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Sire Evaluation and Genetic Trends of Pre-Weaning Growth Traits of Fogera Cattle at Metekel Ranch, Amhara, Region, Ethiopia

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ABSTRACT

The Best Linear Unbiased prediction (BLUP) procedure of animal evaluation using WOMBAT was done for estimation of breeding values of sires. Estimated overall mean breeding values for BWT, AWWT and PADG were 0.046 ± 0.23 kg, 0.26 ± 2.4 kg and 0.0002 ± 0.009kg, respectively. The trends of sire breeding values for all growth traits were negative. The hypothesis, selection based on phenotypic performance of animals can bring genetic progress in the herd was rejected and it is concluded that selection based on physical appraisal did not bring genetic progress. The selection method should be updated and must be based on genetic evaluation of individual animals. The coefficient of change in genetic trends for BWT, AWWT and PADG were -0.00134 ± 0.0012 kg, -0.05 ± 0.011 kg and -0.0001 ± 0.000045 kg respectively. The reduction of genetic potential of sires over years implies that the selection method based on the physical appraisal was not efficient.

Keywords: Fogera Breed, Growth Traits, Metekel Ranch, Sire Breeding Value.

I. INTRODUCTION

Estimation of breeding value of sires is one of the most important aspects of genetic improvement program. From genetic conservation standpoint, sire selection is by far the most speculative part of cattle breeding simply because a single sire can have a large genetic impact on a herd and the genetic makeup of most population encompassed by a few highly selected animals (Tseveenjav *et al*., 2001). Selecting genetically superior bulls is the quickest path to herd genetic improvement. Several methods of estimation of breeding value of sires have been developed to enhance the accuracy and efficiency of sire evaluation under varying management and environmental conditions (Singh and Joshi, 2003; Aynalem *et al*., 2010).

The objective of selection is to choose those animals with the best breeding values to become parents of the next generation. The breeding value for sires should also be computed to help in the design of breeding program. At present, the selection criteria for young males for future breeding at Metekel ranch is based on physical appraisal of the young bulls which may not adequately represent the real potential of the sire. Selection of the sire should thus be based on its breeding value. It is with this underlying fact that this study was initiated with the objective of to estimate the breeding value of sire and with the overall hypothesis that Selection based on phenotypic performance of animals will bring genetic progress in the herd.

II. METHODS AND MATERIAL

Description of the study Area

Metekel Cattle Breeding and Improvement Ranch is found in Guangua district of Awi zone in Amhara

National Regional State, and is situated about 505 km North-west from Addis Abeba. The annual mean relative humidity is 61.7% and it reaches to high from June to October (76.7-83.8%). The ranch receives an average annual rain fall of 1730.0 mm; average temperature ranges from 13.7 to 29.5^0, with monthly mean minimum-maximum occurring in January (9.4^0) and in April (35.0^0), respectively (ENMA unpublished). The rain fall distribution is bi-modal. The area has three rain seasons; long rainy season (June-October), short rainy season (March-May) and dry season (November-February) (Melaku et al., 2011a, b and Addisu and Hegde, 2003).

Breeding Program

The breeding program has two components: selection and crossbreeding. The establishment of the pure breed unit was meant for the conservation of the Fogera breed and for providing heifers to cross- breed to exotic dairy sires (by Artificial insemination). In the selection program or pure breed unit, the tradition was that the Fogera bulls used to run together with the Fogera cows. In cross breeding program; crossbred animals are produced through artificial insemination of Fogera cows with Friesian semen. Around three to six months of pregnancy, the F_1 cross heifers are sold to farmers for milk production (Melaku et al., 2011a, b). Very recently the ranch started to distribute non-pregnant F_1 cross heifers.

Data Source and management system

Data found in Metekel ranch was collected for this study. In the study, farm records of Metekel ranch which was 24 years (i.e. from 1988-2011) data was used. All records of animals born 1988 and 2011 were included in this study. There was a service record loss from 2004-2006 and the sires used during these years were not evaluated. Data which were analyzed include: for BWT, AWWT

$$\text{AWWT} = \frac{\text{actual weaning weight} - \text{birth weight}}{\text{No.of days from birth to weaning}} \text{ x } 240 + \text{birth weight}$$

and PADG.

Statistical analysis

The Best Linear Unbiased prediction (BLUP) procedure of animal evaluation using WOMBAT program was done for estimation of breeding values of sires. Best Linear Unbiased Predictions (BLUP) procedure using the individual animal model has become the worldwide standard for the prediction of breeding values of farm animals (Javed et al., 2001). It can make maximal use of information from relatives and it is the most effective method of separating genetic and environmental effects and permits across year evaluations, provided that there are genetic links between years (Mrode and Thompson, 2005). Sire estimated breeding value obtained from a sire model may be slightly less accurate both due to lower accuracy (in case of few progeny / sire) and potential bias, because there is no correction for differences between dams (Sun et al., 2009). If mates are chosen in some nonrandom manner, and if the model does not account for mating schemes, sire evaluations may be adversely affected and could be biased (Schaeffer, 1983). In addition, the disadvantage of the sire model could be more obvious in genetic evaluations based on data collected over many years from a population under parental selection, because the model does not account for the selection effects on mates. Animal model could provide EBV with higher accuracy than the sire model (Sun et al., 2009). Due to this Animal model was used for sire breeding value estimation. The breeding values of sires for growth performance were estimated by using BWT, AWWT and PADG of their progenies through uni-variate analyses. Sires with at least five daughters were used for the analysis. Trends of sire breeding value were estimated by regression of the average predicted sire breeding values in the particular trait on year.

The model equation used for sire evaluation was:

$Y = Xb + Z_1a + Z_2m + Z_3c + e$ (cova, m = 0)

Where, Y = the vector of records, b = vector of fixed effects, X = incidence matrix of fixed effects, a = vector of direct additive genetic effect, m = vector of maternal additive genetic effect, c = vector of permanent environmental effect, Z_1 = incidence matrix for direct additive genetic effect, Z_2 = incidence matrix for maternal additive genetic effect, Z_3 = incidence matrix

for permanent environmental effect, e = vector of random errors.

III. RESULT AND DISCUSSION

The estimated mean sire breeding values were 0.046 ± 0.23 kg, 0.26 ± 2.4 kg and 0.0002 ± 0.009kg, respectively for BWT, AWWT and PADG (Table 2). As there is no selection done based on any quantitative measurement on the study area this result was expected. There was a notable difference in the range of the breeding values of the sires. The range of the breeding value estimated was 1.22 kg, 14.34kg and 0.05kg of breeding value respectively for BWT, AWWT and PADG and it is important for genetic selection. The top ranking sire for BWT had estimated breeding value of 0.76kg while the bottom ranked sire had -0.47kg. The top ranking sire for AWWT and PADG and had estimated breeding value of 6.01kg and 0.02kg while the bottom ranked sire had -8.32kg and -0.03kg below the population average breeding value respectively for AWWT and PADG (Table 2).

Table 2. Mean SD, minimum, maximum and range value of estimated breeding value of sire for growth traits

Parameters	Mean(kg)	SD	Min (kg)	Max (kg)	Range
BWT	0.046	0.23	-0.47	0.77	1.22
AWWT	0.26	2.4	-8.33	6.01	14.34
PADG	0.0002	0.009	-0.03	0.02	0.05

Trends of sire breeding value for BWT, AWWT and PADG are presented in Figure1, 2 and 3. Genetic trend lines were negatively sloped for all traits. A fluctuating sire breeding value trend was observed across years for all traits. The coefficient of change in genetic trends for BWT, AWWT and PADG were -0.00134 ± 0.0012 kg, -0.05 ± 0.011 kg and -0.0001 ± 0.000045 kg respectively. The genetic progress for all traits was negative. The sire breeding value trends shows an average reduction of 0.00134 ± 0.0012 kg, 0.05 ± 0.011kg and 0.0001 ± 0.000045kg per year, respectively for BWT, AWWT and PADG. Decreasing trends observed in BWT, AWWT and PADG over the years for least square means estimates were consistent with the negative annual sire breeding value trend. It implies inefficiency in selection for growth traits and the selection method based on physical appraisal which is used in the past time doesn't result any genetic gain. Herds selected on the basis of estimated breeding values have higher genetic trends than those selected based on physical appraisal (Hofgren and Schinckel, 1998; Plasse *et al*., 2002; Wasike, 2006). The breeding program was not effective and it needs re-evaluation of management practices and earlier selection programs for efficient growth improvement.

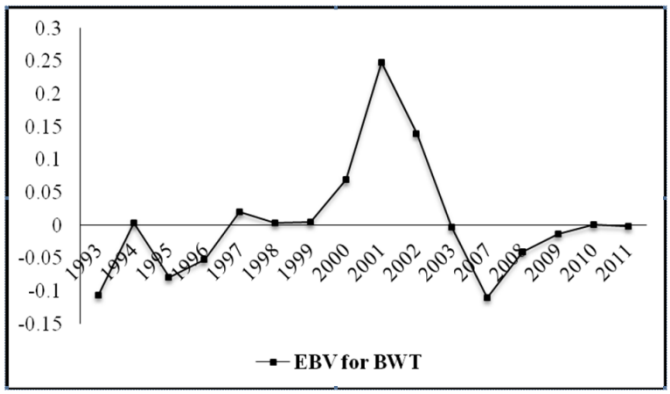

Figure 1. Trend of sire breeding value for BWT

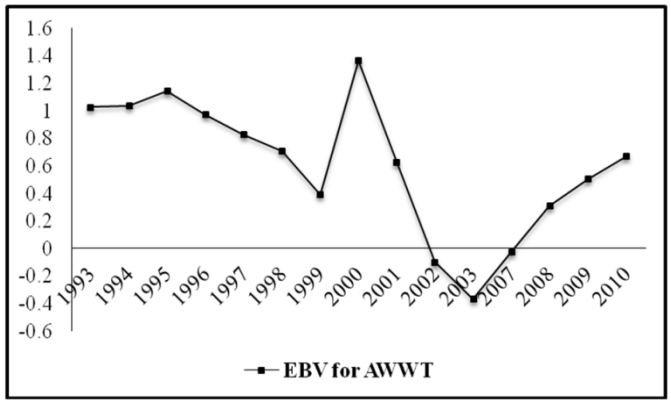

Figure 2. Trend of sire breeding value for AWWT

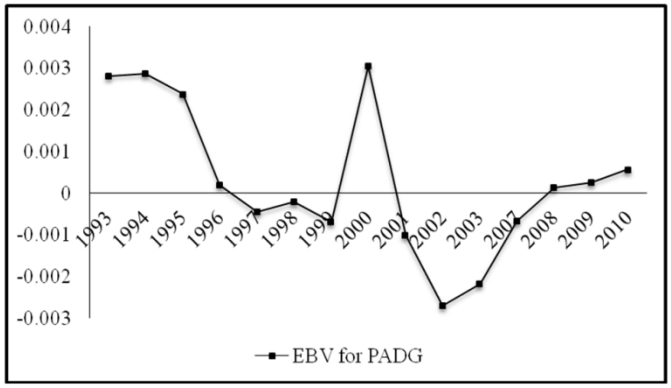

Figure 3. Trend of Sire breeding value for PADG

IV. CONCLUSION

Negative trend of sire breeding value for all growth traits were observed. Results indicate no genetic progress of performance of Fogera cattle on the past selection and management conditions. The selection method adopted by the ranch on the last time based on the physical judgment doesn't result genetic improvement. Therefore, the hypothesis that selection based on phenotypic performance of animals will bring genetic progress in the herd was rejected. There was no apparent voluntary selection practiced with concrete objective. Consequently, there is a need to change the selection method.

V. REFERENCES

[1] Addisu Bitew and Hegde B P 2003 Evaluation of reproductive and growth performance of Fogera cattle and their F1-Friesian cross at Metekel Ranch, Ethiopia. Proceedings of the 10th annual conference of the Ethiopian Society of Animal Production (ESAP) held in Addis Ababa, Ethiopia. ESAP, Addis Ababa.pp119-126.

[2] Aynalem Haile, Joshi B K, workinehi Ayalew, Azage Tegegne and Singh A 2010 Comparison of sire evaluation methods in Holstein Friesian in the central highlands of Ethiopia. Indian Journal of Animal Sciences 80(12).

[3] Hofgren D L and Schinckel A P 1998 Within-herd genetic trends provide important information for breeders. In: Proceedings of the Swine day Symposium, University of Purdue: 185- 187.

[4] Javed K, Mohiuddin G and Akhtar P 2001 Heritability estimates of some productive traits in Sahiwal cattle. Pakistan vet. J., 21(3): 114-117.

[5] Melaku Minale, Zeleke Mekuriya, Getinet Mekuriaw and Mengistie Taye 2011a Pre-weaning growth performances of Fogera calves at Metekel cattle improvement and multiplication ranch, North West Ethiopia. Livestock Research for Rural Development. Volume 23, Article #182. Retrieved November 25, 2011, from http://www.lrrd.org/lrrd23/9/mela23182.htm.

[6] Melaku Minale, Zeleke Mekuriya, Getinet Mekuriaw and Mengistie Taye 2011b Reproductive Performances of Fogera Cattle at Metekel Cattle Breeding and Multiplication Ranch, North West Ethiopia. J. Anim. Feed Res., 1(3): 99-106.

[7] Mrode R A and Thompson R 2005 Linear models for the prediction of Animal Breeding values. Second edition. CABI Publishing. Oxon, UK.

[8] Plasse D, Verde O, Arango J, Camaripano L, Fossi H, Romero R, Rodriguez C M and

[9] Rumbos J L 2002 (Co) variance components, genetic parameters and annual trends for calf weights in a Brahman herd kept on floodable savanna. Genet. Mol. Res. 1(4), 282-297.

[10] Schaeffer L R 1983 Effectiveness of model for cow evaluation intraherd. J. Dairy Sci. 66:874-880.

[11] Singh A and Joshi B K 2003 Practical manual on animal breeding. Division of Dairy cattle breeding, National Dairy research institute, Karanal, India. pp213.

[12] Sun C, Madsen P, Nielsen U S, Zhang Y, Lund M S and Su G 2009 Comparison between a sire model and an animal model for genetic evaluation of fertility traits in Danish Holstein population. J. Dairy Sci. 92:4063-4071.

[13] Tseveenjav B, Maiwashe A, Golden B L and Blackburn H D 2001 Predicted rate of inbreeding for a closed line of Hereford cattle. Proc. Western Section. American Society of Animal Science. 52. Available at http://www.asaa.org/western/02proc/18984.doc.

[14] Wasike C.B 2006 Genetic evaluation of growth and reproductive performance of the Kenya Boran cattle. MSc Thesis. Egerton University, Kenya.pp108.