Inbreeding and Genetic Trend of Dairy Cattle in Baturraden Dairy Cattle Breeding Centre: A Short Communication

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Abstract. The success (or failure) of a breeding centre can be assessed through the genetic trend of trait(s) included in the breeding objective and the inbreeding trend. Through continuous genetic evaluation and structured mating program, positive genetic trend while maintaining inbreeding on the reasonable level will be achieved. Inbreeding level of a population is an important aspect in animal breeding as this may lead to a deteriorating phenomenon called inbreeding depression. This information will guide the animal breeder on how the mating system of their animals will be designed. Inbreeding level of a dairy cow population generally is maintained to be less than 10%. The trend of additive genetic (breeding value) and inbreeding of dairy cattle population in Baturraden Dairy Cattle Breeding Centre (*Balai Besar Pembibitan Ternak Unggul Sapi Perah, BBPTU*) was examined. The pedigree data consisted of 450 animals and 861 records were analyzed. The study included two traits namely milk yield (MY) and calving interval (CI). The pedigree data were collected from 1977 to 1990. The breeding value (EBV) of animals was estimated using DMU computer package applying repeatability animal model and the coefficient of inbreeding was computed with SECATEURS. The study showed zero inbreeding level of the population based on the pedigree available without any single inbred animal. The population showed no genetic progress over years during the period of 1977-1990 based on linear regression of EBVs on the year of birth. This indicated that during the period of 1977 and 1990 the genetic improvement program in *BBPTU* was unsuccessful. The inbreeding level of zero could mean that the designed mating system was successful. However, no genetic progress and no inbreeding trend could mean that no selection program has been introduced in the breeding centre.

Key Words: genetic trend, inbreeding trend, BBPTU Baturraden, dairy cattle

Introduction

BBPTU Baturraden as a dairy cattle breeding centre has at least three important missions to be achieved: (1) to develop national dairy cattle breeding, (2) to optimize both quantity and quality of the breeding dairy cattle, (3) to fulfill dairy cattle market demand (BBPTU, 2010). Animal breeders today have challenge on balancing between intense selections and maintaining enough genetic variation of the relatively small population of the bred animals. Intense selection is required to speed up the genetic progress per generation while genetic variation is absolutely needed as source of selection. The battling between increasing the selection intensity and maintaining enough genetic variation has to be setup in a balance way so that none is sacrificed. The most

applied of genetic improvement method (BLUP; Henderson, 1975) has led to rapid genetic progress and simultaneously increased the inbreeding level of the population. Malécot (1969) defined inbreeding as the probability of two alleles (genes) to be identical by descent which measures the homozygosity.

Selection of animals for future breeding has to be based on their EBVs since only breeding value (additive genetic effect) will be passed onto the offspring. This is true especially for phenotypic traits with low heritability since the risk of falsely ranking animals for selection is higher for traits with low heritability. BLUP method of Henderson that is widely used in animal breeding value evaluation resulted in higher accuracy of EBV than other methods. The drawback of the BLUP method is that it tends to increase the rate of inbreeding trend

due to coselection between relatives (Quinton et al., 1992). Regardless of the genetic evaluation method applied to a population on which subsequently animals selection are based, balancing between selection response and maintaining inbreeding on the acceptable level is a key factor in a breeding centre. Generally, inbreeding is avoided since the negative effect of the decline in performance of the inbred animals (inbreeding depression).

Inbreeding can be deteriorating if it is uncontrolled and not managed properly. Accumulated inbreeding up to a certain level is acceptable but it may result in serious economic losses due to inbreeding depression in production, growth, health, and fertility to which the trait is more profoundly affected. Filippo et al. (1992) did not recommend inbreeding coefficient above 12.5% in dairy cattle as this will lead to serious inbreeding depression. Inbreeding results in serious economic losses with various degrees. For instance, in every lactation, per 1% increase of inbreeding reduces 9.84-29.6 kg of milk yield, 0.55-1.08 kg of milk fat and 0.80-0.97 kg of milk protein (Casanova et al., 1992; Miglior et al., 1992; Wiggans et al., 1995; Smith et al., 1998). Different selection methods have been studied by various authors on how to reduce inbreeding while maintaining high rates of genetic gain (Toro and Perez-Enciso, 1990; Verrier et al. 1993; Wray and Goddard, 1994; Grundy et al., 2000; Sonesson and Meuwissen, 2002). BBPTU Baturraden as a breeding centre also has to take care of these two aspects, i.e. increasing the genetic progress and maintaining the inbreeding level. Computing inbreeding level of a population is a simple task which requires only the pedigree data; a short computer program can be written for instance following Meuwissen and Luo (1992). Though, some computer programs are readily available for the

analysis such as SECATEURS (Meyer, 2003), DMU (Madsen and Jensen, 2008) and Gilmour et al., 2009). DMU computer package (Madsen and Jensen, 2008) which is free and the more advanced though not free computer package, ASReml (Gilmour et al., 2009) are designed for BLUP analyses for simple until complex models. Thus the objective of this paper was to asses the genetic trend of dairy cattle in BBPTU Baturraden as well as its inbreeding level using the readily available computer programs. Since the similar study has never been published, this study becomes essential especially for the policy maker in BBPTU Baturraden as the evaluation tool in running the breeding centre.

Materials and Methods

A pedigree data consisting of 450 animals with 226 animals with phenotypic records of Holstein Frisian (HF) dairy cattle was used. The phenotypic data included milk yield (MY, liters) and calving interval (CI, days) with 861 total number of observation for each trait available. The pedigree was recorded during 1977-1990 period. For simplicity, all of the animals with unknown parents (base population) were assigned year 1976 for their year of birth.

Inbreeding coefficient of animals in the pedigree were computed using SECATEURS (Meyer, 2003), a computer program designed for pruning pedigree data before used in genetic analysis. SECATEURS incorporates a fast procedure (Tier, 1990) to calculate inbreeding coefficients of the population. The rate of inbreeding was calculated by regressing the inbreeding mean of the population on the year of birth.

The predicted breeding values (EBV) of animals were estimated using BLUP method following mixed model of the repeated measures with equal design:

$$\begin{bmatrix} \boldsymbol{y}_1 \\ \boldsymbol{y}_2 \end{bmatrix} = \begin{bmatrix} \boldsymbol{X}_1 & 0 \\ 0 & \boldsymbol{X}_2 \end{bmatrix} \begin{bmatrix} \boldsymbol{b}_1 \\ \boldsymbol{b}_2 \end{bmatrix} + \begin{bmatrix} \boldsymbol{Z}_1 & 0 \\ 0 & \boldsymbol{Z}_2 \end{bmatrix} \begin{bmatrix} \boldsymbol{a}_1 \\ \boldsymbol{a}_2 \end{bmatrix}$$
$$+ \begin{bmatrix} \boldsymbol{W}_1 & 0 \\ 0 & \boldsymbol{W}_2 \end{bmatrix} \begin{bmatrix} \boldsymbol{p}_1 \\ \boldsymbol{p}_2 \end{bmatrix} + \begin{bmatrix} \boldsymbol{e}_1 \\ \boldsymbol{e}_2 \end{bmatrix}$$

where $\boldsymbol{y}_i$ is the vector of observation; $\boldsymbol{b}_i$ is a vector of fixed effects; $\boldsymbol{p}$ and $\boldsymbol{a}$ are vectors of random effect of dam and the additive genetic value of each animal, respectively; $\boldsymbol{e}$ is a residual random effect and i is the phenotypic traits included in the analysis (MY and CI). $\boldsymbol{X}_i$, $\boldsymbol{Z}_i$ and $\boldsymbol{W}_i$ are the design matrices for fixed effects, random effect of genetic additive and permanent environmental effect of dam, respectively. The co(variance) structure of the random effects was assumed as follows: $\boldsymbol{p}$~$N(\boldsymbol{0},\boldsymbol{I}\ \sigma_p^2)$, $\boldsymbol{a}$~$N(\boldsymbol{0},\boldsymbol{A}\ \sigma_a^2)$, $\boldsymbol{e}$~$N(\boldsymbol{0},\boldsymbol{I}\ \sigma_e^2)$ and the model assumes cov($\boldsymbol{a},\boldsymbol{p}$) = cov($\boldsymbol{a},\boldsymbol{e}$) =cov($\boldsymbol{p},\boldsymbol{e}$) = 0. N stands for a multivariate normal distribution; $\boldsymbol{I}$ is an identity matrix; $\boldsymbol{A}$ is the additive relationship matrix of animals; σ_p^2, σ_a^2, and σ_e^2 are variances of permanent effect of dam, additive genetic and residual, respectively. The $\boldsymbol{b}$ vector included lactation number as well as age of dam, number of milking days and number of dry period as covariables. BLUP bivariates analysis was conducted using DMU computer package (Madsen and Jensen, 2008) assuming co(variance) of the random effects of identity. As the emphasis was to study the rate of inbreeding per year, the regression of inbreeding mean on year of birth was limited to the linear and quadratic regression. The genetic trend per year was also analyzed similarly using linear and quadratic regression of EBV mean on the year of birth. The regression analyses was performed using *lm* function of R statistical package (R Development Core Team, 2010).

Results and Discussion

SECATEURS performed a routine check to the pedigree file and reported 162 (36%) animals to be uninformative so that they were removed from the pedigree file since these animals will not affect the result of the genetic analysis. For animal with phenotypic records, the number of records was varied (Table 1). The distribution of animals (percentage) by the year of birth is presented in Figure 1.

Table 1. Distribution of animals expressed in number and percentage

Number of record	Number of animals (%)
1	1 (0.4)
2	56 (24.8)
3	65 (28.8)
4	35 (15.5)
5	38 (16.8)
6	11 (4.9)
7-10	20 (8.8)

There were 77.4% animals without offspring and 22.6% with offspring. Ninety eight animals were with unknown sire and 205 animals with unknown dam. Number of animals which both parents known were only 87. Number of sires and dams in the pedigree file were 25 and 40, respectively. The number animals with known paternal grand sires and paternal grand dam were both void while the number of animals with known maternal grand sire and maternal grand dam were one and two, respectively. The average inbreeding coefficient of the pedigree is zero provided the fact that none of the animal in the pedigree was inbred. The very limited number of paternal/maternal grand sire or grand dam known in the pedigree showed poor recording system of the breeding centre. The zero inbreeding level (no inbred animal) may indicate that the breeding centre did not use the common elite sires in the population. This could also mean that the mating system during 1977-1990 was random and uncontrolled. Assortative mating (both positive and negative) in a relatively small population tends to increase the inbreeding level if the mating were without considering the pedigree information. Thus, inbreeding in a breeding centre is unavoided especially if BLUP method is used in

the genetic evaluation of the animals and is expected in a population applying AI since semen from a sire might be used to sire many dams. The effect of BLUP selection to inbreeding level of the population is well understood since it tends to select animals from the same family (coselection). For instance in the USA, the current inbreeding level of Holstein dairy cattle is 5% (AIPL, 2003) and in Canada the inbreeding level of the same species is 4.91% with an increase of 0.25% per year from 1990 to 2000 (CDN, 2003). Those increases in inbreeding level could be attributed to at least 3 factors (Kearney et al., 2000): (1) tendency to select animals from the same family as a result of BLUP method in the EBV evaluation, (2) to use fewer sires through artificial insemination (AI) and fewer dams facilitated by multiple ovulation and embryo transfer (MOET) and (3) the selection is based only on fewer traits such as milk yield.
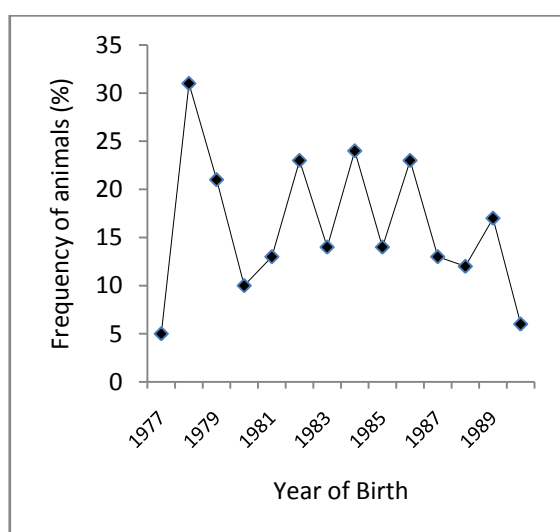

Figure 1. Distribution of animals by year of birth

The genetic trend analysis of the dairy cattle recorded by BPPTU during the period of 1977-1990 was based on the available phenotypic traits (MY and CI) in the breeding centre. The distributions of the EBVs of the two traits estimated by DMU software applying bivariates

repeatability animal models are presented in Figure 2 and 3. Linear regression line is illustrated with solid line while the quadratic line is depicted with dotted line. None of the distribution of the EBVs shows positive trend over year of birth. The linear regression analyses of the MY and CI traits did not find any positive slope (the linear regression coefficient for both traits was not different from zero; P>0.05). This is surprising and unexpected since the breeding centre has its mission to carry out genetic improvement program for the population (BPPTU Baturraden, 2010). The result tells us that there is no genetic progress per year for the traits evaluated. Theoretically, any population undergone selection program will improve its EBV (Falconer and Mackay, 1996) with the slope of the EBV on year of birth bigger than zero. Examples of the success of breeding programs with positive genetic trends are clear for instance studies by Serrano *et al*. (1996) and Gizaw et al., (2007). To asses the pattern of relationship between the EBV mean and the year of birth, a higher degree of regression (quadratic) were sought so that the relationship would be clear. The results of quadratic regression revealed that the relationship between the EBV mean of MY and their birth year was quadratic (P<0.05). In contrast, quadratic regression of EBV mean on year of birth of CI was not significant (P>0.05). Lack of genetic connectedness will cause larger prediction error in the evaluation of animals` BV than those that are genetically well connected (Laloë et al.*,* 1996). Genetic connectedness will serve as benchmark so that EBVs of animals born on different years can be compared fairly. Lack of genetic link between animals born on different years resulted in EBV mean pattern as shown in Figure 2. For illustration purpose, both the linear and quadratic lines of the regression analysis for MY trait is presented in Figure 2.
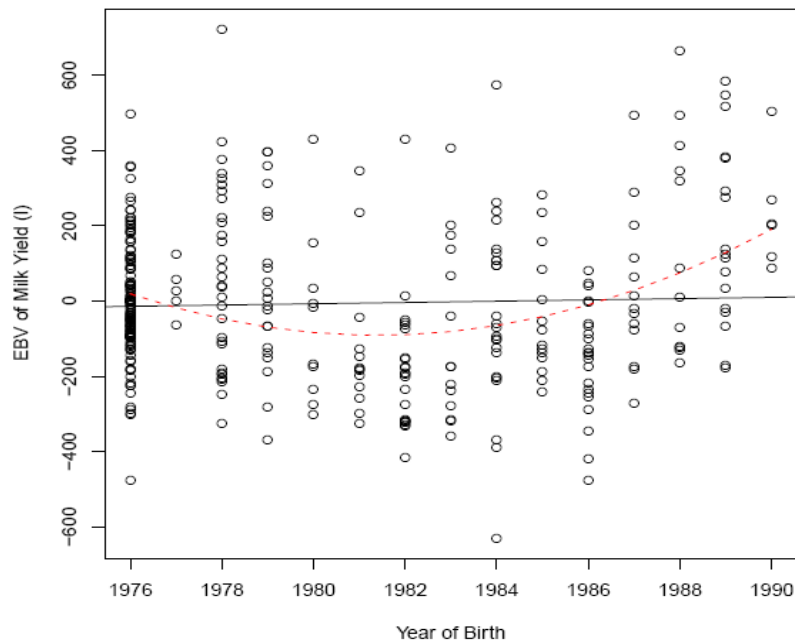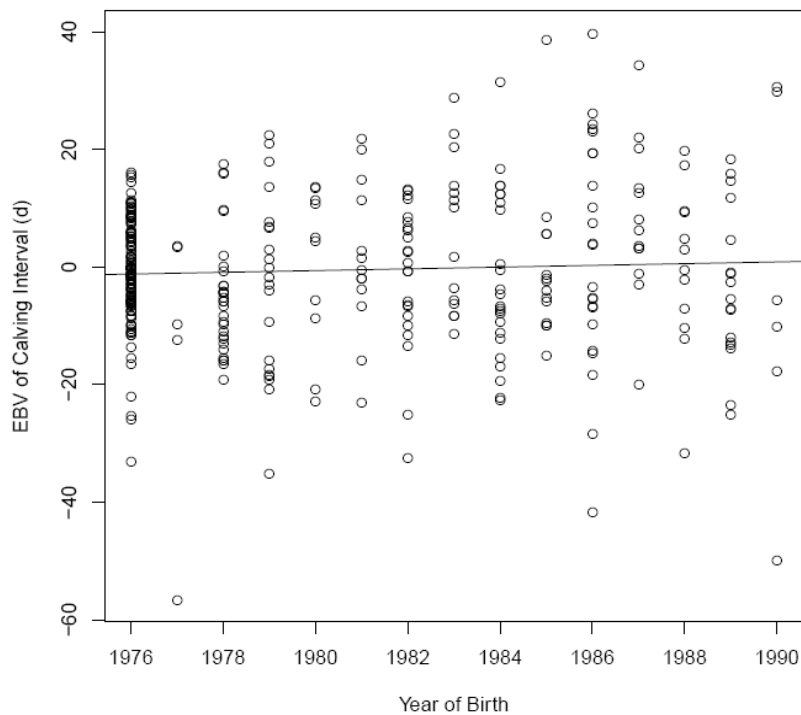
Figure 2. EBV Trend of Milk Yield

Figure 3. EBV Trend of Calving Interval

Conclusions

Genetic improvement of dairy cattle in BBPTU Baturraden was unsuccessful during the period of 1977-1990 even though the rate of inbreeding was zero. The accuracy of recording the pedigree needs to be improved so that the EBV of animals will be accurately predicted in BLUP genetic evaluation routine.

References

Animal Improvement Programs Laboratory (AIPL). 2003. Inbreeding. http://www. aipl.arsusda.gov. Accessed Dec. 10, 2010.

BPPTU Baturraden. 2010. Pembibitan. http://www. bbptusapiperah.org/?page_id=13. Accessed: December 21, 2010.

Canadian Dairy Network (CDN). 2003. Inbreeding. http://www.cdn.ca. Accessed Dec. 1, 2010.

Casanova L, Hagger C, Kuenzi N and M. Schneeberger. 1992. Inbreeding in Swiss Braunvieh and its influence on breeding values predicted from a repeatability animal model. J. Dairy Sci. 75:1119–1126.

Filippo M, Szkotnicki B and EB Burnside. 1992. Analysis of Levels of Inbreeding and Inbreeding Depression in Jersey Cattle. J. Dairy Sci. 75:1112-1118.

Gilmour AR, Gogel BJ, Cullis BR and R Thompson. 2009. ASReml User Guide Release 3.0. NSW Departmen of Industry and Investment. Australia.

Grundy B, Villanueva B and JA Woolliams. 2000. Dynamic selection for maximizing response with constrained inbreeding in schemes with overlapping generations. Anim. Sci. 70:373-382.

Henderson CR. 1975. Best linear unbiased estimation and prediction under a selection model. Biometrics. 31:423–447.

Madsen P and J Jensen. 2008. An Userès Guide to DMU: A Package for Analysing Multivariate Mixed Models. University of Aarhus, Denmark.

Malécot G. 1969. The mathematics of heredity. W.F. Freeman, San Francisco.

Meyer K. 2003. SECATEURS: to prune your pedigree. Animal Genetics and Breeding Unit1, University of New England, Armidale.

Miglior F, Szkotnicki B and EB Burnside. 1992. Analysis of levels of inbreeding and inbreeding depression in Jersey cattle. J. Dairy Sci. 75:1112–1118.

Quinto M, Smith C and ME Goddard. 1992. Comparison of Selection Methods at the Same Level of Inbreeding. J. Anim. Sci. 70:1060-1067.

R Development Core Team. 2010. R: A language and environment for statistical computing. R Foundation for Statistical Computing. http://www.r-project.org/. Accessed Dec. 16, 2010.

Smith LA, Cassell BG and RE Pearson. 1998. The effects of inbreeding on the lifetime performance of dairy cattle. J. Dairy Sci. 81:2729–2737.

Sonesson AK and THE Meuwissen. 2002. Non-random mating for selection with restricted rates of inbreeding and overlapping generations. Genet. Sel. Evol. 34:23-39.

Tier B. 1990. Computing inbreeding coefficients quickly. Genet. Select. Evol. 22:419–425.

Toro M and M Perez-Enciso. 1990. Optimization of response under restricted inbreeding. Genet. Sel Evol. 22:93-105

Verrier E, Colleau JJ and JL Foulley. 1993. Long-term effect of selection based on the animal model BLUP in finite population. Theor. Appl. Gen. 87:446-454.

Wiggans GR, PM VanRaden and J Zuurbier. 1995. Calculation and use of inbreeding coefficients for genetic evaluation of United States dairy cattle. J. Dairy Sci. 78:1584–1590.

Wray NR and ME Goddard. 1994. Increasing long-term response to selection. Genet. Sel. Evol. 26:431-451.