I.J.A.B.R, VOL. 3(2) 2013: 227-230 ISSN 2250 – 3579

INTERNATIONAL JOURNAL OF ADVANCED BIOLOGICAL RESEARCH

www.scienceandnature.org

ESTIMATION OF CORRELATED RESPONSE IN SOME LIFETIME TRAITS ACCORDING TO OTHER TRAITS IN HOLSTEIN COWS

[a]Firas Rashad Al-Samarai, [b]Sadi Shalan Khalaf & [c]Falah Hamad Al-Zaidi
[a]Department of Veterinary Public Health/ College of Veterinary Medicine / University of Baghdad/Iraq
[b]Department of Animal Resources/ College of Agriculture/ University of Anbar/Iraq
[c]Ministry of Agriculture/Directorate of Baghdad Agriculture/Department of Animal Resources/Iraq

ABSTRACT

Data belong to 944 Holstein cows, for the period from 1998 to 2004 in the Nasr dairy cattle station, United Company for Animal Resources Ltd., Al-Soueira (50 km south of Baghdad), were analyzed. The aim of this study is to estimate the expected correlated response in some lifetime traits by using average milk yield per day of age at second calving (AVMSC) as an indicator trait for productive life (PL) and nunber of lactations (NL), whereas, the first milk yield (FMY) was used as an indicator trait for average milk yield per day of productive life (AVMPL), average milk yield per day of lifetime (AVML) and lifetime milk yield (LTMY). The results revealed that using selection intensity 1.64, 1.25 and 0.98 of cows according to the average milk yield per day of age at second calving caused expected increasing by 0.20, 0.15 and 0.12 month/year in productive life and 0.022 , 0.017 and 0.013 lactation/year in number of lactations due to correlated response respectively. The corresponding estimates for the expected correlated response according to selection of sires on the first milk yield were 0.15 , 0.12 and 0.09 kg/year in the average milk yield per day of productive life , 0.10 , 0.07 and 0.05 kg/year in the average milk yield per day of longevity and 278.58 , 212.33 and 166.47 kg/year in the lifetime milk yield respectively.

KEY WORDS: correlated response, lifetime traits, indicator traits, Holstein cattle

INTRODUCTION

Milk yield and its components are the most important traits of selection for dairy cattle, and genetic progress for these traits has been well documented [1,2]. However, high milk yields may be associated with physiological changes that tend to limit further increases in productive economic herd life [3]. Dairy producers should be concerned to more maximizing the profitability of the cow with maximizing milk yield [4], even if that approach implies suboptimal genetic progress for milk yield and component traits [5]. Selection goals for dairy cattle should reflect profit over lifetime of cows [6, 7], but increased milk yield should be considered to be only part of the goal of maximizing profit [8]. In the past, lifetime traits were excluded from most breeding program. Considering lifetime traits in a breeding program was generally thought to increase the generation interval compared with a program considering only production traits, because the information on lifetime traits only becomes available when cows were already culled [9]. However, as a consequence of the last two decades, more emphasis has been put on methods for genetic evaluation of lifetime traits [10]. One alternative is the use of satiability traits, the binomial traits that measure whether a cow has survived to a certain time (*e.g.* 48 mo of age, 300d in lactation) [11]. A second alternative is the use of survival analysis to obtain breeding values [12]. A third alternative is the use of correlated traits (e.g. conformation traits)[13]. Selection for one trait rarely affects just that one trait. Usually other traits are affected as well, genetic

change in one or more traits resulting from selection for another is termed correlated response to selection, number of genetic mechanisms was probably caused correlated response, linkage is one, if major genes affecting two traits are closely linked, they will tend to stick together. Bourdon,[14] thought that linked genes do not remain together forever, because sooner or later recombination breaks the linkage and the major cause is pleiotropy.

From a statistical perspective, genetic correlations between traits which measure the relative importance of pleiotropic effects on two traits caused correlated response to selection. Knowledge of relationships among traits is important for prediction of expected correlated response to selection [8].The present study was undertaken to estimate expected correlated response in some lifetime traits due to phenotypic selection of cows with different selection intensity according to indicator traits.

MATERIALS & METHODS

Data belong to 944 Holstein cows, for the period from 1998 to 2004 in the Nasr dairy cattle station, United Company for Animal Resources Ltd., Al-Soueira (50 km south of Baghdad), were analyzed to estimate the expected correlated response in some lifetime traits (productive life and nunber of lactations, average milk yield per day of productive life, average milk yield per day of longevity and lifetime milk yield) by phenotype selecting of cows according to two indicator traits (average milk yield per day of age at second calving and first milk yield). Due to first milk yield is very important economic trait which is usually use in evaluation the herd, while average milk yield per day of age at second calving might appear to be a useful criterion for comparing the economic merits of dairy animals because this measure combines three very important traits like age at first calving, first lactation yield and first calving interval [15]. The trait was calculated by dividing the first lactation yield by the age at second calving reckoned as the total of the age at first calving and first calving interval. Forage were fed as part of the base ration. A more detailed description on feed intake and its measurement was given by Al-Anbari and Al-Samarai [16]

Statistical analysis

Statistical analysis included 944 records was carried out using SAS [17]. Expected correlated response in lifetime traits as a result of selection cows with different selection intensity according the indicator traits was estimated by using the following equation (Bourdon, 1997):

$\Delta BVy , x / t = rBVx , BVy\ hx\ hy\ ix\ \sigma Py / L$

Where $\Delta BVy , x / t$ = the rate of genetic change in trait Y per unit of time (t) due to phenotypic selection for trait X,

rBVx , BVy = the genetic correlation between traits x and y,

hx = the square root of heritability for trait x,

hy = the square root of heritability for trait y,

ix = selection intensity for trait x,

σ Py = phenotypic variation for trait y,

L = generation interval (5 years)

Because there is a clear point of truncation, selection in this case is termed truncation selection, and a short method for calculating selection intensity is the number of cows chosen to be parents as a proportion of the number of potential parents or the proportion saved. The proportion selection intensity can then read from a certain table [14]. We assumed that the selection included 123 cows out of 944 cows which mean a proportion selection 13% and the corresponding selection intensity 1.64 and the selection of 246 and 368 cows with a proportion selection 26, 39% and selection intensity 1.25 and 0.98 respectively. To determine whether selecting for an indicator trait is more effective than selecting directly for a trait of interest, we estimated response from both types of selection and expressed the results as a ratio by using the following equation [14]:

$\Delta BVy , x / \Delta BVy = r\ BVx , BVy\ hx\ ix / hy\ iy$

All notations in the equation are the same to notations of equation 1 except iy which denote to selection intensity in trait y.

All genetic and phenotypic parameters were taken from two researches for the same data [16, 18].

Several notions are using in this research and the meaning of each of them as following:

AVMSC = average milk yield per day of age at second calving, PL = productive life NL = number of lactations, FMY = first lactation milk yield, AVMPL = average milk yield per day of productive life, AVML = average milk yield per day of lifetime milk yield, LTMY = lifetime milk yield, PL = productive life, NL = number of lactations.

RESULTS & DISCUSSION

Tables 1 and 2 show the genetic parameters used in this research, whereas table 3 show the expected correlated response in productive life at different intensities of selection 1.64, 1.25 and 0.98 which represent 123, 246 and 368 cows out of 944 cows respectively, due to selection according to average milk yield per day of age at second calving at the the different selection intensities mentioned above, the expectation of correlated response in PL are 0.20, 0.15 and 0.12 month/year respectively. The corresponding estimates for number of lactations are 0.022, 0.017 and 0.013 lactation/year.

Concerning other life time traits, table 4 show the expected correlated response at selection intensity 1.64, 1.25 and 0.98 of cows were 0.15, 0.12 and 0.10 (kg/year) for average milk yield per day of productive life, 0.09, 0.07 and 0.05 (kg/year) for average milk yield per day of lifetime and 278.58, 212.33 and 166.47 (kg/year) for lifetime milk yield respectively. One way to determine whether selecting for an indicator trait is more effective than selection directly for a trait of interest is to estimate response from both types of selection and express the result as a ratio[14]. It‘s obvious from table 5 that most traits were dominated in response by selection for an indicator trait compared with directly selection. In view of the present results we support using an indicator trait because it will reduce the generation interval and increase the annual gain and profitability of dairy project. Similar conclusions were reported by Pryce *et al.*, [19] who pointed to the importance of using indicator traits in selection indexes for improve function traits. It should be clear that the rate of genetic change in a population depends to a large degree on accuracy of selection or, more precisely, accuracy of breeding value prediction.

Some traits had low estimate of heritability such as fitness traits (lifetime traits) and the information on these traits only becomes available when animals are already culled which means longer generation interval and low rate of genetic change, some else traits such as threshold traits which were defined as polygenetic traits that are not continuous in their expression, tend to have small selection intensity and then low rate of genetic change. One important alternative way to improve these traits is using indicator traits to selection for these traits particularly, when an indicator trait has a high heritability and can measured at early age.

TABLE 1. Genetic parameters of average milk yield per day of age at second calving, productive life and number of lactations

Trait / Trait	AVMSC	PL	NL
AVMSC	**0.39**	**0.43**	0.47
PL		**0.02**	
NL			0.02

Estimates in diagonal represent the heritability (h^2) of the traits

Estimates upper diagonal represent genetic correlations (rG)

TABLE 2. Genetic parameters of first milk yield and some lifetime traits

Trait Trait	FMY	AVMPL	AVML	LTMY
FMY	0.19	0.91	0.92	0.90
AVMPL		0.20		
AVML			0.17	
LTMY				0.10

Estimates in diagonal represent the heritability (h^2) of the traits
Estimates upper diagonal represent genetic correlations (rG)

TABLE 3. Expected correlated response in PL and NL according to selection the cows for average milk yield per day of age at second calving at different selection intensities

Trait	Selection intensity		
	1.64	1.25	0.98
PL (kg/year)	0.20	0.15	0.12
NL (lactation/year)	0.022	0.017	0.013

Table 4. Expected correlated response in AVMPL, AVML and LTMY according to selection the cows for first lactation milk yield at different selection intensities

Trait	Selection intensity		
	1.64	1.25	0.98
AVMPL (kg/year)	0.15	0.12	0.10
AVML (kg/year)	0.09	0.07	0.05
LTMY (kg/year)	278.58	212.33	166.47

TABLE 5. Selection for indicator traits and selection directly for traits expressed as ratio.

Trait	Ratio of response
PL (months)	1.90
NL (lactation)	2.08
AVMPL (kg)	0.90
AVML (kg)	0.97
LTMY (kg)	1.23

REFERENCES

[1]. Van Vleck, L.D. (1985) Including records of daughters of selected bulls in estimation of sire components of variance. J.Dairy Sci., 68: 2396 – 2402.

[2]. Van Tassell, C.P., and Van Vleck, L.D. (1991) Estimates of genetic selection defferentials and generation intervals for four paths of selections. J. Dairy Sci.,74: 1078 – 1083.

[3]. Solkner, J. (1989) Genetic relationships between levels of production in different lactations, rate of maturity and longevity in a dual purpose cattle. Livest. Prod. Sci., 23: 33 – 38.

[4]. Lin, C.Y., and Allaire, F.R. (1978) Efficiency of selection on milk yield to a fixed age. J. Dairy Sci., 61: 489 – 497.

[5]. Pearson, R.B., and Miller, R.H. (1981) Economic definition of total performance, breeding goals, and breeding values for dairy cattle. J.Dairy Sci., 64: 857 – 863.

[6]. Burnside, E.B., McClintock, A.E., and Hammond, K. (1984) Type, production and longevity in dairy cattle: a review. Anim. Breed. Abstr.52: 171.

[7]. Van Arendonk, J.A.M. (1989) Use of profit equations to determine relative economic value of dairy cattle herd life. J. Dairy Sci., 74: 1101 – 1109.

[8]. Jairath, L. K., Hayes, J. F. and Cue, R.I. (1994) Multitrait restricted maximum likelihood estimates of genetic traits for Canadian Holsteins. J. Dairy Sci., 77 : 303-312.

[9]. Vollema, A. R. and Groen, A. F. (1998) A comparison of breeding value predictors for longevity using linear model and survival analysis. J. Dairy Sci., 81: 3315-3320.

[10]. Vukasinovic, N. (1999) Application of survival analysis in breeding longevity. Interbull Bulletin, 21: 3-10.

[11]. Hudson, G. F. and Van Vleck, L.D. (1981) Relationship between production and stayability in Holstein cattle. J. Dairy Sci., 64 : 2246-2250.

[12]. Ducrocq, V. (1994) Statistical analysis of length of productive life for dairy cows of the Normande breed. J. Dairy Sci., 77: 855-866.

[13]. Brotherstone, S., Veerkamp, R.F. and Hill, W.G. (1998) Predicting breeding values for herd life of Holstein – Friesian dairy cattle from lifespan and type. Anim. Sci., 67: 405-411.

[14]. Bourdon, R. M. (1997) Understanding Animal Breeding. Prentice Hall, Upper Saddle River, NJ. 07458.

[15]. Deshpande, K.S., and Bonde, H.S. (1983) Genetic aspects of milk yield per day of age at second calving in Friesian x Sahiwal cross breed. Indian J. Anim.Sci., 82: 362 – 367.

[16]. Al-Anbari, N.N., and Al-Samarai, F.R. (2007) Average milk yield per day of age at second calving as an indicator of productive life in Holstein. Iraqi Journal of Agriculture Sciences. 38: 87 – 93. (In Arabic).

[17]. SAS.2001.SAS/STAT Users Guide for Personal Computer. Release 6.12.SAS Institute, Inc., Cary, N.C., USA.

[18]. Al-Samarai, F.R. (2007) Genetic and phenotypic correlations between first milk yield and some lifetime traits in Holstein cows. Journal of Tikrit University for Agricultural Sciences.7: 41 – 50. (In Arabic).

[19]. Pryce, J. E., Veerkamp, R. F. and Simm, G. (2000) Expected correlated response in health and fertility traits to selection on production in dairy cattle. 6th World Congress on Genetics Applied to Livestock Production. Jan, 12-16, Armidale N.S.W., Australia.