



Comparison of linear and threshold models for estimation genetic and phenotypic parameters of success of conception at first service and inseminations to conception in Holstein Cattles in East Azarbayjan province

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ABSTRACT

In this research genetic and phenotypic parameters were estimated using linear and threshold models, for reproductive traits, data from 6 large industrial dairy herd of East Azerbaijan province collected by Agriculture Jihad Organization during 10 years (2001-2010). Best linear unbiased predictions of traits breeding values were estimated using Restricted Maximum Likelihood method by WOMBAT software. Marginal posterior distributions under Bayesian approach via Gibbs sampling algorithm were estimated using repeatability analysis under animal model by Thrgibbs1f90software, in threshold model. Heritability's of inseminations to conception and success at first insemination traits were estimated 0.078 ± 0.014 and 0.068 ± 0.013 respectively, in linear model and in threshold model, the means of posterior distributions of heritability's were estimated 0.07 ± 0.0001 and 0.136 ± 0.0022 respectively. The research results showed that although the amount of heritability's for reproductive traits are low using linear and threshold models, but using threshold model in contrast with linear model cause increasing accuracy of evaluation and increasing rate of response to selection.

Key words: Heritability, Linear model, Threshold model, Genetic and Phenotypic parameters, Holstein Cattle

INTRODUCTION

With regard to the selection of animals for increase the milk production and due to the existence of an adverse relationship between the milk production and other economic traits such as fertility, performance of fertility is reduced during recent years (Weigal and Rekaya, 2000; Weller and Ezra, 2004). On the other hand, because of a low heritability for reproductive traits, these traits haven't enough regard as compared to the productive traits (Mac Daniel and Bell 1989). Nevertheless, in addition to the productive traits that are effective on the profitability, the reproductive performance of dairy cows is very important too. Because of the importance of the reproductive traits, in many countries, these traits have been selected into the index in recent years. Some of reproductive traits have discrete distribution in animal breeding unlike most economic traits, so these traits are called discontinuous traits. Phenotypic manifestations of these traits have

two unique situations with two groups, or their phenotypic manifestations are several groups. These variables haven't normal distribution and simple regression analysis assumptions and analysis of variance such as being normal model error variances and being constant for dependent variables for all values of the independent variables are not honest about their (Kaps and Lamberson, 2004). The design methods used in the estimation of the parameters of these traits are based on the of threshold model. It is necessary that the components of (co)variance and genetic and phenotypic parameters of traits be determined to import various traits in selection index in choosing cattle (honorvar et al, 1383). In fact genetic parameters must be estimated in order to select programs in animal breeding, by prediction of genetic values for the desired traits (Tekreli and Gundoghan, 2005). In order to improve the economic traits such as reproductive traits, estimation of variance components of these traits seems essential. Boosting accuracy of genetic evaluation is one of the best available tools for the progress of response to selection. (Ghavi Hossein Zadeh and Ardalan, 2010). Therefore, having the information about the genetic parameters and heritability is very important in genetic evaluation and choose the best corrective program (Maxa et al. 2007). In addition traits functional should be accurate, using an appropriate model for a correct estimation of the genetic parameters and assessments in analysis. Often the assessments of threshold traits with the help of linear models have a little reliability in one trait analysis (Hagger and Hofer, 1990). Because the distribution of these traits is not normal. For single-mode trait, Meijering and Gianola(1985) found that a threshold model for analysis of traits that have two categories with low heritability, are more desirable than which has several categories. Carlen et al. (2006) found that a threshold model is preferred to other models to justifying for parameters of two traits. Ramirez et al. (2001) also reported a threshold model is better for estimate the parameters of multinomial traits, such as the number of inseminations to conception. However Silvestre et al. (2007) reported no significant difference between the results of linear models and a threshold model in connection with the Estrella mountain dog's hip joint abnormalities. The aim of the present research is study and comparison of linear and threshold models in estimating parameters for number of services per conception (NSPC) and the success or failure of conception to first service (SF) for Holstein Cattles in East Azarbaijan province.

MATERIALS AND MTHODS

Genetic and phenotypic parameters were estimated using linear and threshold models, for reproductive traits, data from 6 large industrial dairy herd of East Azerbaijan province collected by Agriculture Jihad Organization under the supervision of the country's livestock breeding Center during 10 years (2001-2010). Data edited using SQL and Excel software's. Pedigree software used to check the structure of pedigree (Sargolzaei et al, 2006). Before doing any analysis, Variance analysis of affecting fixed effects on traits was carried out using the General linear model by SAS 9.1 software. The results showed a significant effect of the herd, the period of calving, season and year of calving and sperm on the traits. Linear unbiased prediction of breeding values of traits using WOMBAT software and Restricted Maximum Likelihood method (REML) was used. The estimation of the parameters in threshold model was performed using Marginal posterior distribution with Gibbs sampling algorithm - from a Bayesian approach under Repeatability model of by software Thrgibbs1f90(Misztal et al, 2002). 200 000 sample cycles were taken to analyze the traits and 20,000 samples were taken as a burn in samples. Gibbs sampling methods were used for estimating the average of marginal posterior distribution of the genetic parameters.

RESULTS

Descriptive Statistics of reproductive traits in Holstein cows are given in Table 1. Average of the number of inseminations to conception were estimated 1.404 that was Similar to values obtained by Raheja et al. (1989) and Hansen et al. (1983) that reported the mean of this trait 1.4 in successful pregnancy in heifers.

Average of estimate of this trait in the present study was less than amounts reported by Aslama et al. (1976), Dematawewa et al. (1998), Biffani et al. (2005), Jamrozik et al. (2005), Gonzalez-Recio et al. (2005) values were 1.95, 1.83, 1.7, 1.64 and 1.87 respectively. Average obtained in this study is somewhat better than other research. Of course, in some cases, that number is more than one insemination, it may only last service is registered by husbandry. This reduces the average number of the insemination rate per conception (Farhang far and naeemipour, 2007). In this study the mean of success or failure at first insemination was estimated 0.74 that is same Ranberg et al. (2003), Haile-Mariam et al. (2003) and Jamrozik et al. (2005) that they reported 0.74, 0.71 and 0.74 respectively. The value in this research is more than of results in Muir et al. (2004) research for cows' selected and unselected values were 0.64 and 0.68 respectively. In Table 2 the results of the posterior distribution of Bayesian approach using Gibbs sampling based on animal models and a comparison with the results of the linear model using restricted maximum likelihood method is presented. In this study, the heritability values obtained for number of insemination and success or failure at first service were estimated that values were 0.07 and 0.136 While the results of linear model parameters for these traits were estimated 0.07 and 0.068. The differences in the results of two different models indicate that a threshold model is based on the underlying values but the linear model results are based on the observed values. The results of this study for insemination to conception were similar in the two models. The main reason for this result is that there can be polynomial discrete distribution for this trait, because the numbers are closer to the normal distribution, despite the binomial distribution for success or failure at the first insemination. Threshold model is preferred over other methods to explain the parameters for the binary traits (all or none traits). The threshold model can be preferable for binary traits using a threshold model for genetic evaluation (Gianola and Foulley 1983). As expected, the estimates of linear and threshold models, for success of conception at first service had different values in comparison of number of services per conception in linear and threshold models. The results of this research for number of services per conception did not match with results of Abdollahi et al. (2012) that values of heritability of they result were 0.04 and 0.165 in linear and threshold models respectively. But it is almost identical with the results obtained for the success at the first service with sequential values 0.039 and 0.091 and the ratio of one to two for these. In this research, the values of repeatability and heritability is not significant difference related to these traits based on a linear model due to the small variance of permanent environmental. The values of repeatability for number of services per conception and success at first service were estimated 0.077 and 0.177 respectively. While these results was 0.078 and 0.068 using a linear model. Abdollahi et al. (1391) reported similar results with the estimates of the present research that values were 0.078 and 0.081 respectively while he reported values with a threshold were 0.29 and 0.27 respectively. In some of the research the difference between linear and threshold analysis p has been reported 0.01 (Carlen et al. 2006). In many researches, the estimation of genetic parameters for many of the multiple trait analysis was difference using a linear-linear model with linear-threshold model (Varona et al, 1999). Abdollahi and Abbasi (2009) were also reported estimation of genetic parameters is insignificant in between linear-linear and linear-threshold models ($P > 0.05$). The superiority of the threshold models has been reported in estimate genetic parameters of a threshold trait in many researches (Schaeffer, 2004). The marginal posterior distribution of heritability of success or failure at first insemination and number of services per conception are shown in charts 1 and 2. The results of the present study showed that although the heritability of reproductive traits using linear and threshold model are little and responses to selection for these traits will be slow, but these traits analysis using a threshold model, especially for binary traits, increases assessment accuracy in Comparison with a linear model (reducing the standard error), thus increase the speed of response to selection. Because the estimations of this model is greater than the estimate derived from the linear model as well as the standard error is less than the linear model.

Table 1- statistical informations

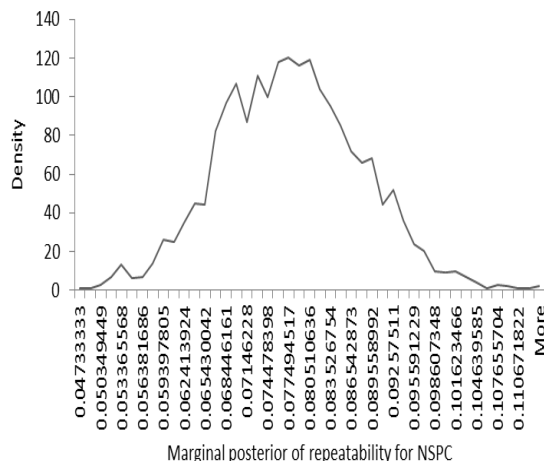
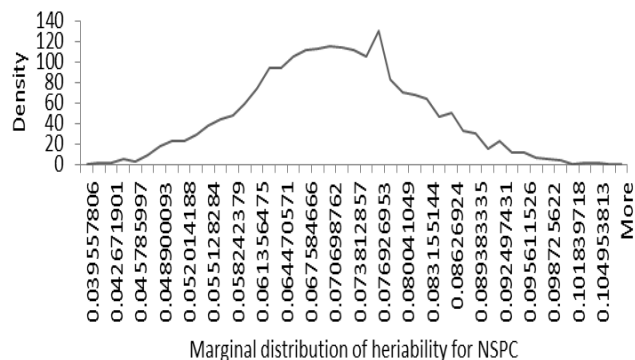
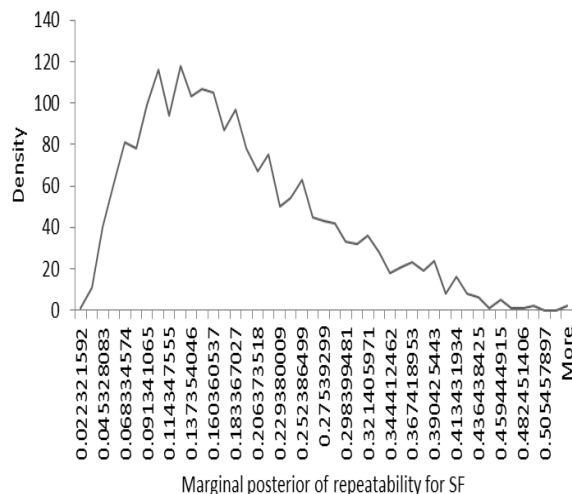
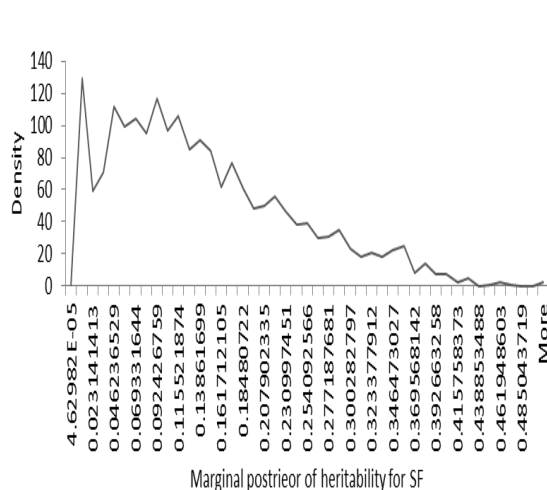
traits	Record number	mean	min	max	std	Cv
SF	10346	0.746	0	1	0.437	58.82
NSPC	10346	1.4	1	10	0.87	62.14

SF: success or failure at first insemination, NSPC: number of services per conception

Table 2- Linear and threshold model comparison

parameters	Linear model		Threshold model	
	SF	NSPC	SF	NSPC
σ_a^2	9.14E-)0.0498(3)	1.082E-2(2.054E-3)	0.045(1.55E-4)	0.004(6.17E-5)
σ_{pe}^2	1.7E-6(9.48E-3)	1.261E-6(2.257E-3)	0.004(7.83E-5)	5.58E-)0.0011(5)
σ_e^2	9.985E-)0.5877(3)	0.148(2.51E-3)	0.584(7.83E-5)	0.022(8.14E-6)
h^2	0.078(0.014)	0.068(0.013)	0.07065(2.4E-4)	2.182E-)0.1366(3)
C^2	0.000(0.015)	0.000(0.014)	0.0065(1.24E-4)	2.2542E-)0.0406(4)
R^2	0.922(0,011)	0.932(0.011)	0.9229(2.28E-4)	2.096E-)0.8227(3)
R	0.078(0.012)	0.068(0.011)	2.281E-)0.0771(4)	2.097E-)0.1773(3)

σ_e^2 : additive genetic variance, permanent environmental varianc, residual variance $\sigma_{pe}^2, \sigma_a^2, \sigma_e^2$
 h^2 : heritability, C^2 and R^2 : ratio of permanent environmental and residual variances on phenotypic variance
R: repeatability



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