

# *Technological Economic for an Aggregate During Modernization Parameters of Milk Traits Weights of Healthy Dairy Cattle*

Ward M. Ashraf<sup>1</sup>, Hdud M. Ismail<sup>2</sup>, Al Zlitne A. Rabia, Aswehli A. Abdelatef<sup>1</sup>, Elgusbi M. Tarek<sup>3</sup>

<sup>1</sup> Department of Preventive Medicine, Faculty of Veterinary Medicine,  
University of Tripoli, Tripoli, Libya

<sup>2</sup> Department of Pathology and Clinical Pathology, Faculty of Veterinary Medicine,  
University of Tripoli, Tripoli, Libya

<sup>3</sup> Department of public health, Faculty of Medical Technology.  
University of Tripoli, Tripoli, Libya



**Abstract** - the conditions for increasing the efficiency of milk production is the modernization of farms with the introduction of technologies for loose maintenance and maintenance of livestock. Mainly the transition to a loose-fitting content allows to significantly reducing labour costs and the number of employees, to facilitate the work of operators directly servicing animals. At the same time, problems of mechanization and automation of processes are more easily solved. Productive longevity, expressed as the number of lactations per year or the milk yield per year during the lifetime, is a function of three or four variables: age at the first calving, calving interval, number of lactations during the lifetime and, respectively, milk / fat / protein yield in the standard lactation. Because these two functions are not linear, their expressions are approximated as linear functions of the considered variables. These functions express the phenotypic value of the trait, the number of lactation per year or the milk yield per year during the lifetime. Each of these functions is used to define an aggregate genotype.

The calculated aggregate genotypes put together usual traits, which are difficult to be used in an index-based selection. If these traits are genetically evaluated, the selection index for an animal results directly from the aggregate genotype by replacing the true breeding values with the estimated breeding values. The expected number of lactations may substitute the number of lactations of a cow, which did not finish its career.

**Keywords** - Dairy Cattle, Economic Parameters, Modernization, Aggregate Genotype

## **I. INTRODUCTION**

In spite of the state support measures taken in recent years, low productivity, severe and unattractive working conditions for cattle breeders due to the use of outdated technologies and equipment, and an acute shortage of qualified personnel still remain serious problems in livestock production. Theory concerning linear index based selection (1,4,12,16) is well known, but weighting of the traits in the aggregate genotype is a special and unsolved problem. It is difficult to obtain economic weights for an aggregate genotype of milk traits (milk, fat or protein yield), reproductive traits (calving interval), precocity traits (age at

the first calving) and longevity traits (number of lactations during the lifetime). the main welfare problems that may arise through breeding, feeding, housing, managing or otherwise manipulating cows for high productivity as follows:

- Hunger or acute metabolic disease, due to an imbalance between nutrient supply and demand;
- Chronic discomfort, through bad housing, loss of condition, etc.

- Chronic pain or restricted movement due to distortion of body shape, bad housing or management;
- Increased susceptibility to infectious or metabolic disease;
- Metabolic or physical exhaustion after prolonged high production.

A solution for this problem could be to have an aggregate genotype based on an optimum or prospective genotype, but it is difficult to know this one.

If it is interesting to select for a composite trait, which is expressed as function of usual traits, but difficult to put them together into a selection index, the solution could be to make an approximation of the aggregate genotype. But, on the other hand, at times the role of technology specialists increases. They should have a broad erudition in matters of animal maintenance and maintenance, livestock house planning, mechanization and automation of production processes and herd management(6,8,15), the specifics of preparation for the transition and the transition to new methods of dairy farming .

Defining a composite trait, like the number of lactations per year or the milk yield per year during the lifetime, it is possible to obtain, in the same aggregate genotype, the weights of age at the first calving, calving interval, lifetime lactations' number and milk traits. Further, one demonstrates that weights are function of the implied traits means. In livestock, unlike industry, the main means of production, processing raw materials in the final product, are living beings with all the diversity of their individual characteristics and behavioural responses. In this case, the cow acts not only as a means of processing feed in milk, but also as a means of reproduction of the herd. The economic future of the dairy industry is related directly to public acceptance of its breeding and production practices. It is important to the dairy industry that welfare problems should be addressed before there is widespread condemnation of breeding and management practices. A new breeding goal aimed at improving fitness and tolerance of metabolic stress is necessary to prevent the decrease in the quality of life of dairy cows and instead, perhaps, enhance it.

## II. MATERIALS AND METHODS

The method applies to productive or functional longevity traits in dairy cattle, but may be extended to similar species. The longevity traits may have different expressions, but the number of lactations per year and the milk yield per year during the lifetime are some of the most important. In this study, the number of lactations per year during the lifetime

was not neglected, because no cow with low yield is maintained in a herd.

The method consists in building for each phenotypic value of a longevity trait a linear combination of the phenotypic values of some important usual traits. On this basis, one obtains definitions of the aggregate genotypes.

It is possible to demonstrate that the number of lactations per year during the lifetime (L) is a function of three variables: age at the first calving (v), calving interval (c), and number of lactations during the lifetime (n). Indeed, the length of productive life is  $v+n \cdot c$ , where  $c=(c_1+c_2+\dots+c_n)/n$ , and  $c_k$  is the calving interval after the parturition of rank k. This trait is used as a repeated one. By consequence, the number of lactations per year during the lifetime (L) is given by the function:

$$L(v, c, n) = n / (v + n \cdot c)$$

Similarly, the milk / fat / protein yield per year during the lifetime (Y), which are considered as repeated traits, is a function (Y) of four variables, given by the formula:

$$Y(v, c, n, p) = n \cdot p / (v + n \cdot c) \quad ,$$

with

$$p = (p_1 + p_2 + \dots + p_n) / n$$

where  $p_k$  is the milk /fat / protein yield in the standard lactation of rank  $k=1,2,\dots,n$ .

More generally, let us consider

$$P = f(P_1, P_2, \dots, P_n)$$

a phenotypic value (P) of a composite trait, as a function of  $P_1, P_2, \dots, P_n$ , which are phenotypic values of other n traits.

If it is possible to expand this function into series, by denoting the means,  $\mu = E(P)$  and  $\mu_k = E(P_k)$ , and limiting resulted expression to the linear terms, one obtains:

$$P = f(P_1, P_2, \dots, P_n) \approx \mu + Q_1 \cdot (P_1 - \mu_1) + Q_2 \cdot (P_2 - \mu_2) + \dots + Q_n \cdot (P_n - \mu_n)$$

where  $Q_k$  is the value of the derivative  $\partial f / \partial P_k$  for  $P_1 = \mu_1, P_2 = \mu_2, \dots, P_n = \mu_n$

From this formula, using substitution

$$P = a + e \quad \text{and} \quad P_k = a_k + e_k$$

Where a and e,  $a_k$  and  $e_k$  are breeding values and residuals respectively, it results the definition of an

aggregate genotype (H) of  $a_1, a_2, \dots, a_n$ , based on the approximate breeding value (a):

$$a \approx Q_1 \cdot a_1 + Q_2 \cdot a_2 + \dots + Q_n \cdot a_n = H$$

The above procedure was applied to obtain aggregate genotypes based on the functional longevity, expressed as number of lactations per year and the milk yield per year during the lifetime.

### III. RESULTS

An algorithm was developed for the technological calculation of livestock, taking into account the pace and rhythm of grouping, the working hours of sections.

□ rate complete (  $m_i$  ) - number of animal heads (  $T_f$  ) entering the shop average daily

$$m_i = T_p / 365;$$

□ the picking rhythm (  $P_i$  ) is the interval between two consecutive receipts to the given workshop of technological groups of animals.

□ the duration of use of the section, or the cycle of operation of the section (  $T_i$  ) is the interval between two consecutive arrivals of groups of animals into this section.

The smaller the pick-up rhythm, the less the difference in age or physiological state of the animals in one technological group, the more aligned the composition will be, and the easier it will be to maintain it.

It should be noted that the size of the technological group, the pace and rhythm of the assembly of the section, as well as the number of seats in it, are in close relationship and cannot be chosen arbitrarily. The more the assembly rate, the more for a given rhythm will be the size of the technological group, and the more the number of seats in the section. If the picking rhythm is a multiple of the week, i.e. is divided into the number 7, then all the movements of technological groups of animals from the shop to the workshop always fall out on the same day of the week, which contributes to the improvement of technological discipline.

The work cycle of the section is equal to the sum of the duration of the period of keeping the animals (  $P_i$  ) and the duration of its sanitation (  $D_i$  ):

$$T_i = P_i + D_i$$

In order to successfully combat infectious diseases, sections of livestock premises should be sanitized when the livestock is changed. This is possible only if one of the basic rules of industrial livestock - the use of sections on the principle of "empty-busy." To comply with this principle, it is necessary that the duration of the operation cycle of the

sections in each workshop satisfies two conditions. First, it must be a multiple of the accepted rhythm, i.e. contain an integer number of rhythms:

$$T_i = C_i \cdot P_i$$

Where  $C_i$  is an integer

Secondly, the duration of the measure should be longer than the period of keeping the animals in this shop. Thus, the cycle time of the sections and the rhythm of their configuration cannot be chosen arbitrarily. The cyclic transition of animals from phase to phase creates a kind of biological conveyor, the average rate of movement of which depends on the number of forage cows on the farm and on the average duration of the inter-ovary cycle. It is important to modernize the dairy farms in accordance with the physiological requirements of animals to the conditions of the production process at each phase of this conveyor.

Any project should begin with the definition of the technological parameters of the projected farm, such as the planned livestock(5,10), the number and size of technological groups in each phase and in each workshop (2,3). The number of livestock necessary for them. At the same time, it is very important in industrial livestock production to take into account the pace of movement of the live conveyor on the farm, the rhythm of the formation and movement of technological groups. The method refers to dairy cattle, but may be extended to similar species. Productive or functional longevity may have different expressions, but the number of lactations per year and the milk yield per year are the most important. Currently, the calculation is done automatically on the computer. The results of the technological calculation are summarized in several compact tables (7,13,14) containing the main parameters of all sectors, shops and sections of the farm. The table shows an example of a calculation for the production sector of a farm for 6850 dairy cows.

An increase in milk production was observed in the early lactation and followed by a gradual decrease until the end of lactation (Table 1). Thus, the average test-day milk yield was the highest during the beginning of lactation. The trend of standard deviation for test-day milk yield across lactation was almost same. The number of observations decreased as the lactation progressed (Table 1).

Table 1. Days in milk (DIM), number of observation (N), means and standard deviation (SD) for milk yield

| DIM     | N    | Mean | SD   |
|---------|------|------|------|
| 5-30    | 601  | 12.9 | 3.98 |
| 31-60   | 729  | 12.9 | 3.75 |
| 61-90   | 733  | 12.1 | 3.75 |
| 91-120  | 730  | 11.5 | 3.76 |
| 121-150 | 743  | 11.0 | 3.64 |
| 151-180 | 738  | 10.7 | 3.70 |
| 181-210 | 713  | 10.3 | 3.82 |
| 211-240 | 658  | 10.0 | 3.76 |
| 241-270 | 606  | 9.8  | 3.67 |
| 271-305 | 599  | 9.3  | 3.61 |
| All     | 6850 | 11.1 | 3.93 |

Calving interval was derived as the interval between consecutive calving for the first three lactations. Means, standard deviations (SD) and coefficients of variation (CV %) for LMY, LL, AFC CI are given in Table 2.

The large CV% for LMY reflects the great variation between individual cows in these traits.

Table 2. Descriptive statistics of lactation milk yield (LMY), age at first calving (AFC), calving interval (CI) and lactation length (LL)

| Trait       | No. of records | Mean   | SD    |
|-------------|----------------|--------|-------|
| LMY, kg     | 1841           | 1287.9 | 509.6 |
| AFC, months | 1767           | 44.1   | 7.2   |
| CI, days    | 1841           | 474.5  | 125.5 |
| LL, days    | 1837           | 287.1  | 50.7  |

lactation milk yield (LMY), lactation length (LL), age at first calving (AFC) and calving interval (CI) using the following animal model:  $Y = Xb + Za + e$

where  $y$  is a vector of observations for LMY, LL, AFC and CI in each lactation,  $b$  and  $a$  and  $e$  are vector of fixed effects, random animal effects, and random residuals, respectively and  $X$  and  $Z$  are the incidence matrices relating fixed and random animal effects to observations, respectively. The random effects will be assumed to be normally distributed with a mean=0 and variance as follows:  $a \sim N(0, A I \sigma^2_a)$  and  $e \sim N(0, I \sigma^2_e)$  where  $\sigma^2_a$  and  $\sigma^2_e$  are animal and residual variances, respectively, and  $A$  and  $I$  are the numerator relationship and identity matrices, respectively. The models for LMY, CI and LL included fixed effects of year-season of calving and age at calving.

The number of lactations during the lifetime ( $L$ ) is a function of three variables: age at the first calving ( $v$ ), calving interval ( $c$ ) as an average, and number of lactations during the lifetime ( $n$ ):

$$L(v, c, n) = n / (v + n \cdot c)$$

By denoting  $\mu_L = E(L(v, c, n))$ ,  $\mu_v = E(v)$ ,  $\mu_c = E(c)$ ,  $\mu_n = E(n)$ , the expansion into series of this function limited to the linear terms is:

$$L = L(v, c, n) \approx \mu_L + Q_v \cdot (v - \mu_v) + Q_c \cdot (c - \mu_c) + Q_n \cdot (n - \mu_n),$$

where

$$\begin{aligned} Q_v &= -(\mu_v + \mu_c \mu_n)^{-2} \cdot \mu_n \\ Q_c &= -(\mu_v + \mu_c \mu_n)^{-2} \cdot \mu_n^2 \\ Q_n &= (\mu_v + \mu_c \mu_n)^{-2} \cdot \mu_v \end{aligned}$$

If we denote breeding values of  $v$ ,  $c$ ,  $n$  by  $a_v$ ,  $a_c$ ,  $a_n$ , one results the approximate breeding value  $a$  of the composite trait  $L$  and the aggregate genotype:

$$a \approx Q_v \cdot a_v + Q_c \cdot a_c + Q_n \cdot a_n = H_L$$

For example, if  $\mu_v = 2.8$  years,  $\mu_c = 1.1$  years and  $\mu_n = 5$ , then

$$H_L = -0.073 \cdot a_v - 0.363 \cdot a_c + 0.041 \cdot a_n$$

The milk / fat / protein yield per year during the lifetime ( $Y$ ) is a function of four variables: age at the first calving ( $v$ ), calving interval ( $c$ ), number of lactations during the lifetime ( $n$ ), and milk yield per year during the lifetime ( $p$ ).

If a trait may be repeated, then it is supposed that its phenotypic value is the average of measurements. The resulted expression of  $Y$  is

$$Y(v, c, n, p) = n \cdot p / (v + n \cdot c)$$

By denoting  $\mu_L = E(L(v, c, n, p))$ ,  $\mu_v = E(v)$ ,  $\mu_c = E(c)$ ,  $\mu_n = E(n)$ ,  $\mu_p = E(p)$ , the expansion into series of this function, limited to the linear terms is:

$$Y = Y(v, c, n, p) \approx \mu_Y + S_v \cdot (v - \mu_v) + S_c \cdot (c - \mu_c) + S_n \cdot (n - \mu_n) + S_p \cdot (p - \mu_p),$$

where

$$\begin{aligned} S_v &= \mu_p \cdot Q_v = -(\mu_v + \mu_c \mu_n)^{-2} \mu_p \mu_n \\ S_c &= \mu_p \cdot Q_c = -(\mu_v + \mu_c \mu_n)^{-2} \mu_p \mu_n^2 \\ S_n &= \mu_p \cdot Q_n = (\mu_v + \mu_c \mu_n)^{-2} \mu_p \mu_v \\ S_p &= (\mu_v + \mu_c \mu_n)^{-1} \mu_n \end{aligned}$$

Denoting by  $a_v$ ,  $a_c$ ,  $a_n$  and  $a_p$  the breeding values of  $v$ ,  $c$ ,  $n$  and  $p$ , one results the approximate breeding value  $a$  of the composite trait and the aggregate genotype

$$a \approx S_v \cdot a_v + S_c \cdot a_c + S_n \cdot a_n + S_p \cdot a_p = H_Y$$

or

$$H_Y = \mu_p \cdot H_L + (\mu_v + \mu_c \mu_n)^{-1} \mu_n \cdot a_p$$

For example, if  $\mu_v = 2.8$  years,  $\mu_c = 1.1$  years,  $\mu_n = 5$ , and  $\mu_p = 120$  kg fat, then

$$\begin{aligned} H_Y &= -8.71 \cdot a_v - \\ &43.548 \cdot a_c + 4.877 \cdot a_n + 0.602 \cdot a_p \end{aligned}$$

For the breeding and fattening sectors, in addition to these parameters, the age and weight of animals are also indicated when entering the workshop and transferring from the workshop, which is very important in the future to determine the dimensions of the boxes(17). It is important to note that the technique allows to provide rhythmic movement of technological groups of animals in phases of the biological cycle, i.e. shops and sections of the farm, which cannot be done using the generally accepted method of determining the number of livestock in per cent of the livestock or in the herd turnover.

$$H_Y = -(\mu_v + \mu_c \mu_n)^{-2} \mu_p \mu_n \cdot a_v - (\mu_v + \mu_c \mu_n)^{-2} \mu_p \mu_n^2 \cdot a_c + (\mu_v + \mu_c \mu_n)^{-2} \mu_p \mu_v \cdot a_n + (\mu_v + \mu_c \mu_n)^{-1} \mu_n \cdot a_p$$

and

$$H_Y = -8.71 \cdot a_v - 43.548 \cdot a_c + 4.877 \cdot a_n + 0.602 \cdot a_p,$$

$$\text{if } \mu_v = 2.8 \text{ years, } \mu_c = 1.1 \text{ years, } \mu_n = 5 \text{ and } \mu_p = 120 \text{ kg fat}$$

$$H_L = -(\mu_v + \mu_c \mu_n)^{-2} \cdot \mu_n \cdot a_v - (\mu_v + \mu_c \mu_n)^{-2} \cdot \mu_n^2 \cdot a_c + (\mu_v + \mu_c \mu_n)^{-2} \cdot \mu_v \cdot a_n$$

and

$$H_L = -0.073 \cdot a_v - 0.363 \cdot a_c + 0.041 \cdot a_n,$$

$$\text{if } \mu_v = 2.8 \text{ years, } \mu_c = 1.1 \text{ years and } \mu_n = 5.$$

Based on the results of the technological calculation, cyclograms of livestock movement can be constructed, which allow one to plan work in each workshop and with each technological group on a daily basis(15,18).

In addition, in the lactation shop, the movement of groups is clearly linked to the feeding classes. The proposed algorithm, programs and methods of graphical representation of calculation results are repeatedly tested and are constantly used in the development of farm modernization projects. They allow not only to determine the rational parameters of the enterprise, but also to control the effectiveness of its operation, using information on the dynamics of changes in the mass and productivity of animals, the consumption of feed, water and other resources, the amount of waste, etc. and comparing the actual figures with the calculated ones.

#### IV. CONCLUSIONS

1. It is difficult to put together in the same index milk traits (milk, fat or protein yield), reproductive traits (calving interval), precocity traits (age at the first calving) and longevity traits (number of lactations during the lifetime). Defining a composite trait, like the number of lactations per year or the milk yield per year during the lifetime, it is possible to obtain, in the same aggregate genotype, the weighting of age at the first calving ( $v$ ), calving interval ( $c$ ), lifetime lactations' number ( $n$ ) and milk yield ( $p$ ) traits.
2. The longevity traits implied being nonlinear functions, their expressions are approximated as linear functions. The presented results are based only on the linear terms, but the procedure may be extended.
3. For the aggregate genotype ( $H$ ) based on the number of lactations during the lifetime, as a linear combination of age at the first calving breeding value ( $a_v$ ), calving interval breeding value ( $a_c$ ), number of lactations during the lifetime breeding value ( $a_n$ ) and fat yield one obtains for given means:

4. If the breeding value of each considered trait is predicted, for example by a BLUP procedure, the selection index for an animal results directly from the aggregate genotype by replacing the true breeding values with the estimated breeding values.
5. It is very useful to have pedigree information and phenotypic information of relatives. An unhappy but necessary approximation is to substitute the number of lactations of a cow that did not finish its career with the expected number of lactations.

## REFERENCES

- [1] Albuquerque L G, Keown J F and Van Vleck L D 1996 Genetic parameters of milk, fat and protein yields in the first three lactations, using an animal model and restricted maximum likelihood. *Brazilian Journal of Genetics* 19: 79-86.
- [2] De Varies M J, Van Der Waaij E H and Van Arendowk J A M 1998 Estimation of genetic parameters for litter size in sheep: A comparison of repeatability and a multivariate model. *Animal Science*. 66: 685-688.
- [3] Dong M C, Van Vleck L D and Wiggans G R 1988 Effect of relationships on estimation of variance components with an animal model and restricted maximum likelihood. *Journal of Dairy Science* 71: 3047-3052.
- [4] Madalena, F.E., Peixoto, M.G.C.D. & Gibson, J., 2012. Dairy cattle genetics and its applications in Brazil. *Livestock Res. Rural Dev.* 24, Article #97. <http://doi.org/http://www.lrrd.org/lrrd24/6/made24097.htm>
- [5] Meyer K 2008 WOMBAT A program for Mixed Model Analyses by Restricted Maximum Likelihood. USER NOTES. Version 1.0, Animal Genetics and Breeding Unit, University of New England, Armidale, NSW 2351, Australia.
- [6] Santos, D.J.A., Peixoto, M.G.C.D., Borquis, R.R.A., Verneque, R.S., Panetto, J.C.C. & Tonhati, H., 2013. Genetic parameters for test-day milk yield, 305-day milk yield, and lactation length in Guzarat cows. *Livest. Sci.* 152, 114-119.
- [7] Statistical Analysis Systems (SAS). 2011. SAS/STAT User's guide, Release 9.3. SAS Institute Inc, Cary, North Carolina, USA.
- [8] Andersen-Ranberg, I.M., Klemetsdal, G., Heringstad, B. & Steine, T. 2005. Heritabilities, genetic correlations, and genetic change for female fertility and protein yield in Norwegian dairy cattle. *J. Dairy Sci.* 88, 348-355.
- [9] Gilmour, A.R., Gogel, B.J., Cullis, B.R., Welham, S.J. & Thompson, R. 2006. ASReml User Guide Release 2.0 VSN International Ltd., Hemel Hempstead, HP1 1ES, UK.
- [10] Haer, L.C.M. de. 2009. Estimation of genetic parameters of fertility traits for dairy cattle in The Netherlands and Flanders. CRV Report, Arnhem, The Netherlands.
- [11] Jamrozik, J., Fatehi, J., Kistemaker, G.L. & Schaeffer, L.R. 2005. Estimation of genetic parameters for Canadian Holstein female reproduction traits. *J. Dairy Sci.* 88, 2199- 2208.
- [12] SAS 2009 User's guide, Release 9.2. SAS Institute Inc., Cary, NC, USA.
- [13] Torres V, Ramos N, Lizazo D, Monteagudo F and Noda A 2008 Statistical model for measuring the impact of innovation or technology transfer in agriculture. *Cuban Journal of Agricultural S.* Torres V, Martínez O, Noda A, Medina Y and Rodríguez Y 2010 Evaluation of the statistical suppositions in the statistical model of impact measuring (MEMI), in a case study. II Workshop of Computer Science and Applied Biostatistics to the Agricultural Sciences, III Congress of Animal Production, 15-19 November, Havana, Cuba (CD-ROM) *Sience*, 42, 131-137
- [14] Torres V, Martínez O, Noda A, Medina Y and Rodríguez Y 2010 Evaluation of the statistical suppositions in the statistical model of impact measuring (MEMI), in a case study. II Workshop of Computer Science and Applied Biostatistics to the Agricultural Sciences, III Congress of Animal Production, 15-19 November, Havana, Cuba (CD-ROM)
- [15] Urioste J I, Rekaya R, Gianola D, Fikse W F and Weigel K A 2003 Model comparison for genetic evaluation of milk yield in Uruguayan Holsteins. *Livestock Production Science* 84: 63-73.
- [16] WOLF, J., WOLFOVÁ, M. and KRUPA E. (2013) User's Manual for the program Package ECOWEIGHT (C Programs for Calculating Economic Weights in Livestock), Version 6.0.4. Part 1: Programs EWBC (Version 3.0.4) and EWDC (Version 2.2.3). Prague-Uhřetěves: Research Institute of Animal Production. 222 p.

- [17] ZAVADILOVÁ, L. et al. (2011) Genetic parameters for somatic cell score in the first three lactations of Czech Holstein and Fleckvieh breeds using a random regression model. Czech Journal of Animal Science, vol. 56, no. 6, pp. 251–260.
- [18] Zeleke, B., Kebede, K. & Kumar, B.A., 2016. Estimation of genetic parameters for reproductive traits of Fogera and Holstein Friesian crossbred cattle at Metekel Ranch, Amhara region, Ethiopia. Online J. Anim. Feed Res. 6, 90-95.