



Calculating daughter yield deviations for production traits in Holstein cattle using repeatability animal and random regression test day models



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ABSTRACT

In the present study, the records of milk yield and fat and protein contents collected by the Animal Breeding Center of Iran between 2001 and 2010 were used to estimate the daughter yield deviations of Iranian Holstein bulls. The results were compared with the conventional method of the estimation of breeding values for bulls. The results obtained from a repeatability animal model and random regression test day model were compared. Correlations of bulls' daughter yield deviation with estimated breeding value were 0.65, 0.71 and 0.58 with repeatability animal model and 0.76, 0.92 and 0.91 with random regression test day model for milk yield and fat and protein contents, respectively. Correlation of bulls' daughter yield deviation with estimated breeding value in both models was dependent on the number of daughters and when this factor increased, the correlation of bulls' daughter yield deviation with estimated breeding value increased consistently. Correlation also increased along with increase in the lactation number of daughters and number of test day records for daughters in the repeatability and random regression models, respectively. Correlation between bulls' daughter yield deviation and estimated breeding value in random regression model was greater than that of the repeatability model for all studied traits.

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1. Introduction

Besides estimated breeding value (EBV), yield deviation (YD) of cows and daughter yield deviation (DYD) of bulls are important quantities used in dairy cattle selection (Szyda et al., 2008). The YD is a weighted average of the cows' yields adjusted for all effects of the model other than genetic merit and error. The DYD of bulls is average performance of their daughters that are adjusted for fixed and non-genetic random effects of the daughters and genetic effect of their mates (Freyer et al., 2002; Liu et al., 2004;

Vanraden and Wiggans, 1991). DYD is not regressed on breeding value of bulls and is the most independent and accurate measure of phenotypic performance of a bull's daughters (Liu et al., 2004; Vanraden and Wiggans, 1991). It was initially the variable of choice in international evaluations by Interbull but due to the inability of several countries to calculate DYD, de-regressed proofs were used (Sigurdsson and Banos, 1995). Secondly, some of the Interbull methods for validation of trends in national evaluations prior to acceptance for international evaluations utilize DYDs (Boichard et al., 1995). Moreover, DYDs are commonly used in dairy cattle studies aimed at detecting quantitative trait loci based on the grand-daughter design (Kim, 2008; Kim and Georges, 2002; Weller, 2001). The recent trend in dairy cattle genetic evaluations is towards application of random regression models (RRM) using test day (TD) records (Mrode and

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Swanson, 2004). Due to the advantages of random regression model over the conventional animal model in increasing the accuracy of estimating genetic parameters and predicting breeding values, application of this model is expanding. Although, the subject of this study has been investigated by other researchers, but the novel items in this study included the use of national data set of dairy herds in Iran and the interest of comparing RRM with repeatability animal model in the context of calculating YD and DYD. On the other hand, comparison of the calculated DYDs and YDs in Iranian dairy herds with other dairy production systems could be interesting. Therefore, the primary objective of this study was to calculate bulls' DYD using random regression test day model (RRTDM) and repeatability animal model and the other objective was to compare the results obtained by two models.

2. Materials and methods

Data of 515,049 daily records (TD records) of first lactation yields and 239,028 adjusted records for 305-d milk yield and fat and protein contents of the first three lactations of Holstein cows with calvings between 2001 and 2010 were obtained from the Animal Breeding Center of Iran. The GLM procedure of SAS software (SAS, 2002) was used for fitting the fixed effects in the statistical models of analysis.

2.1. Genetic analysis

Records of 305 day productive traits were analyzed using a single-trait repeatability animal model. The statistical model in matrix notation was as follows:

$$Y = Xb + Za + Wp + e$$

where:

Y: vector of observations for 305 day adjusted records of milk yield and fat and protein contents.

X: design matrix for the fixed effects.

b: vector of fixed effects of herd-year of calving, season of calving, parity, linear and quadratic regression coefficients for age at calving.

Z: design matrix for the random effect of animal.

a: vector of animal additive genetic effects.

W: design matrix for the random permanent environmental effects of animal.

p: vector of random animal permanent environmental effects.

e: vector of random residual error.

Test day records were analyzed with the following random regression model (RRM):

$$y_{imnptv} = HTD_m + \sum_{f=1}^2 C_f(age_n)^f + \sum_{r=0}^k \beta_r \varnothing_r(dim_t) + \sum_{r=0}^{k_a-1} \alpha_{pr} \varnothing_r(dim_t) + \sum_{r=0}^{k_p-1} \gamma_{pr} \varnothing_r(dim_t) + e_{imnptv}$$

where,

y_{imnptv} ; test day record i obtained at dim_t of cow p calved at the n th age in herd-test date m ,

HTD_m ; fixed effect of m th herd-test date,

C_f ; the f th fixed regression coefficient for calving age,

age_n ; the n th calving age,

k ; the order of fit for fixed regression coefficients ($k=2$),

β_r ; the r th fixed regression coefficient,

k_a ; the order of fit for additive genetic random regression coefficients,

k_p ; the order of fit for permanent environmental random regression coefficients,

α_{pr} ; the r th random regression coefficient of additive genetic value for p th cow,

γ_{pr} ; the r th random regression coefficient of permanent environmental effect for p th cow,

$\varnothing_r(dim_t)$; the r th coefficient of Legendre polynomials evaluated at days in milk t ,

e_{imnptv} ; the random residual error.

First lactation records were used in RRM while first three lactation records in the repeatability model. In order to achieve the appropriate RRM for the analysis of TD milk yield and fat and protein contents, with the minimum number of parameters, different orders of fit for random regression coefficients of additive genetic and permanent environmental effects were evaluated. Optimum set of various orders of polynomials was selected based on the logarithm of the likelihood function at the point of conversion and total number of parameters to be estimated. Different orders of fit for various RRM which were evaluated in the current study are presented in Table 1. All analyses (repeatability and RRM) were performed using the AIREML algorithm of the WOMBAT program (Meyer, 2006) on a Linux operating system.

2.2. Calculating yield deviations

An animal predicted transmitting ability (PTA) can be partitioned into three sources of information which are consisted of the weighted parent average, half of its yield deviation and progeny contribution. Thus information from lactation records of a cow included in the cow's PTA through her YD (Vanraden and Wiggans, 1991). For calculating YD of cows in a repeatability animal model,

Table 1
Different orders of fit for random regression coefficients in this study.

Model	Order of fit		np	log _l _{milk}	log _l _{fat}	log _l _{protein}
	k_a	k_{pe}				
1	3	3	13	-1,001,060.81	-39,354.59	402,203.76
2	3	4	17	-996,471.47	-38,283.34	404,519.72
3	3	5	22	-992,612.86	-37,428.65	407,466.96
4	3	6	28	-990,376.63	-37,015.54	409,554.58
5	4	4	21	-992,473.04	-36,534.80	406,060.75
6	4	5	26	-989,945.79	-36,021.88	408,193.03
7	4	6	32	-987,708.55	-35,659.16	410,164.44
8	5	5	31	-987,115.20	-35,293.54	410,601.61
9	5	6	37	-985,738.50	-35,057.76	411,791.91

k_a and k_{pe} : orders of fit for additive genetic and permanent environmental effects, respectively; np: number of parameter for estimated variance function, log_l: maximum log likelihood.

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