection possible through A.I. The greatest advantage of A.I. is the genetic improvements possible for quantitative traits through intensive sire selection. The other advantages of A.I. include more productive offspring, less venereal disease, removal of the danger of personal injury associated with keeping a bull and reduction in the frequency of recessive lethal genes (Brackett et al., 1981).

MATERIALS AND METHODS

Data

A total of 18, 000 records for the black and white cows (Holstein/Friesian) extending over a period of 7 years from 1980-1986 were extracted from the Zimbabwe milk recording scheme of Dairy Services (M.R.S) in the Department of Research and Specialist Services. These records are from a relatively few herds (about 127) in Zimbabwe. This is because only 20% of the approximately 520 milk producers are members of the M.R.S. And of these herds approximately 80 % of the black and white herds use A.I.

The Zimbabwe black and white cows can be divided into two population groups, daughters of imported sires which are Holsteins with sire codes beginning with "7" and those of locally-bred sires which are locally called Friesians with sire codes beginning with "2". Some locally-bred sires are descendants of imported bulls. Imported bulls are mainly North American, i.e., U.S. and Canadian Holsteins with a few Friesians from the U.K.

As in other countries, Zimbabwe has registered and unregistered animals. Breeders registration is with the Zimbabwe Herd Book (ZHB). Dairy cows are divided into 3 classes: pedigree, grade and appendix. Grade cows are unregistered animals, i.e., their parents are not registered and not identified. Grade animals can be graded up. A grade

cow mated to a registered bull will produce appendix A offspring. Appendix cattle are only those registered with ZHB. Thus many cows from grade dams and registered bulls are not listed as appendix A cows. By continued use of registered parents, offspring from succeeding generations go from appendices A to B to C and finally to pedigree (these are registered and identified).

General Characteristics

The M.R.S divide Zimbabwe into 4 major geographic areas (Figure 1). 1. Matabeleland, with an altitude of about 1, 350m is the driest part of the country and the hottest. Temperatures are normally in the range of 27-30C in summer and the minimum is 7 c in winter and rainfall of about 450-650mm. Therefore farmers have to grow irrigated pastures to supplement their dairy feeds. 2. Midlands, this area has an altitude of about 1, 400m an annual rainfall of about 650-800mm and temperatures maximum of about 28 C in summer and a minimum of 0 C in winter. 3. Mashonaland, with an altitude of about 1, 500 m is the greater part of the country which has temperatures of about 29 C in summer and a minimum of 6 C in winter and annual rainfall of between 750 and 1000 mm but is seasonal. 4. Manicaland, which has an altitude of over 1, 860 m receives the highest annual rainfall of greater than 1000 mm and rainfall is throughout the year. The temperatures are always around 21 C, the maximum temperature is 24 C in summer and the minimum is 4 C in winter and is also the coolest part of the country.

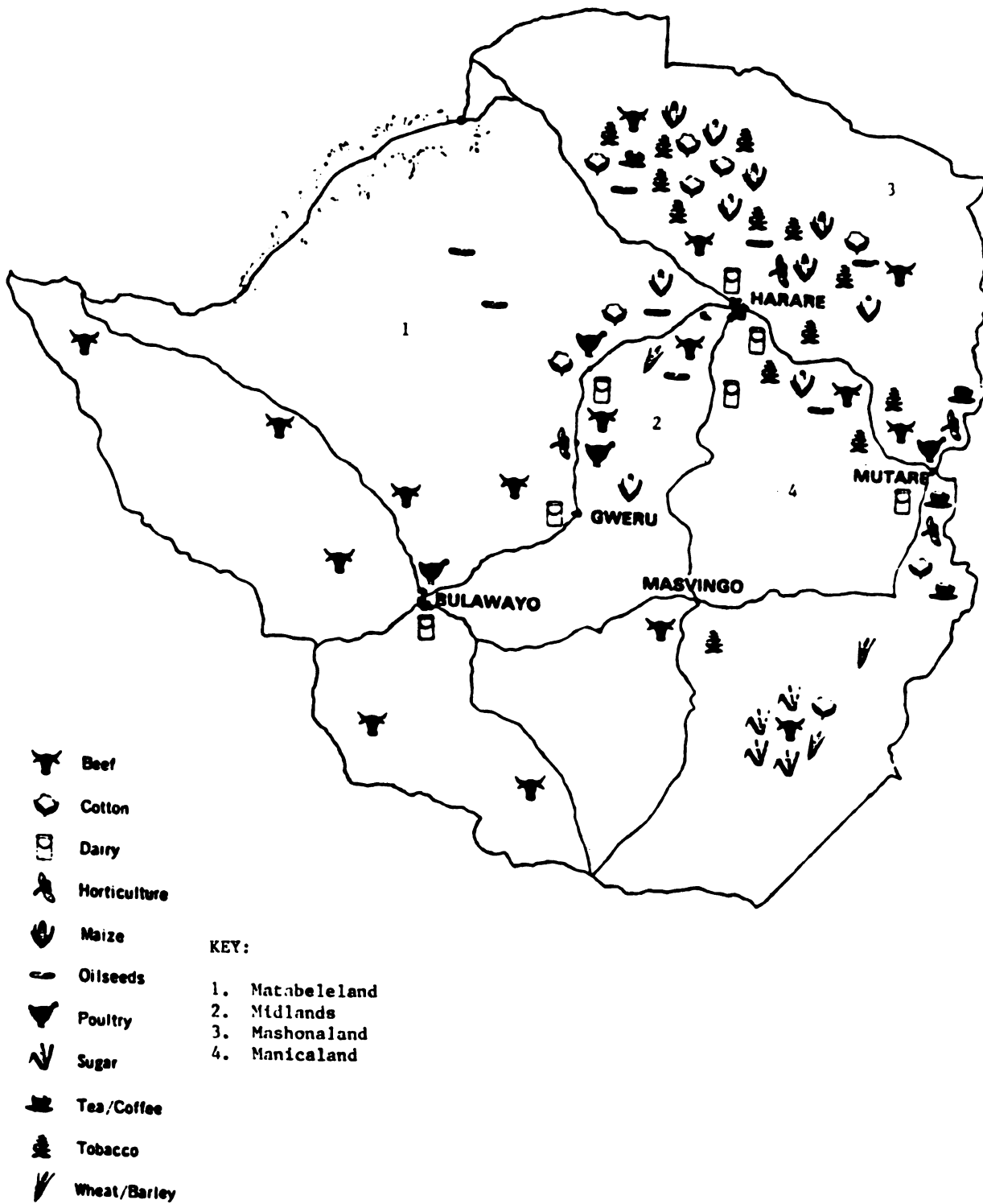


Figure 3. Map of Zimbabwe showing the four areas (regions).

In Zimbabwe, rainfall decreases from East to West i.e., from area 4 to area 1. As a result, area four is the best suited for dairying and area one is the least suited for dairy production. The natural vegetation of the whole country is basically savanna consisting of savanna woodland and grassland. In Manicaland some montane and tropical forests are found. In all areas the basic summer feed is grass. There are large yearly variations in rainfall which influence grass yield. These yearly changes significantly affect dairy production and reproduction.

Three seasons were used: 1. November to February (wettest); 2. March to June (cold and dry); 3. July to October (hot and dry).

Production Systems

Feeding systems and management are the two primary sources of herd differences in the tropical areas. Feeding systems in Zimbabwe are based on maize and its by-products for energy, and cotton-seed and soya-oil cakes for protein. The major roughage source is natural summer veld grass, veld hay (i.e., natural or indigenous grass hay which are of the predominant species / varieties), maize silage and where irrigation is available, oats, midmar rye, lucerne and planted pastures. With the price of concentrates rising sharply, many farmers are now looking to growing their sources of protein in the form of pastures, legumes and high protein crops. Therefore the feeding systems used in the four areas vary depending on the ability to economically produce home-grown feeds. In Midlands and Matabeleland, the majority of the farmers purchase their concentrate requirements and use natural grazing in the summer months as

a form of roughage. Maize silage combined with cut veld hay is used in the winter months. In Mashonaland farmers grow maize both for silage as a source of roughage, and as grain meal to make up the energy part of the concentrate mix. They normally only purchase high protein concentrate mixes. While many farmers still put their cattle out to normal grazing during the summer months, there is an ever-increasing trend towards zero grazing with maize silage forming the bulk of the roughage intake.

Where irrigation is available in either of the above areas, the majority of producers tend to use this irrigation for green feed during the winter months and the most popular forages are oats, midmar rye grass and grass pastures. The majority still, depend on natural grazing. Grass is at its best in November to January, thus milk intakes at Dairy Marketing Board (D.M.B) are at the highest levels in November to January and lowest in June and July. The D.M.B pays seasonal prices to farmers, to tend to level production over the year.

Method of Taking and Testing Samples

For the MRS there are two methods of taking milk samples. In both cases, the milk is agitated well before taking a sample.

The first method is from a Danish Bucket. At the first milking, select the number of turns on the sampling tap which one is going to make for that particular cow. Weigh the milk and draw off that number of turns on the tap. For subsequent milkings of that cow during that visit, take the same number of turns of the tap regardless of how much milk the cow delivers.

The second method is sampling from milk meters and volumetric bowls. A certain number of millilitres of milk for each kg of milk delivered by a particular cow at the first milking is sampled. Then the same number of ml's/kg of milk delivered at subsequent milkings is taken.

The Gerber test

Fat testing occurs on the farm immediately after sampling. The method used for determining the percentage of fat in milk in Zimbabwe is the Gerber Method using isoamyl alcohol and sulphuric acid (Martin, 1978). The milk sample is warmed for five minutes at 40 C in a water bath (which is at about 55 C). The sample is then immediately cooled down to 18-22 C. After mixing the sample thoroughly, 10.94 ml are pipetted into a butyrometer containing 10 ml concentrated sulphuric acid (98 %). Then 1ml of amyl alcohol is added to the contents to dissolve the fat. The butyrometer is stoppered and the contents are thoroughly mixed until no white milk particles are visible. The butyrometer is then inserted upside-down in the Gerber centrifuge container, and the contents are centrifuged for 7 minutes at 700 revolutions per minute. The butyrometer is transferred to a water bath at 63 C, where it is immersed to the level of the upper fat layer for 3 minutes. Before taking the reading, the position of the fat column is adjusted so as to bring the lower end of the column on to a main graduation mark. This is done by slightly withdrawing the stopper. The reading is taken with the butyrometer held with the graduated portion vertical at an eye level, and is the difference between

the readings at the bottom of the fat meniscus and the surface of separation between fat and acid (the interface).

Production Traits

Important traits in dairy production in Zimbabwe at present are milk yield and fat percentage. These are the basis for payment, with milk yield being the main determinant of income for the dairy farmers. Thus, selection is primarily focused on these two traits. Zimbabwe records are truncated at 300 days such that yield after 300 days and the first five days are not used on record calculation. For this study, only butterfat content and basic price based on the amount of milk produced were the factors considered in computing milk price (Zimbabwean dollar value). The exchange rate in 1984 was approximately Z\$1.00 = US\$0.80. The milk producers' basic prices used in this study to determine dollar value were for 1984 when the basic price for milk volume was 34.2 cents per kg of milk produced. Although the milk prices have changed in recent years, the change is not that much and therefore the trend should be the same as in 1984.

The dependent variable dollar value was computed using the following formula:

Dollar value = $(.342 + (\text{butterfat percent} - 3.2) * .0342) * \text{milk yield(kg)}$.

The variable fat yield was computed using the following formula:

fat yield = fat percent * milk yield / 100.

An example of how dollar values were calculated is: A cow produced 5,000kg of milk with 4.2% butterfat percentage content would have a dollar value of Z\$1, 881.00.

Data Editing

Restrictions were imposed on the data set as an attempt to remove incorrect data. The restrictions are shown below:

Table 2. Restrictions imposed on the data set.

Variable	Minimum	Maximum
Calving Interval(d)	313	513
Days dry (d)	0	120
Lactation Days	280	300
Age at First Calving (mo)	18	36

Lactation number was restricted as follows:

Table 3. Restrictions imposed on Lactation number.

Lactation Number	Age (months)	
	Minimum	Maximum
1	18	36
2	30	57
3	42	72
4+	54	none

Lactation number 4+ included animals with lactation number 4 and greater. Cows with unknown sires and missing values for milk yield, age at calving, fat percentage, and date of calving were excluded from the data set. Further edits included checks on outliers for milk yield, fat percentage and consistency in birth dates, calving dates and age at calving. The restriction was imposed that a sire had to have 2 daughters in a herd.

The number of records which were obtained are listed in Table 4:

Table 4. Records used in the Analysis^a.

	Lactation Number			
	1	2	3	4+
Total no. of Records	6206	3875	2746	5173
Total no. of Sires	460	376	311	390
Imported Sires	184	139	95	98
Imported Records	2302(37)	1485(38)	1011(37)	1731(33)
Local Sires	276	237	216	292
Local Records	3904(63)	2390(62)	1735(63)	3442(67)

^a Values in parenthesis are percentages of source of sire records in the total data set.

Table 5. Frequency distribution of classes of cows^a.

Class of	Lactation number			
	1	2	3	4+ Cow.
Pedigree	751(12)	359(9)	250(9)	390(8)
Grade	4,104(66)	2,565(66)	1,800(66)	3,518(68)
Appendix	1,351(22)	950(25)	696(25)	1,265(24)

^a Values in parenthesis are percentages.

The Model

The first lactation heifers (2 year olds) do not have a calving interval nor do they have previous days dry. As a result two different covariate models were fitted, one for first lactation records and the second for the second and subsequent lactations. For the first lactation heifers (2 year olds) the model [1] was:

$$Y_{ijklmnop} = U + A_i + C_j + HY_k + SS_l + SC_m + ASC_{im} + AC_{ij} + Ag_n + S_{om} + bl(L-L) + E_{ijklmnop} \quad [1]$$

Where:

$Y_{ijklmnop}$ is the record/dependent variable i.e., milk yield, fat yield, fat percentage or dollar value.

U is the overall mean common to all observations.

A_i is the fixed effect of area $i = 1, 2, 3$, and 4 which are Matabeleland, Midlands, Mashonaland and Manicaland, respectively.

C_j	is the fixed effect of the jth class of cow $j = 1, 2, \text{ and } 3$; where 1 = pedigree 2 = grade and 3 = appendix.
HY_k	is the fixed effect of the kth herd-year.
SS_l	is the fixed effect of the lth season, $l = 1, 2, \text{ and } 3$; where 1 = November to February, 2 = March to June and 3 = July to October, respectively.
SC_m	is the fixed effect of the mth source of bulls $m = 1, 2$; where 1 = local and 2 = imported.
ASC_{im}	is the source by area interaction.
AC_{ij}	is the class of cow by area interaction.
A_{gn}	is the fixed effect of age at first calving of cow (in months).
S_{om}	is the random effect of the oth sire in the mth source/group, with no relationship matrix considered except for the paternal half-sisters having a relationship of .25.
$b_1(L-L)$	is the length of lactation fitted as a linear regression variable.
$E_{ijklmnop}$	is the random residual error term associated with each record.

The covariate model for the second, third and fourth lactation cows was an extension of that of the first lactation heifers. In this model age at first calving was not fitted and days dry and days dry squared and calving interval were fitted and included as regression covariates. Everything else is as described for the first lactation model [1].

Model [2] for second and subsequent lactation cows is:

$$Y_{ijklmno} = U + A_i + C_j + HY_k + SS_l + SC_m + ASC_{im} + AC_{ij} + S_{nm} + b_1(L-L) + b_2(D-D) + b_3(D-D)^2 + b_4(C-C) + E_{ijklmno}. \quad [2]$$

Where:

$b_2(D-D)$ is the number of days dry.

$b_3(D-D)^2$ is days dry squared.

$b_4(C-C)$ is the length of the calving interval (days).

In matrix notation the model used is a sire model with group effect. Grouping is by source of sire/germ plasm.

$$\underline{Y} = \underline{X}\underline{b} + \underline{Z}_s\underline{Q}\underline{g} + \underline{Z}_u\underline{U} + \underline{e}$$

Where:

Y is a vector of observations

b is a vector of fixed factors

U is a vector of random sire effects

g is a vector of group effects where grouping by source of germ plasm.

e is a vector of random environmental effects and

X is the incidence matrix associating records with elements of b

Z is the incidence matrix associating records with elements of U

Q is the incidence matrix connecting sires to the group

$$\text{var} \begin{pmatrix} s \\ e \end{pmatrix} = \begin{pmatrix} S & 0 \\ 0 & R \end{pmatrix}$$

$$\text{var}(s) = S = \begin{pmatrix} s_{11} & s_{12} & s_{13} & s_{14} \\ & s_{22} & s_{23} & s_{24} \\ & \text{symmetric} & s_{33} & s_{34} \\ & & & s_{44} \end{pmatrix}$$

where s_{ij} is the sire variance covariance for the trait i and j .

$$\text{var}(e) = R = \begin{pmatrix} r_{11} & r_{12} & r_{13} & r_{14} \\ & r_{22} & r_{23} & r_{24} \\ & \text{symmetric} & r_{33} & r_{34} \\ & & & r_{44} \end{pmatrix}$$

where r_{ij} is the residual variance-covariance for the trait i and j .

The mixed model equations are as follows:

$$\begin{bmatrix} X'X & X'Q & X'Z \\ Q'X & Q'Q & Q'Z \\ Z'X & Z'Q & Z'Z + Ik \end{bmatrix} \begin{bmatrix} b \\ g \\ u \end{bmatrix} = \begin{bmatrix} X'Y \\ Q'Y \\ Z'Y \end{bmatrix}$$

where $s = \hat{g} + \hat{u}$ i.e., $E(s) = \text{group} + \text{sire}$ or $U = Qg + \underline{u}$

k is the variance ratio i.e., $\frac{\text{Residual variance}}{\text{Sire variance}}$

Assumptions

In fitting the above models the following assumptions were considered.

- 1) All other interactions were not significant or are unimportant.
- 2) Relationships between sires were ignored. Therefore, all relationships except for paternal half-sibs were ignored.
- 3) The sires in each group are regarded as a random sample from that group.
- 4) No covariance between sire and residual i.e., $\text{COV}(s, e) = 0$.

Statistical Analysis

For the Least Square means and interactions, SAS's Generalized Linear Models (GLM) program was used. For the variance-covariance components (i.e., for the estimation of genetic parameters between and within sires)

an EM-REML with some transformations program developed by Just Jensen at Michigan State University was used.

As regards estimability of fixed factors, the variable source was not an estimable function, but the differences between sources of sire/germ plasm were estimable functions, i.e. the marginal means are estimable functions.

RESULTS AND DISCUSSION

Differences due to Source

The least square means in Table 6 show that daughters of imported sires out-performed local sires in the first lactation by 304 kg of milk; this increased to 476 kg in the second then decreased to 463 kg in the third lactation and is highest in the fourth lactation when they produced 666 kg more milk. This increase in production with lactations may be due to both selection and age effect. When averaged over all lactations, daughters of imported sires produced 477 kg more milk than local sires. Similarly daughters of imported sires made Z\$101.00, Z\$141.00, Z\$140.00 and Z\$218.00 more than the local sires in the first, second, third and fourth lactation, respectively; giving an average of about Z\$150.00 more in favor of daughters of imported sires. This same trend is repeated for fat yield where daughters of imported sires yielded 8, 9, 10 and 19 kg of fat more than local sires in the first, second, third and fourth lactation, respectively. On the average, over all lactations, daughters of imported sires produced 12 kg more fat than local sires. However, the trend was reversed for fat percent where the daughters of local sires produced about .07%, .14% ,.14% and .08% more fat than imported sires for the first, second, third and fourth lactation, respectively.

Table 6: Least square means within a lactation^a.

Trait	Source	Lactation Number			
		1	2	3	4+
Milk(kg)	Imported	4720(65)	5626(65)	5892(75)	6130(52)
	Local	4416(42)	5150(44)	5429(50)	5464(35)
	Difference	304	476	463	666
Dollar value (Z\$)	Imported	1681(23)	1991(23)	2080(26)	2157(18)
	Local	1580(15)	1850(15)	1940(18)	1939(12)
	Difference	101	141	140	218
Fat(kg)	Imported	170(3)	200(3)	208(3)	214(2)
	Local	162(2)	191(2)	198(2)	195(1)
	Difference	8	9	10	19
Fat%	Imported	3.64(.03)	3.60(.03)	3.55(.03)	3.52(.02)
	Local	3.71(.02)	3.74(.02)	3.69(.02)	3.60(.01)
	Difference	-.07	-.14	-.14	-.08

^a In parenthesis are the standard errors of least square means.

On average daughters of local sires had about .11% higher fat test than imported sires. The estimates based on the BLUE (Best Linear Unbiased Estimate) solutions show similar differences between the daughters from the two groups of sires Tables 7 and 8.

Table 7: BLUE estimates for single trait analysis (STA).

Trait	Source	Lactation Number			
		1	2	3	4+
Milk (kg)	Imported	0	0	0	0
	Local	-271	-291	-257	-506
Dollar Value (Z\$)	Imported	0	0	0	0
	Local	-96	-89	-73	-187
Fat (kg)	Imported	0	0	0	0
	Local	-9.2	-2.1	-1.2	-18.4
Fat (%)	Imported	0	0	0	0
	Local	.03	.18	.14	.01

Table 8: BLUE estimates for multiple trait analysis (MTA) for milk, fat yield and fat percent.

Trait	Source	Lactation Number			
		1	2	3	4+
Milk (kg)	Imported	0	0	0	0
	Local	-268	-305	-250	-488
Fat (kg)	Imported	0	0	0	0
	Local	-9.0	-5.0	-2.0	-14.0
Fat (%)	Imported	0	0	0	0
	Local	.03	.12	.12	.06

The major advantage of MTA versus STA is the use of genetic, residual and phenotypic correlations between traits to increase accuracy and precision of BLUP (Best Linear Unbiased Predictors) solutions and BLUE estimates and reduce selection bias. Dollar value was not included in the MTA solutions.

Differences due to other fixed factors

Tables 9-12 show GLM (SAS's Generalised Linear Models) analysis of variance tables for all traits throughout lactations. Herd-year and age at first calving are significant at ($P < .001$) for all traits throughout all lactations. A preliminary analysis showed that age for second and subsequent lactations was significant at ($P < .001$) for fat yield, milk yield and dollar value and at fat percentage in lactation 4+ only and near the end of the analysis it was suggested age should be included as a variable within each lactation but due to time restraints it was felt uneconomical to go back and reanalyse the data. Age at first lactation is not fit in all lactations. Class of cow is significant at at least ($P < .05$) for milk yield, dollar value throughout all the four lactations and for fat yield in lactation 1 and 4+ but do not appear to be significant ($P < .05$) for fat yield in lactation 2 and 3 and fat percent for all lactations. Season of calving is significant at least at ($P < .05$) in lactation 2, 3 and 4+ for milk yield, dollar value and fat yield and for fat percent in lactation 2 and 3. Geographic area does not seem to have any large effects.

All the covariates lactation days, days dry, days dry squared and calving interval are highly significant ($P < .001$) for all traits except fat percentage throughout all lactations.

Table 9. GLM (Generalized Linear Models) analysis of variance table for milk (values divided by 100, 000).

Variable		Lactation Number							
	DF	1		2		3		4+	
		MS	P	MS	P	MS	P	MS	P ^c
Source	1	135.6	***	178.6	***	81.3	**	513.4	***
Class	2	129.5	***	51.1	**	59.7	**	105.6	***
Season	2	17.2	NS	83.8	***	33.1	*	200.7	***
Area	3	20.2	NS	32.1	*	.06	NS	17.8	NS
Herd-Year ^b	369	136.0	***	120.7	***	86.3	***	140.6	***
Source-Area	3	3.9	NS	17.2	NS	5.8	NS	10.8	NS
Class-Area	6	45.4	***	11.3	NS	5.4	NS	28.8	**
Age at 1st Calving	18	89.3	***						
Lactation Days	1	1,017.6	***	1,332.7	***	547.8	***	1,846.6	***
Days dry	1			295.4	***	276.3	***	198.7	***
Days dry Sq	1			152.2	***	242.2	***	249.1	***
Calving Interval	1			1,243.1	***	875.7	***	1,335.6	***
Error ^a	5959	7.2		9.6		10.0		10.1	

^aThe error degrees of freedom are 3939, 2681 and 5237 for the second, third and fourth lactation, respectively.

^bThe herd-year degrees of freedom are 349, 331 and 347 for the second, third and fourth lactation, respectively.

^c P Level of significance: *** ($P < .0001$); ** ($P < .001$);

* ($P < .05$); NS non-significant at $P < .05$).

Table 10. GLM (Generalized Linear Models) analysis of variance for dollar value (values divided by 100, 000).

Variable		Lactation Number							
		1		2		3		4+	
	DF	MS	P	MS	P	MS	P	MS	p ^b
Source	1	14.2	***	16.0	***	5.2	*	64.1	***
Class	2	12.7	***	5.5	**	6.0	**	12.5	***
Season	2	2.4	NS	9.5	***	4.6	*	24.6	***
Area	3	2.4	NS	3.7	*	.03	NS	1.7	NS
Herd-Year	369	16.8	***	14.5	***	10.6	***	17.2	***
Source-Area	3	.3	NS	1.9	NS	1.4	NS	.7	NS
Class-Area	6	5.1	***	1.1	NS	.9	NS	3.4	*
Age at 1st Calving	18	11.2	***						
Lactation Days	1	121.2	***	164.7	***	68.3	***	221.7	***
Days dry	1			34.6	***	28.8	***	24.6	***
Days dry Sq	1			19.1	***	28.2	***	33.1	***
Calving Interval	1			137.9	***	119.1	***	165.4	***
Error ^a	5959	.87		1.13		1.22		1.25	

^{abc} same as Table 9.

Table 11. GLM (Generalized Linear Models) analysis of variance for fat yield.

Variable	Lactation Number								
	1			2		3		4+	p ^b
	DF	MS	P	MS	P	MS	P	MS	
Source	1	9,588	**	6,722	*	265	NS	64,175	***
Class	2	7,314	**	4,447	NS	3,902	NS	11,621	**
Season	2	3,161	NS	9,739	**	5,754	*	25,270	***
Area	3	2,754	NS	3,045	NS	467	NS	893	NS
Herd-Year	369	18,491	***	15,512	***	11,910	***	18,622	***
Source-Area	3	525	NS	1,683	NS	3,637	NS	81	NS
Class-Area	6	4,311	**	960	NS	1,907	NS	3,112	NS
Age at 1st Calving	18	11,700	***						
Lactation Days	1	110,291	***	161,247	***	68,160	***	204,837	***
Days dry	1			30,371	***	19,190	***	24,319	***
Days dry Sqd	1			19,363	***	24,377	***	37,072	***
Calving Interval	1			107,437	***	139,085	***	162,611	***
Error ^a	5959	1,173		1,524		1,751		1,755	

^{abc} same as Table 9.

Table 12. GLM (Generalized Linear Models) analysis of variance table for fat percentage.

Variable	Lactation Number								
		1			2		3		4+
	DF	MS	P	MS	P	MS	P	MS	p ^b
Source	1	.52	NS	.89	*	2.82	**	.003	NS
Class	2	.62	NS	.24	NS	.23	NS	.12	NS
Season	2	.33	NS	.96	*	.06	NS	.92	*
Area	3	.52	NS	.02	NS	.01	NS	.05	NS
Herd-Year	369	1.18	***	.90	***	.68	***	.89	***
Source-Area	3	.32	NS	.03	NS	.58	NS	.17	NS
Class-Area	6	.17	NS	.21	NS	.21	NS	.14	NS
Age at 1st Calving	18	.29	NS						
Lactation Days	1	.37	NS	.07	NS	.02	NS	.10	NS
Days dry	1			.25	NS	.99	*	.03	NS
Days dry Sq	1			.03	NS	.27	NS	.04	NS
Calving Interval	1			1.58	**	.43	NS	.003	NS
Error ^a	5959	.21		.22		.23		.24	

^{abc} same as Table 9.

The null hypothesis stated in the justification is rejected. Thus importation of Holstein sires has increased the dollar value of dairy production for all ages of cows and across all regions of the country.

Interaction

G X E interactions

The source x area interaction was not significant ($P < .05$) for all the four traits throughout the 4 lactations (Table 9-12). Figure 4 gives a graphic comparison of the two sources of semen across the four areas for milk production for lactation 1 (all the other graphs show a similar trend).

Class X area interaction

There seems to be a significant class x area interaction for milk and fat yield and dollar value in lactation 1 and 4 ($P < .05$) (Table 9-12). Figure 5 gives a graphic comparison of the three classes of cows across the four areas for milk production for lactation 1 (all the other graphs for four production traits show a similar trend throughout the four lactations). In areas 2 and 4 (Midlands and Manicaland) pedigree cows tend to do better than appendix cows whereas in areas 1 and 3 (Matabeleland and Mashonaland) appendix cows were better than pedigree cows. Grade cows were outperformed by both pedigree and appendix cows for all traits throughout the four lactations in all the four areas. Fat percent did not appear to show an interaction in all the four lactations (Table 12).

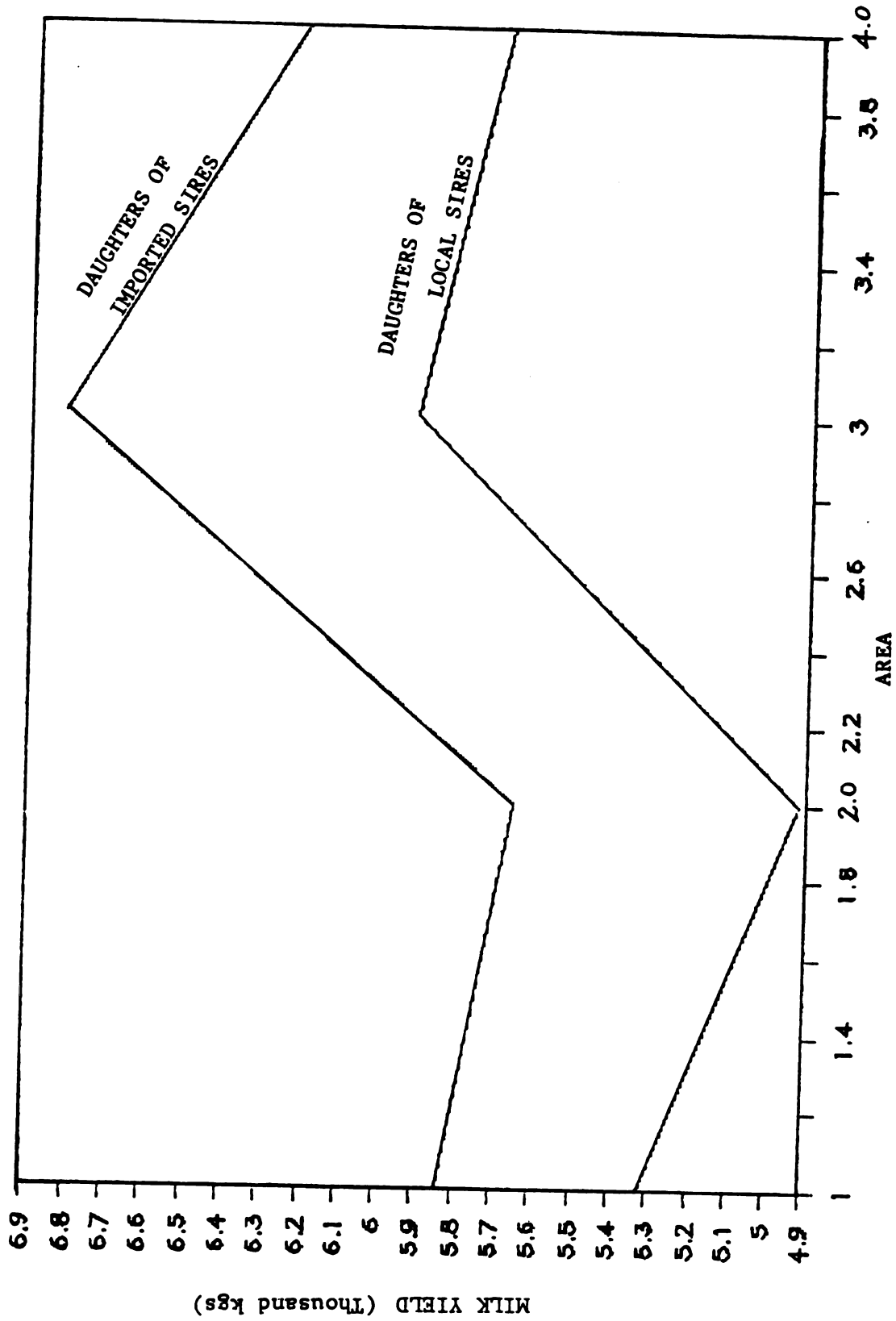


Figure 4. Source x area interaction for Lactation 4

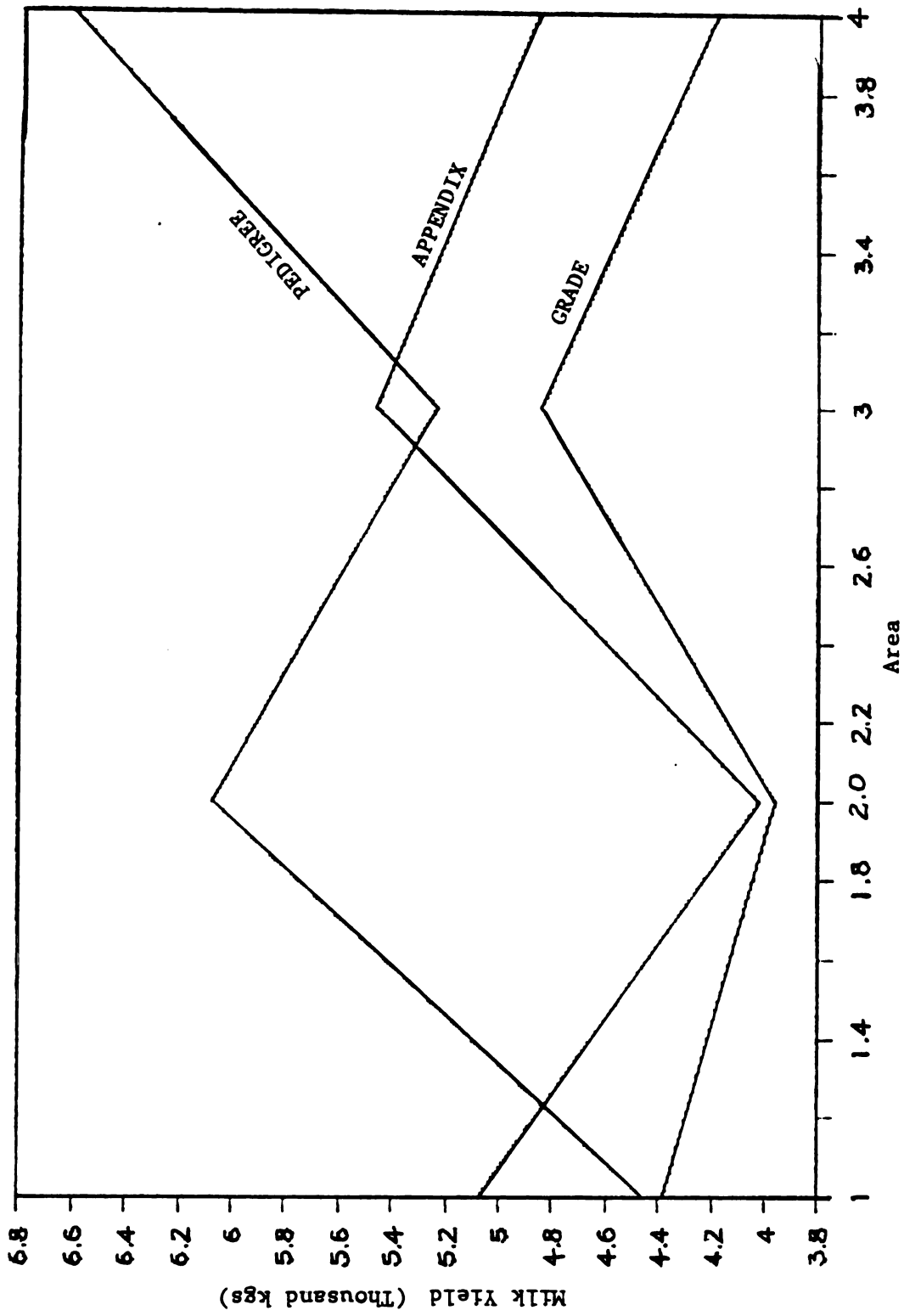


Figure 5. Class x Area interaction for Lactation 1

Variance components

The phenotypic, sire and residual variances within source by lactation are shown in Table 13. Phenotypic sire and residual variances increased from lactation 1 to lactation 4 for milk yield and dollar value. This might partly be due to selection and genetic age effect. Van Vleck (1963) reported that variance increases with an increase in production. Similarly, Hill et al. (1983) reported the same trend with heritability.

Phenotypic, sire and residual variances in the imported sires are higher than the variance associated with local sires for all the traits except the sire variance for fat yield for all the 4 lactations. The sire variance component constitutes about 6 % of the total variance in the daughters of imported sires for all traits throughout lactations compared to 4 % for the local sires. This means that the imported sires are significantly more variable than the local sires. This implies that the imported sires have more genetic variation or there is less environmental variation associated with the daughters of imported sires than the local sires. This may be due to the fact that imported sires are from different populations and are a restricted sample of bulls from these populations. This could also be partly explained by different production levels. Higher variances are found in high yielding compared to low yielding herds. The imported sires are a mixture from more than one country with different mean yields (recombination of genes from different countries of origin gives higher genetic variances). With little phenotypic variation or with a low heritability little progress can be made even with

Table 13. Sire, Residual, Phenotypic variances components within source within a lactation (values divided by 1,000 for milk and dollar value)^a.

Trait	Source	Variance	Lactation Number			
			1	2	3	4+
Milk	Imp.	Sire-V	68.4(.09)	89.1(.09)	155.9(.14)	130.6(.11)
		Res-V	686.8(.91)	932.0(.91)	974.3(.86)	1040.0(.89)
		Phen-V	755.1	1,021.0	1,130.2	1,170.6
	Loc	Sire-V	59.2(.08)	50.1(.06)	22.6(.02)	56.7(.06)
		Res-V	667.7(.92)	822.2(.94)	891.5(.98)	859.0(.94)
		Phen-V	726.9	872.4	914.1	915.7
Doll.	Imp.	Sire-V	6.6(.07)	9.0(.07)	6.5(.05)	12.4(.08)
		Res-V	82.0(.93)	111.7(.93)	125.3(.95)	128.7(.92)
		Phen-V	88.6	120.7	131.8	141.1
	Local	Sire-V	6.6(.08)	4.1(.04)	3.7(.03)	7.0(.06)
		Res-V	81.4(.92)	100.9(.96)	107.8(.97)	107.9(.06)
		Phen-V	88.1	105.0	111.5	114.9
Fat (kg)	Imp.	Sire-V	28(.02)	67(.04)	33(.02)	73(.04)
		Res-V	1,179(.98)	1,610(.96)	1,937(.98)	1,845(.96)
		Phen-V	1,207	1,677	1,970	1,918
	Loc	Sire-V	47(.04)	30(.02)	63(.04)	92(.06)
		Res-V	1,116(.96)	1,384(.98)	1,519(.96)	1,549(.94)
		Phen-V	1,163	1,414	1,582	1,641
Fat (%)	Imp.	Sire-V	.006(.04)	.011(.05)	.011(.04)	.017(.08)
		Res-V	.218(.96)	.225(.95)	.252(.96)	.205(.92)
		Phen-V	.224	.236	.263	.222
	Local	Sire-V	.003(.02)	.009(.04)	.004(.02)	.009(.04)
		Res-V	.202(.98)	.200(.96)	.220(.98)	.220(.96)
		Phen-V	.205	.209	.224	.229

^a Values in parenthesis are variance component percentages.

intense selection and high accuracy of evaluation. The variation required to practice an effective selection program in Zimbabwe is present for both the imported and the local sires.

Heritabilities

Heritabilities within source of germ plasm and within a lactation are given in Table 14. The estimates are not greatly different for the first three lactations, and the fourth lactation appears to have higher heritability. This may be due to the fact that cows that reach the fourth lactation are genetically superior due to selection and age effect as the cows are mature and produce more milk. The heritability estimates for milk yield are higher than the range quoted by Maijala and Hanna (1974) but lower than .41 for the first lactation found by Mpofu (1986) working with Zimbabwean data. The estimates for fat yield and fat percent are lower than literature values from other countries. This maybe due to large residual variances caused by measurement error as testing is done manually by technicians. It might also be a reflection of a large environmental influence within the country. A possible explanation might be that there is very low or little genetic variation for fat test in the sires used.

Table 14: Heritabilities and standard errors of heritabilities by source within a lactation.^{ab}

Trait	Source	Lactation Number			
		1	2	3	4+
Milk yield(kg)	Imported	.36(.13)	.35(.15)	.55(.22)	.45(.14) ^{ab}
	Local	.33(.12)	.23(.10)	.10(.06)	.25(.10)
Dollar value (Z\$)	Imported	.30(.12)	.30(.13)	.20(.10)	.35(.12)
	Local	.30(.11)	.16(.07)	.13(.07)	.24(.10)
Fat yield (kg)	Imported	.09(.06)	.16(.08)	.07(.05)	.15(.06)
	Local	.16(.04)	.08(.04)	.16(.09)	.22(.09)
Fat (%)	Imported	.10(.04)	.19(.09)	.17(.09)	.31(.11)
	Local	.07(.03)	.17(.08)	.07(.04)	.16(.07)

^a Heritability was calculated as: $h^2 = \frac{4 \times \text{sire variance}}{\text{phenotypic variance}}$

^b Standard error of heritability = $\frac{4B(B + KA)}{(A + B)^2 * ((.5(K - 1) KN))}^{.5}$

Where:

$B = \sigma^2_E$

$A = \sigma^2_S$

K = number of sires and

N = number of offspring per sire (Hazel and Terrill, 1945).

Addition of the relationship matrix may have resulted in higher heritability estimates (Lawlor and Pollack, 1983). Heritability appears lower in the data for local sires for all traits throughout lactations.

Sampling errors in determining the fat percentage using the Gerber Method.

The source of error when using the Gerber Method could be due to the following: 1. The scales not adjusted to zero. 2. The meters might have chips and milk will leak. 3. The jars might not have been agitated well or jars and plastic bags used for taking samples not kept at proper or correct conditions. 4. The real procedure for testing the fat percentage e.g., the strength of sulphuric acid and isoamyl alcohol might be wrong, the water temperature might not be optimum and the cooling and centrifuge rotations might be inadequate and may be samples are not thoroughly mixed and the general atmospheric conditions might not be suitable for the Gerber test e.g., darkness.

Genetic and phenotypic correlations

The genetic and phenotypic correlations for the three natural traits within source by lactation are in Table 15. The genetic correlations for milk and fat yield are not greatly different for the two populations whereas the phenotypic correlations are slightly higher for daughters of local sires compared to imported sires. The genetic correlations between milk and fat percent is more negative in the imported and more negative than quoted general literature values, and the phenotypic correlations are not significantly different for the two populations and agree with general literature values. The genetic correlation between fat and fat percent of $-.95$ for imported sires in lactation 1 and that between milk yield and fat percent of $.93$ in lactation 3 for local sires are way out

Table 15: Genetic, Phenotypic and Residual Correlations for the three Production Traits Within Source by Lactation ^a.

Traits	Source	Lactation Number			
		1	2	3	4+
Milk & Fat(kg)	Imported	rg .99(.007)	.81(.11)	.91(.06)	.77(.10)
		rp .70	.70	.68	.72
		re .69	.69	.70	.73
	Local	rg .98(.008)	.76(.14)	.96(.03)	.83(.09)
		rp .76	.74	.72	.75
		re .74	.74	.71	.75
		rg -.99(.005)	-.68(.17)	-.89(.07)	-.70(.12)
		rp -.26	-.23	-.17	-.18
		re -.23	-.20	-.11	-.13
Milk & Fat(%) Import.	Local	rg -.67(.15)	-.69(.17)	.93(.06)	-.08(.29)
		rp -.22	-.23	-.18	-.12
		re -.21	-.20	-.21	-.12
	Imported	rg -.95(.04)	-.15(.34)	-.61(.27)	-.09(.26)
		rp .49	.51	.58	.53
		re .52	.54	.62	.57
	Local	rg -.52(.17)	-.07(.34)	.97(.02)	.48(.23)
		rp .45	.47	.52	.54
		re .47	.48	.51	.55

^a Values in parenthesis are approximate standard errors for the genetic correlations calculated using the formula by Falconer (1981).

$$S.E. (rg) = \frac{1-rg^2}{2} \sqrt{\frac{S.E. (h1^2) * S.E. (h2^2)}{h1^2 * h2^2}}$$

of the biological range and might be an indication of large sampling errors. The same is true for genetic correlations between fat yield and fat percent. The phenotypic correlations between fat yield and fat percent are slightly higher in the daughters of imported sires compared to local sires. Milk and fat yield are almost perfectly positively correlated (.99) in the first lactation. Selection for one in all cases improves the other to almost the same extent. The genetic correlations between yield traits were large and positive showing that many genes affect both traits and intensive selection for one should bring about improvement in the other. The genetic correlation between milk yield and fat percentage was highly negative, indicating that many of the genes responsible for high milk yields cause the production of a lower percentage of fat in the milk.

This also indicates that any selection indices constructed to improve overall genetic merit may well need to be restricted to ensure a legally acceptable minimum concentration of fat percentage. The high negative genetic correlation between fat yield and fat percentage may be due to the low genetic variation in fat test of the sires. Misgrouping of sires is another possible reason as local sires are better in fat percent whereas imported sires are better in fat yield. The very high positive genetic correlation between fat yield and milk yield might also explain this high negative correlation between fat percent and fat yield.

CONCLUSIONS

1. Daughters of imported sires gave higher milk, dollars and fat yields compared to those of local sires but had a lower fat test for all four lactations.
2. Variance components (sire, phenotypic and residual) were larger in the daughters of imported sires than daughters of local sires for all four lactations.
3. Heritabilities for milk yield were higher than general literature values but those for fat yield and fat percent were lower than general literature values. Heritabilities were higher in the daughters of imported sires compared to those of local sires for all four lactations.
4. There were no source x area interactions for all the four traits and the four lactations (i.e., no GxE interaction as daughters of imported sires gave higher yields of milk, fat yield and dollars in all the 4 areas and those of local sires gave higher fat percentages in all the 4 areas).
5. Class x area interaction was significant for milk yield, dollar value and fat yield in lactations 1 and 4+.
6. Genetic correlations were higher than general literature values whereas phenotypic and residual correlations were within the range. Genetic correlations were slightly higher in the daughters of

imported sires whereas phenotypic correlations seem to be higher in the daughters of local sires.

RECOMMENDATIONS

1. Zimbabwe should continue to import semen and frozen embryos.
2. The sources of error with the fat test by the Gerber method should be identified and corrected.
3. An effective breeding program should be established for sire evaluation, young sire sampling and progeny testing.

APPENDICES

APPENDIX

Table A.A1. Least square means for source x area interaction for milk yield for lactation 4+

Area					

Source	1	2	3	4	Mean
Imported	5836	5654	6811	6217	6130
Local	5323	4923	5919	5692	5464
Mean	5580	5289	6365	5955	5797

Table A.A2. Least square means for class x area interaction for milk yield for lactation 1.

AREA					

Class	1	2	3	4	Mean
Pedigree	4465	6065	5233	6616	5595
Grade	4381	3957	4841	4186	4341
Appendix	5075	4016	5466	4862	4855
Mean	4640	4679	5180	5221	4930

Table A.A3 Description of Data Files

COL 1	ENTRY TYPE	
2-7	COW NUMBER	(M.S.R.N.)
8	CLASS:	1 = PEDIGREE
		2 = GRADE
		3 = APPENDIX
	BREED:	1 = AYRSHIRE 5 = RED SOIL
		2 = FRIESLAND 6 = CROSSBRED
		3 = GUERNSEY 7 = NIL
		4 = JERSEY 8 = SIMMENTALER
		9 = RED DANE
10-13	DATE OF BIRTH (MONTH AND YEAR)	
14-17	HERD CODE	
18	AREA 1 = MATEBELEAND	AREA 3 = MASHONALAND
	2 = MIDLANDS	4 = MANICALAND
19-24	SIRE'S CODE	
25-30	DAM'S M.R.S.N. (MILK RECORDING SCHEME NUMBER)	
31-34	AGE AT CALVING (MONTHS)	
35-38	CALVING INTERVAL (DAYS)	
39-42	DAYS DRY	
43-46	DATE OF CALVING	
47-48	LACTATION NUMBER	
49-54	YIELD (KG)	
55-58	LACTATION NUMBER	
59-62	MILK DAYS TIMES 3	
63-66	FAT PERCENTAGE	
67-68	NUMBER OF TESTS	
69-72	LACTATION END DATE	
73-74	LACTATION END CODE	
	1 = LP	4 = NURSE COW 7 = SLAUGHTERED
	2 = DRY	5 = SOLD (R/H) 8 = DIED
	3 = DRY - SICK	6 = SOLD (N/R/H) 9 = ABORTED
		(W/O)
75	QUARTER	
76-80	YEAR DATA COLLECTED	
78-80	EMPTY	

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