IJAS Iranian Journal of Applied Animal Science

Genetic Trends for Milk Yield, Persistency of Milk Yield, Somatic Cell Count and Calving Interval in Holstein Dairy Cows of Iran

Research Article

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Received on: 19 Jul 2012
Revised on: 13 Dec 2012
Accepted on: 31 Dec 2012
Online Published on: Sep 2013

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ABSTRACT

The objective of the present study was to estimate genetic trends for lactation milk yield, persistency of milk yield, somatic cell count and interval between first and second calving in Holstein dairy cows of Iran. The dataset consisted of 210,625 test day and 25,883 first parity cows with milk yield recorded from July 2002 to September 2007 comprising 97 herds in Iran. Breeding values of animals were predicted with Best Linear Unbiased Prediction methodology under multi-trait animal model. Model included region, herd–year–season of calving and age at first calving as fixed effects and Holstein percentage (covariate) and random animal additive effect. Genetic trends of studied traits were estimated by regressing mean of breeding values on calving year. Phenotypic trends were estimated using annual averages of first lactation traits on calving year weighted by the number of animals in each year. Genetic trend was positive and significant for lactation milk yield (21 kg/yr; $p < 0.01$). Although not significant, favorable genetic trends for most studied traits were reported. Considering that selection emphasis in Iran was on lactation milk yield, progress for this trait was low during the years of the study.

KEY WORDS Best Linear Unbiased Prediction, Holstein, persistency, somatic cell count.

INTRODUCTION

Estimation of genetic trends is necessary to monitor and evaluate selection programs. Evaluation of important traits (such as reproduction and health traits) other than milk yield should provide dairy producers with more useful information upon which to base their genetic decisions (Mahoney *et al.* 1986). In previous studies on genetic trends, researchers focused mostly on yield traits. Studies on genetic trends in secondary traits such as persistency of milk yield, somatic cell count and calving interval are scarce (Roman *et al.* 1999; Abdallah and Mc Daniel, 2000). Little is known about the genetic change in these secondary traits due to indirect selection or as a correlated response for yield traits. The majority of the Iranian dairy cattle population consists of several domestic breeds and their crosses with Holsteins. Only approximately 800000 animals are purebred Holsteins. These are either descendant of the cows originally imported from North America and Europe or Holstein upgrades of domestic breeds over 50 year (Ghavi Hossein-Zadeh *et al.* 2008). Despite remarkable changes in selection indices in different Countries (Interbull, 2000) in the last fifteen years, the main emphasis in selecting bulls and cows in Iran was on estimated breeding value of milk yield (Sadeghi Sefidmazgi *et al.* 2009).

Although several investigations have been carried out in Iranian Holstein cows on the genetic trend of 305-day milk yield (Razmkabir, 2005; Sahebhonar, 2007; Khorshidie *et al.* 2012) and one research on the genetic trend of persistency of milk yield (Khorshidie *et al.* 2012), the genetic trends for somatic cell count and calving interval have not yet been evaluated. The objective of this study was to obtain the genetic and phenotypic trends for lactation milk yield, several measurements of persistency of milk yield, somatic cell count and interval between first and second calving in Holstein dairy cows of Iran.

MATERIALS AND METHODS

Test day records on milk yield, somatic cell count and calving events of Holstein cows were obtained from the Animal Breeding Center (ABC) of Iran. The herds used in this study are among the crossbred and purebred Holsteins (≥50% Holstein blood) managed under conditions similar to those in most other developed countries. The herds were under the official performance and pedigree recording program. Artificial insemination is used almost exclusively, and 60 to 80% of the semen is from US and Canadian proven sires (Ghavi Hossein-Zadeh *et al.* 2008). Summary pedigree information of animals is presented in Table 1.

Table 1 Summary of pedigree information

Description	Total
Total number of animals	38291
Animals with record	20544
Animals without progeny	19022
Animals with progeny	4382
Animals with progeny and record	1522
Base animals	3026
-Sires	837
-Dams	3545
Grand parents	2717
-Grand sires	385
-Grand dams	2332
Great grand parents	54
-Great grand sires	25
-Great grand dams	29
Average inbreeding coefficient	0.0021 (%)
Number of herd-year-season	1324

Herds with over 500 test-day records and more than three sires were considered in analysis. Then, cows that calved for the first time between 20 and 40 months of age with at least 6 test-day records were maintained in the final data set. Tests before 6 days in milk (DIM) and after 305 DIM and also calving intervals less than 290 and more than 600 days were excluded from the data set. Daily milk production records of < 10 kg or > 80 kg were deleted. Records of cows with unknown parents or cows with registration number smaller than parent's registration number were also discarded. The final dataset consisted of 210625 test day records of 25883 cows with first calving from July 2002 to September 2007 in 97 herds. The average and maximum number of daughters per sire were 23.28 and 382, respectively, and about 6% of the sires had more than 100 daughters. The total number of sires was 1112. Descriptive statistics of the phenotypic values of the traits measured in various forms is shown in Table 2, and a summary of genetic values is presented in Table 3.

Statistical methods

Lactation milk yield was retrieved using two different methodologies.

According to the first method, so called the test interval method (ICAR, 2004) and being used by ABC agency in Iran, the average milk yield measured between two consecutive test date were multiplied by number of days interval, and the results for all intervals were accumulated to obtain lactation milk yield (MILK (ABC)). As the second method of choice, Wood's gamma function was fitted on test day records of each individual cow using programming language of Matlab, to estimate lactation milk yield (MILK (WOOD)), as well as the first 100-day milk yield and the second 100-day milk yield. The gamma function described by Wood (1967) is as follows:

$$Y_t = at^b \times e^{-ct}$$

Where:
y_t: milk yield on day.
t, a: a scaling factor to represent yield at the beginning of lactation.
b and c: are factors associated with the inclining and declining slopes of the lactation curve.

Typical lactation curves have positive b and c, and curves with negative b or c were considered to be from atypical lactations (Tekerli *et al.* 2000). Atypical lactation curves in our dataset were about 20.6% and were excluded from further analysis. Two types of persistency measures were used in this study. The first type uses ratios between yield of different parts of the lactation (P2:1, P3:1 and P_{weller}) and the second one uses a mathematical function (s from the gamma function):

$$s = -(b+1) \times \ln \times (c)$$

The measures of P2:1 and P3:1 was introduced by Johansson and Hansson (1940) and is milk yield ratios of the second and third 100 days of lactation to milk yield of first 100 days. Weller *et al.* (2006) defined milk persistency as estimated milk production at 180 day after peak divided by estimated peak production as:

$$P_{weller} = 100\% \times \text{PROD}(270) / \text{PROD}(90)$$

They assumed peak production at first lactation occur at 90 DIM. PROD (270) is considered the production at 270 DIM and was calculated by Wood's function.

Table 2 Summary of descriptive statistics of phenotypic values[a] (based on 20544 first lactation records)

Trait	Mean	SD	CV (%)	Minimum	Maximum
Milk (ABC) (kg)	7646.4	1232.5	16.12	2644	12567
Milk (WOOD) (kg)	9065.2	1521.5	16.78	3106.8	15243.3
CI (mo)	13.287	2.223	16.71	9.67	20
P2:1	1.063	0.216	20.32	0.458	5.196
P3:1	0.915	0.246	26.88	0.163	7.616
P_{weller}	0.803	0.157	19.55	0.134	3.532
s	7.709	1.039	13.48	5.446	18.492
SCC ('000)	245.1	343.8	140.27	9.67	6962
LnSCC	4.869	1.109	22.78	2.269	8.848
stdSCC	318.5	541.2	169.92	2.24	6448

[a] Milk (ABC): total milk yield calculated by ICAR's method; Milk (WOOD): total milk yield calculated by Wood's gamma function; CI: calving interval; P2:1: [(milk yield second 100 days) / (milk yield first 100 days)] × 100; P3:1: [(milk yield third 100 days) / (milk yield first 100 days)] × 100; P_{weller}: (milk yield 270 d) / (milk yield 90 d) × 100; s= -(b+1) × ln × (c); SCC: mean somatic cell count; LnSCC: mean $\log_e$ somatic cell count and stdSCC: standard deviation of somatic cell count.

SD: standard deviation and CV: coefficient of variation.

Table 3 Summary of descriptive statistics of genetic values[a] (based on 20544 first lactation records)

Trait	Mean	SD	CV (%)	Minimum	Maximum	Skewness	Kurtosis
EBV for Milk (ABC)	21.392	355.4	1661.4	-1537.8	1213.8	-0.158	0.219
EBV for Milk (WOOD)	30.03	415.7	1384.3	-1798	1505	-0.186	0.221
EBV for CI	-0.0145	0.161	1110.3	-0.5196	0.5632	0.139	0.06
EBV for P2:1	-0.00049	0.0149	3040.8	-0.0822	0.1374	0.522	2.314
EBV for P3:1	0.0276	0.748	2710.1	-0.163	0.473	0.748	6.981
EBV for P_{weller}	0.00046	0.0208	4521.7	-0.0973	0.2318	0.0649	1.642
EBV for s	-0.00292	0.0749	2565.1	-0.287	0.443	0.229	0.985
EBV for SCC ('000)	-0.0229	17.514	76480	-65.44	179.2	1.109	4.74
EBV for LnSCC	0.00123	0.093	7561	-0.322	0.479	0.381	0.486
EBV for stdSCC	0.753	15.014	1993.9	-40.56	126.58	1.025	3.575

[a] Milk (ABC): total milk yield calculated by ICAR's method; Milk (WOOD): total milk yield calculated by Wood's gamma function; CI: calving interval; P2:1: [(milk yield second 100 days) / (milk yield first 100 days)] × 100; P3:1: [(milk yield third 100 days) / (milk yield first 100 days)] × 100; P_{weller}: (milk yield 270 d) / (milk yield 90 d) × 100; s= -(b+1) × ln × (c); SCC: mean somatic cell count; LnSCC: mean $\log_e$ somatic cell count and stdSCC: standard deviation of somatic cell count.

SD: standard deviation; CV: coefficient of variation and EBV: estimated breeding value.

Higher values of the above mentioned criteria indicated greater persistency. The reason for choosing these measures as persistency measures was their ease of calculation, ease of interpretation and those have moderate heritability and relatively high genetic correlation with milk yield (Solkner and Fuchs, 1987).

Calving interval was calculated using dates of first and second calving. In addition to mean for somatic cell count (SCC) two relevant measures were calculated: mean $\log_e$ somatic cell count (LnSCC) and standard deviation of somatic cell count (stdSCC).

Among various measures of somatic cell count introduced in the literature, a measure which has rarely been considered is stdSCC. Although the distribution of stdSCC is not normal, it is similar to the distribution of SCC and can be referred as variability of somatic cell count. A single-trait analysis was performed, using the WOMBAT 1.0 software (Meyer, 2007).

The fixed part of the model included the effect of region and herd-year-season of calving, with age at first calving (months) and Holstein percentage being considered as a covariate effect. The following linear model was used for the analysis of data:

$$Y_{ijklmn}= \mu + R_i + HYS_j + aAFC_k + bHP_l + A_m + e_{ijklmn}$$

Where:

Y_{ijklmn}: is the observation on TMY (total milk yield), PMY (persistency of milk yield), mean SCC, mean of $\log_e$ somatic cell count (LnSCC), standard deviation of somatic cell count (stdSCC) and interval between first and second calving (CI).

μ: is the mean of population.

R_i: is the fixed effect of region.

HYS_j: is the fixed effect of herd-year-season of calving (four seasons of winter, spring, summer and fall).

AFC_k: is the fixed effect of age at first calving.

HP_m: is the covariate effect of Holstein percentage.

a and b: are the linear regression coefficient of traits on age at first calving and Holstein percentage, respectively.

A_n: is the random genetic effect of the animal.

e_{ijklmn}: is the random residual error.

After performing analyses, WOMBAT 1.0 software produces random solution files that contain estimated breeding values of all animals in pedigree. Genetic trends of studied traits were estimated by regressing mean of breeding values on calving year. Also, phenotypic trends were estimated using annual averages of first lactation traits on calving year weighted by the number of animals in each year using REG procedure of SAS (SAS, 2002).

RESULTS AND DISCUSSION

Total milk yield estimated using WOOD's function was higher than the estimate of test interval method. Similarly Atashi *et al.* (2007) reported 1,311kg difference between estimates of total milk yield using WOOD's function and test interval. Phenotypic trend of MILK (ABC), MILK (WOOD) and CI by year of calving is shown in Figure 1.

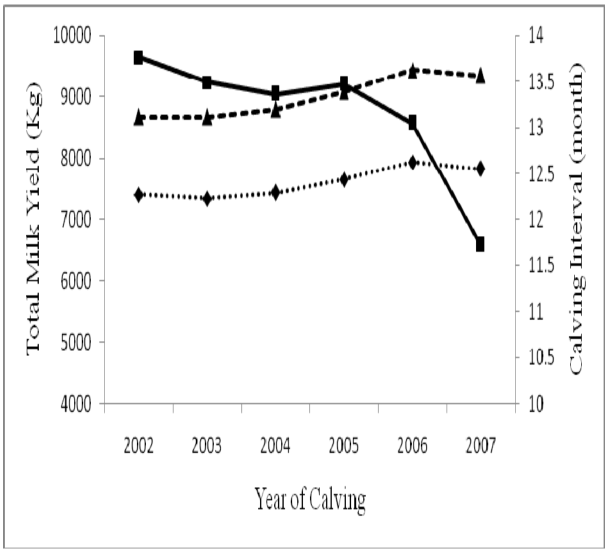

Figure 1 Measurses of total lactatioin milk yield and calving interval by year of calving. solid line= CI; Dashed line= MILK (WOOD) and Dotted line= MILK (ABC)

The phenotypic average for CI decreased from 13.765 mo in 2002 to 11.728 mo in 2007. Contrary to the result of this study, De Vries and Risco (2005) reported that the average calving interval increased from 399 d in 1976 to 429 d in 2000 in dairy herds of Florida and Georgia. Also, they stated that a greater 305-d milk production was associated with a longer calving interval at a rate of 9.5d per 1000 kg milk. Hare *et al.* (2006) reported average of first calving interval for Holstein cows 13.433 mo in United States, with annually one day increase in calving interval. The reason for declining phenotypic trend of CI in current study can be the increasing calf price relative to milk price in recent years that encourages farmers to reduce waiting period and open days after calving. The average annual phenotypic trends (Table 4) obtained from fitting the linear regression of annual phenotypic mean for MILK (ABC), MILK (WOOD) and CI were 116.8 (kg/yr), 172.5 (kg/yr) and -0.326 (mo/yr), respectively (P<0.05). Negative significant (P<0.05) annual phenotypic trend for P2:1 and s was observed (-0.0116 and -0.05174, respectively), but those of P3:1 and P$_{weller}$ were not significant (Table 4).

Table 4 Estimated phenotypic trend function for different traits^{a}

Function	R-square
Milk (ABC)= 7190 + 116.766 × Year*	0.8017
Milk (WOOD)= 8397 + 172.522 × Year**	0.8813
CI= 14.285 - 0.32631 × Year*	0.697
P2:1= 1.10618 - 0.0116 × Year*	0.7314
P3:1= 0.93285 + 0.00669 × Year	0.3603
P$_{weller}$= 0.78706 + 0.00185 × Year	0.044
s= 7.90061 - 0.05174 × Year*	0.7066
SCC= 337.36 - 26.19 × Year**	0.868
LnSCC= 5.30287 - 0.011763 × Year**	0.8917
stdSCC= 342.87 - 11.06 × Year	0.1328

[a] Milk (ABC): total milk yield calculated by ICAR's method; Milk (WOOD): total milk yield calculated by Wood's gamma function; CI: calving interval; P2:1: [(milk yield second 100 days) / (milk yield first 100 days)] × 100; P3:1: [(milk yield third 100 days) / (milk yield first 100 days)] × 100; P$_{weller}$: (milk yield 270 d) / (milk yield 90 d) × 100; s= -(b+1) × ln × (c); SCC: mean somatic cell count; LnSCC: mean log$_e$ somatic cell count and stdSCC: standard deviation of somatic cell count. EBV: estimated breeding value.

* P<0.05 and ** P<0.01.

Considering the nature of measures of milk yield persistency, this result suggests that in the studied population milk production in second part of lactation decreased over time. Annual phenotypic trend for SCC (-26.2) and LnSCC (-0.0118) was significant (P<0.01), while that of stdSCC was not significant (Table 4), showing variability of somatic cell count being unaltered over studied time period. Values for SCC, LnSCC and stdSCC in calving years of 2002-2007 are presented in Figure 2.

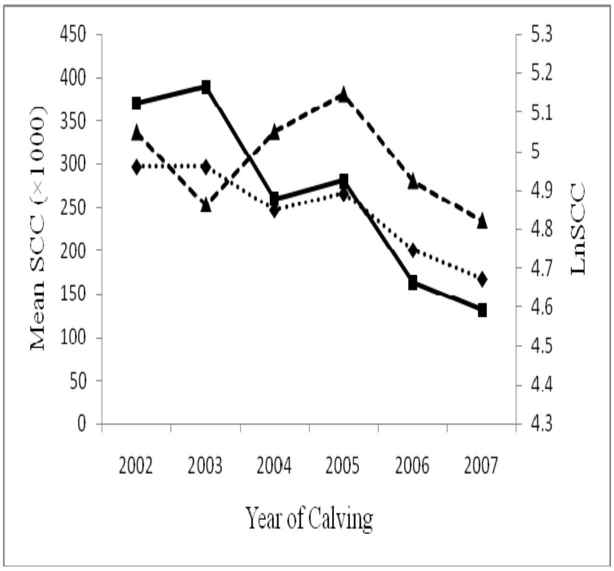

Figure 2 Average mean log$_e$ somatic cell count (LnSCC) (solid line), somatic cell count (SCC) (dotted line) and standard deviation of somatic cell count (dashed line) by calving year

The declining trend for SCC is similar to the report of Ødegard *et al.* (2003) in which they found a favorable downward phenotypic trend over a 17-years period.

Positive genetic trends (Table 5) of about 21 kg/yr were observed ($P<0.05$) for MILK (ABC) and MILK (WOOD), as well.

Table 5 Estimated genetic trend function for different traits[a]

Function	R-square
EBV Milk (ABC)= -60.64 + 20.93 × Year**	0.9098
EBV Milk (WOOD)= -54.93 + 21.14 × Year**	0.8804
EBV CI= -0.64276 + 0.06671 × Year	0.1182
EBV P2:1= -0.00157 + 0.00029461 × Year	0.576
EBV P3:1= -0.00083746 + 0.0001762 × Year	0.1052
EBV P_{weller}= 0.00122 - 0.00020548 × Year	0.1386
EBV s= -0.00583 + 0.00080079 × Year	0.2973
EBV SCC= 0.77259 - 0.25185 × Year	0.4349
EBV LnSCC= 0.00060077 - 0.00021273 × Year	0.007
EBV stdSCC= 1.19641 - 0.15994 × Year	0.2519

[a] Milk (ABC): total milk yield calculated by ICAR's method; Milk (WOOD): total milk yield calculated by Wood's gamma function; CI: calving interval; P2:1: [(milk yield second 100 days) / (milk yield first 100 days)] × 100; P3:1: [(milk yield third 100 days) / (milk yield first 100 days)] × 100; P_{weller}: (milk yield 270 d) / (milk yield 90 d) × 100; s= -(b+1) × ln × (c); SCC: mean somatic cell count; LnSCC: mean $\log_e$ somatic cell count and stdSCC: standard deviation of somatic cell count.

EBV: estimated breeding value.

* $P<0.05$ and ** $P<0.01$.

The genetic trend of lactation milk production for Holstein cows in Iran was lower than the estimates for some other countries such as northeastern states of United States (34.9 and 94.7 kg/yr) (Van Tassell and Van Vleck, 1991; Abdallah and McDaniel, 2000) and Italy (173 kg/yr) (Burnside *et al.* 1992). Recently, Khorshidie *et al.* (2012) estimated a higher genetic trend for 305-day milk yield in Iranian Holstein cows by regressing the weighted average EBVs of the sires on the birth year of their daughters. The reason for higher estimate in Khorshidie *et al.* (2012) (52.54 kg/yr) might be that they employed genetic values of sires to estimate the trend instead of using genetic values of all individual including males and females.

Although a positive genetic trend was obtained for lactation milk yield, the genetic trend in CI was not significantly different from zero ($P>0.05$). Most studies (Hansen *et al.* 1983; Haile Mariam *et al.* 2003; Grosshans *et al.* 1997; Muir *et al.* 2004) used field data to investigate the relationships between milk yield and measures of reproductive performance and found unfavorable genetic associations between those.

In spite of considering persistency measures that have high genetic correlation with milk yield, there was no significant ($P>0.05$) trend in genetic values for different measurements of milk yield persistency (Table 5), although phenotypic trends for some of them were significant. Estimates of the trend for milk yield persistency are rare in the literature, though Weller *et al.* (2006) remarked an increase from 57 to 68% over a 20 yr period. Khorshidie *et al.* (2012) reported a positive, but no significant genetic trend for persistency. Considering the obtained genetic correlation between 305-day milk yield and persistency, they stated that selection for higher 305-day milk yield might not result in selection of sires that are genetically higher in lactation persistency and therefore, simultaneous evaluation for milk yield and lactation persistency would be necessary.

Small negative genetic trends for SCC, LnSCC and stdSCC were obtained (Table 5), although they were not significant ($P>0.05$). Since 60 to 80% of semen using in Iran is usually of US and Canadian proven sires (Ghavi Hossein-Zadeh *et al.* 2008), a marginal decrease in SCC was expected, because of indirect selection for mastitis resistance in those countries. Similar to this study in Finnish Ayrshire, highlighting main emphasis on milk production, mastitis and fertility, Juga *et al.* (1999) reported a downward genetic trend for SCC, while a desired genetic response was obtained for milk production. This supports the findings in this study, and indicates that genetic progress in milk production traits is feasible without deteriorating SCC.

CONCLUSION

Favorable genetic trends for all studied traits (except CI and P_{weller}) were reported. Considering that most emphasis in Iran is on TMY, progress for TMY has not been satisfying through these years. Although genetic trend for different measures of SCC was not significant, downward phenotypic trend was considerable. Also, genetic trend for different measures of PMY was not significant, and considering the economic value of PMY and its correlation with fertility and health traits (Solkner and Fuchs, 1987), it can be suggested to set a new and effective selection index to accelerate progress for this trait.

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