Effects of herd origin, AI stud and sire identification on genetic evaluation of Holstein Friesian bulls

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ABSTRACT

The purpose of this study was to estimate the effects of herd origin of bull, AI stud and sire identification number (ID) on official estimated breeding values (EBV) for production traits of Holstein Friesian proven bulls. The data included 1,005 Italian Holstein-Friesian bulls, sons of 76 sires, born in 100 herds and progeny tested by 10 AI studs. Bulls were required to have date of first proof between September 1992 and September 1997, to be born in a herd with at least one other bull and to have sire and dam with official EBV when bull was selected for progeny testing. Records of sires with only one son were also discarded. The dependent variable analyzed was the official genetic evaluation for a "quantity and quality of milk" index (ILQ). The linear model to predict breeding values of bulls included the fixed class effects of herd origin of bull, AI testing organization, birth year of bull, and estimated breeding values of sire and dam, both as linear covariates. The R^2 of the model was 45% and a significant effect was found for genetic merit of sire (P < 0.001) and dam (P < 0.014), for herd origin of bull (P < 0.01) and for birth year of bull (P < 0.001). The effect of AI testing organization was not significant. The range of herd origin effect was 872 kg of ILQ. However, in this study, the causes of this result were not clear; it may be due to numerous factors, one of which may be preferential treatment on dams of bulls. Analyses of residuals on breeding value of proven bulls for ILQ showed a non significant effect of sire ID, after adjusting for parent average, herd origin effect and birth year effect. Although the presence of bias in genetic evaluation of dairy bulls is not evident, further research is recommended firstly to understand the reasons of the significant herd origin effect, secondly to monitor and guarantee the greatest accuracy and reliability of genetic evaluation procedures.

Key words: Dairy cows, Holstein breed, Genetic evaluation, Preferential treatment, Potential biases.

RIASSUNTO
EFFETTI DELL' ALLEVAMENTO DI ORIGINE, DEL CENTRO DI INSEMINAZIONE ARTIFICIALE E DELL'IDENTIFICATIVO DEL PADRE SULLA VALUTAZIONE GENETICA DEI TORI DI RAZZA FRISONA ITALIANA

Obiettivo della presente ricerca è di stimare gli effetti dell'allevamento di origine del toro, del centro di inseminazione artificiale (FA) e dell'identificativo del padre sulla valutazione genetica per i caratteri produttivi dei tori di razza Frisona ufficialmente provati in Italia. I dati considerati nella presente ricerca sono risultati 1.005 tori di razza Frisona Italiana, figli di 76 padri, nati in 100 allevamenti ed avviati alle prove di progenie nazionali da 10 centri di FA. I tori considerati nella pre-

sente ricerca hanno soddisfatto le seguenti caratteristiche: avere la prima valutazione genetica compresa tra Settembre 1992 e Settembre 1997, essere nati in un allevamento con almeno un altro toro ufficialmente valutato dal programma nazionale di prove di progenie e di avere un padre ed una madre con la valutazione genetica ufficiale quando il toro è stato selezionato per le prove di progenie nazionali. Le osservazioni relative ai padri di toro con un unico figlio provato sono state scartate dall'analisi. La variabile dipendente analizzata è stata l'indice latte qualità (ILQ). Il modello lineare per predire il valore riproduttivo dei tori ha previsto quali fonti di variazione gli effetti fissi dell'allevamento di origine del toro, il centro di FA, l'anno di nascita del toro e gli indici genetici del padre e della madre come covariate lineari. L' R^2 del modello è risultato pari al 45%. Un significativo effetto è stato evidenziato per il valore genetico del padre (P < 0,001) e della madre (P < 0,014), per l'allevamento di origine del toro (P < 0,01) e per l'anno di nascita del toro (P < 0,001). L'effetto del centro di FA non è risultato statisticamente significativo. L'effetto dell'allevamento di origine del toro ha evidenziato una differenza tra il livello minimo e massimo di 872 kg per l'ILQ. Tuttavia, in questo studio, non risultano chiare le cause che hanno determinato la significatività dell'effetto dell'allevamento di origine del toro le quali potrebbero essere dovute da una serie di fattori tra i quali si indicano eventuali trattamenti preferenziali (PT) sulle madri di toro.

L'analisi dei residui non ha evidenziato un significativo effetto dell'identificativo del padre sull'indice genetico del figlio per l'ILQ, a parità di indice pedigree, allevamento di origine ed anno di nascita. In conclusione, sebbene nessuna evidente presenza di distorsione sistematica negli indici dei tori è stata rilevata nel presente lavoro, si suggerisce di condurre ulteriori ricerche sull'argomento, in primo luogo per capire le ragioni della significatività rilevata per l'effetto allevamento di origine ed in secondo luogo per monitorare e garantire la massima accuratezza e precisione delle procedure di valutazione genetica dei riproduttori avviati al programma nazionale di prove di progenie per la razza Frisona Italiana.

Parole chiave: Bovine da latte, Razza Frisona Italiana, Valutazioni genetiche, Trattamento preferenziale, Campionamento mendeliano.

Introduction

The development of the dairy breeding industry is based on a global market that requires accurate EBV. The ability to statistically compare sires across countries (Schaeffer, 1994; Banos and Sigurdsson, 1996) has provided international evaluations with great accuracy (Weigel, 1997) and has intensified international competition. Over time, AI studs are gradually increasing the number of bulls sampled and the average size of progeny groups (Dekkers *et al.*, 1996). In Italy, the number of bulls authorized for progeny testing by ANAFI (National Breeders Association of Italian Holstein Friesian cattle) increased from 201 in 1987 to 534 in 1998 and the number of herds of origin of bulls increased from 89 to 177 during the same time period (ANAFI, 2000). Despite this latter trend, the AI studs are sampling many bulls born in relatively few herds given that in Italy there are more than 15,000 herds of Italian Holstein Friesian cattle enrolled in the national herd book (ANAFI, 2000). This trend might compromise the genetic gain of the national population if some bias affects the genetic evaluation of bull dams in these few herds. Therefore, competi-

tive AI markets urge that AI studs select the best bulls on pedigree merit and sample those bulls in an unbiased manner to demonstrate the genetic merit of each bull accurately (Meinert *et al.*, 1992; Meinert *et al.*, 1997; Vierhout *et al.*, 1998; Vierhout *et al.*, 1999). The interest to guarantee a quality assurance system of national and international genetic evaluation is considered an important issue (Dommerholt *et al.*, 1995). Real biases in EBV of parents hinder the selection of truly superior bulls for AI studs. Selection of bulls accounts for about 75% of the total genetic gain that is possible to realize in a dairy cattle population (Vierhout *et al.*, 1998). In particular, the potential for bias in the EBV of elite cows is a concern, and this bias has been shown to increase as preferential treatment increases (Kuhn *et al.*, 1994). Different studies have shown that BLUP more accurately predicted parent average EBV than did alternative genetic evaluation methods (Ferris and Wiggans, 1991; Samuelson and Pearson, 1995) but it cannot correct for preferential treatment. Therefore, the potential for biased evaluations in dairy populations was investigated by other researchers (Kuhn *et al.*, 1994; Kuhn *et al.*, 1999; Meinert *et al.*, 1992). Recently, some methods to

validate EBV have been proposed (Bonaiti *et al.*, 1993), but few studies in the literature have examined the effectiveness of progeny testing to assure adequacy of genetic evaluation estimate.

The aim of the present study was to estimate the effects of critical factors such as herd origin of bull, AI stud and sire ID on estimated breeding value of proven bulls for production traits in the Italian progeny testing program for Holstein-Friesian cattle.

Material and methods

Data and Computations

Official Holstein-Friesian proven bulls computed by National Breeder Association of Italian Holstein Friesian cattle in September 1997, were used. Editing procedures removed data from all herds only one bull and from all bulls that either 1) were born prior to September 1992, or 2) had no paternal half-sibs, or 3) had parents with missing EBV. A total of 1005 bulls, sons of 76 sires (50 USA, 13 ITA, 12 CAN and 1 NLD), born in 100 herds and owned by 10 national AI studs were available for statistical analyses.

The dependent variable was EBV for the Italian milk quantity and quality index (ILQ). The ILQ is expressed in kg of milk and it was the major component (80%) of ILQM that was the official selection index in Italy for Holstein breed (ANAFI, 1994) until December 2001 (ILQM combines ILQ and udder index). The ILQ is obtained by combining EBV for milk yield (with a negative weight of -27%), fat yield (with a positive weight of 6%) and protein yield (with a positive weight of 67%). The genetic evaluations in Italian Holstein Friesian cattle for production traits are currently generated by the animal model procedure including herd-year-season effect and animal random effect with relationship matrix (Interbull, 2000).

The independent variables were herd origin of bull, AI studs, and sire and dam EBV. The parental information were not the most updated EBV, but rather, those recorded when bull was first officially approved for progeny testing (at age around 12 mo.). Use of these historical EBV avoided auto-correlation between indexes of parents and sons, generated by animal model procedure, and allowed

analysis of the situation when AI studs decided to select young bulls for the progeny testing program. The effects of EBV of sires and dams were used to account for pedigree value and for different genetic level of herd origin of bull. All EBV used in the present study were based or rescaled on the genetic base of 1990.

Statistical Models

Statistical analysis was performed using the GLM procedure of SAS (1989) according to the following fixed linear model:

$$Y_{ijklm} = H_i + C_j + B_k + b_1 S_{ijklm} + b_2 D_{ijklm} + e_{ijklm}$$

where

Y_{ijklm} = EBV for ILQ of each bull ;
H_i = effect of herd origin i (i= 1, 2 ... 100);
C_j = effect of AI studs j (j = 1, 2 ... 10);
B_k = effect of birth year k (k = 1, 2 … 6);
b_1 = linear regression coefficient of the observation on EBV of sire for ILQ;
b_2 = linear regression coefficient of the observation on EBV of dam for ILQ;
S_{ijklm} = EBV of sire for ILQ of the ijklm bull observation (linear covariate);
D_{ijklm} = EBV of dam for ILQ of the ijklm bull observation (linear covariate);
e_{ijklm} = random effect of error ~ N (0, σ2e).

The birth year effect of bull (6 levels: from 1987 to 1992) was included to adjust for annual genetic trend, using a linear regression model of EBV on birth year of bulls, because of preliminary analyses which showed that genetic trend was statistically significant and equal to +156 kg for ILQ. Another preliminary analysis of variance discarded the use of accuracy of EBV effect in the statistical model because a non significant effect was detected.

To test the hypothesis that herd origin of bull might be assumed as an indication of non-random Mendelian sampling, we examined the genetic trend in each herd origin. Indeed, if it is true that favourable Mendelian sampling effects are unusually common in the extremely high herd effects, then the genetic trend within those herds

Figure 1.   Distribution of herd origin per size of bulls.

Classes of herd origin of bull
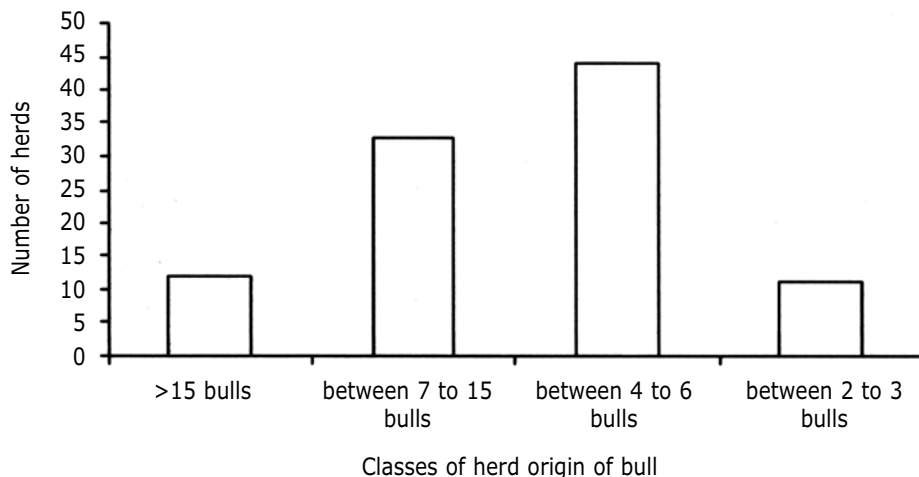
should be much greater than expected under the assumption of random Mendelian sampling. Likewise, the genetic trend should be much lower in herds with extremely low herd effects. Therefore, solutions for the herd origin effect were regressed on the genetic trend within herd of bull using EBV of bulls or dams of bulls.

The effect of sire ID was detected using a GLM procedure that considered the residuals obtained by previous linear models as the dependent variable and the official herd-book sire ID as the independent variable.

Results and discussion

Data Characteristics
The frequency distribution of herds origin of bulls per size of bulls is shown in Figure 1. Seventy-seven percent of herds had between 4 and 15 proven bulls. The average number of bulls per herd origin was 10 (standard deviation of ±12) with a minimum of 2 and a maximum of 60 bulls. Figure 2 shows the number of proven bulls per AI stud. Average number of bulls per AI stud was 101 (±82), with a minimum and maximum of 6 and 218

Figure 2.   Distribution of AI centers for number of bulls owned.
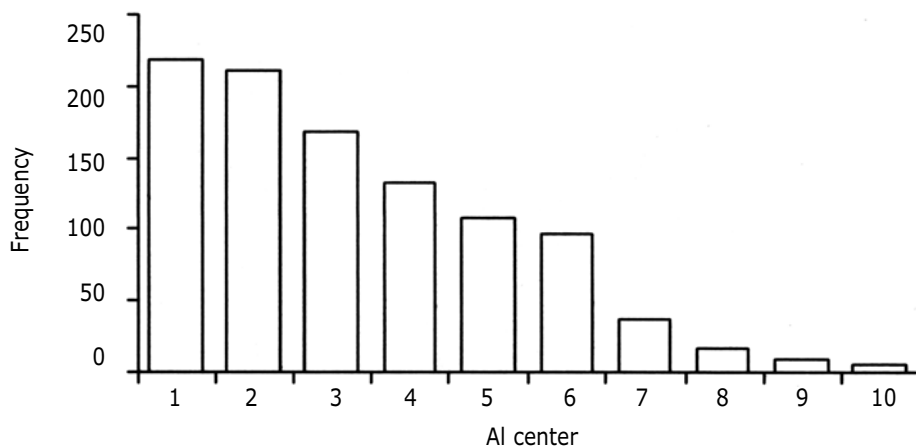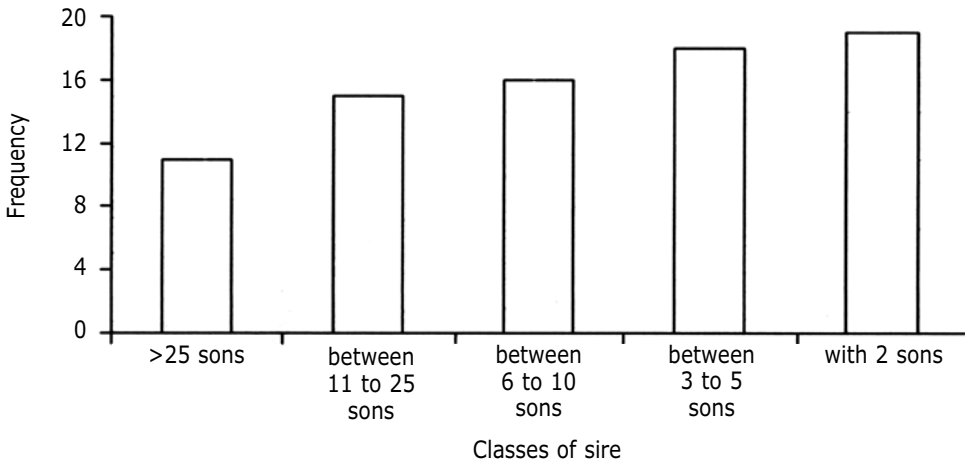

AI center

Figure 3.   Distribution of sire classes for proven sons size.

bulls, respectively. The three largest AI studs accounted for 60% of the total bulls that were born in 92% of the herds analyzed. Figure 3 shows the distribution of number of progeny tested sons per sire. The largest frequency resulted for the class of sires with 2 sons (19 observations), however a uniform distribution was evidenced for the 5 classes defined. On average, the number of bulls per sire was 13 (±18) with a minimum of 2 and a maximum of 83 bulls. The 5 most common sires of bulls accounted for 34% of total bulls analyzed. These sires were: To-Mar Blackstar with 83 sons, Nowerland Trifecta with 73 sons, Bis-May Tradition Cleitus with 69 sons, Rothrock Tradition Leadman with 67 sons and Walkway Chief Mark with 50 sons. The total number of dams was 771 and the average number of bulls per dam was 1.3 (±0.68) with a minimum of 1 and a maximum of 6 bulls. The dams with more than 2 bulls accounted for 16.3% of total bulls analyzed.

Overall, the average number of herds origin of bull per AI studs was 2.8 (±3.0) with a minimum of 1 and a maximum of 26 records. Approximately 15% of the total bulls analyzed were born in herds that provided only one AI stud. Consequently, in the present study a negligible confounding effect between herd and AI stud was assumed.

Summarizing, 50% of bulls used in this research were: born in 15% of the herds, were sons of 13% of sires and owned by 30% of the AI studs analyzed. More than 15,000 herds are

recorded in the Italian Holstein herd-book (ANAFI, 2000) but fewer than 200 (1.3% of total herds) herds were involved in the national progeny testing scheme. This situation is effectively an open nucleus scheme where these 200 herds can be considered the breeders that made up the true nucleus of selection of the Italian Holstein population and the other farms have carried out the role of multipliers. Until now, this circumstance was probably a strong point for a young breeding program but in the future more attention should be paid to involving other herds to avoid a reduction in selection intensity. Use of the same few herds (1.3% of the total herds) in the national progeny test might limit selection intensity and increase risk for biased genetic evaluations, in particular with preferential treatment on potential dams of bulls.

Descriptive statistics regarding the EBV for traits used in the analyses are described in Table 1. The mean EBV of bulls for ILQ was 969 kg with a standard deviation of ± 459 kg. The mean reliability of EBV of bulls for ILQ was 88 % (±5 %) with a minimum of 68 % and a maximum of 98 %. The average EBV of dams of bulls, when son was selected for progeny testing, was 728±471 kg of ILQ. Predicted breeding values of sires of bull was 1359 kg with a standard deviation of ± 450 kg of ILQ. The parent average for ILQ was 1043 kg (±344) confirming that this preliminary index is a good predictor of EBV for a group of bulls.

Table 1.   Descriptive statistics of data set used.

	Mean	SD	Minimum	Maximum
Bulls (1,005 observations):				
- Birth year	89.6	1.51	87	92
- ILQ[1] EBV[2], kg [1]	969	459	-485	2578
Dams (771 observations):				
- ILQ EBV, kg	728	471	-881	2151
Sires (76 observations):				
- ILQ EBV, kg	1359	450	82	2335

[1] ILQ = 4.5 x ((-0.173 x milk yield) + fat yield +(11.3 protein yield)

[2] EBV = Estimated Breeding Value

Sources of Variation Affecting Breeding Values

The factors included in the analysis of variance (Table 2) accounted for 45% of total variation and all effects significantly affected EBV for ILQ of Holstein proven bulls, except for AI effect which accounted for 1% of the total sum of squares. Herd origin of bull (P < 0.01) absorbed 14% of the total sum of squares whereas the birth year effect accounted for 18% of total sum of square (P<0.0001). Dam's information accounted for 3% of total sum of square of ILQ, showing a smaller effect than EBV of sire that absorbed 22%. Moreover, the linear regression coefficients for dam and sire of bulls resulted 0.25 with a standard error of ±0.04 and 0.38 with a standard error of ±0.03, respectively. In both cases the expected linear regression coefficient was 0.50.

*Effect of Herd Origin of Bull on Breeding Values*

Average least square means for herd origin of bull was 953 kg with a standard deviation of 191 kg. Figure 4 shows the distribution of frequency of herd origin effects for ILQ classes with a large range equal to 872 kg. Standard errors of estimates ranged from 233 to 361 kg. This high effect of herd origin of bull might be due to potential preferential treatment of dams of bulls. Indeed, preferential treatment of females often occurs inadvertently through the use of routine management practices that are not applied to all cows equally, as feeding cows according to their level production. Kuhn *et al.* (1994) found that preferential treatment applied to elite cows causes a bias on their PTA that ranges from 6 to 39% of the preferential treatment effect. Moreover, in this study, the significant effect of herd origin might also be caused by a herd-

Table 2.   Analyses of variance for ILQ[1] of bulls.[2]

Source of variation	df	MS	P	ΔR[2]%
Herd origin	99	216,474	0.0060	14
AI center	9	229,981	NS	1
Birth year of bull	6	2,593,020	<0.0001	18
Dam's ILQ	1	7,221,957	<0.0001	3
Sire's ILQ	1	22,669,898	<0.0001	9
MSE	kg	152,026		

[1] Breeding values for milk quality index = 4.5x((-0.173 x milk yield)+fat yield+(11.3 x protein yield)).

[2] R^2 = 0.45

Figure 4.   Distribution of herd origin of bull effects for classes of ILQ [1]
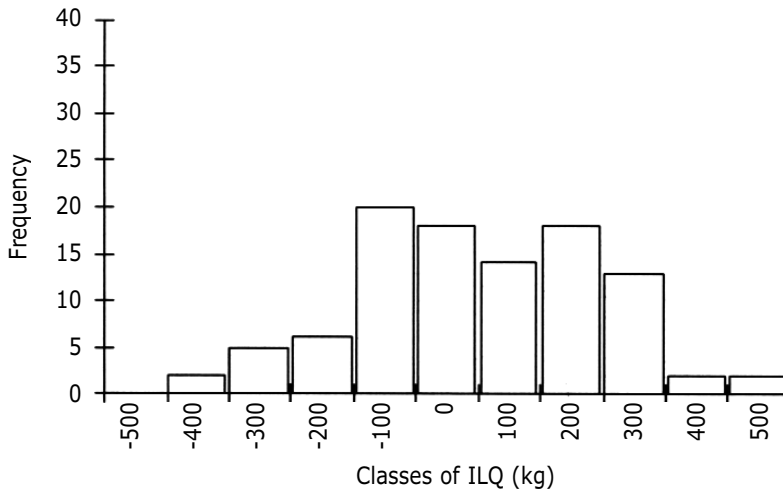
[1] ILQ = 4.5 x (-0.173 x milk yield) + fat yield + (11.3 protein yield)

Figure 5.   Relation between effect of herd origin of bull and genetic trend of dams of bulls within herd for ILQ. [1]
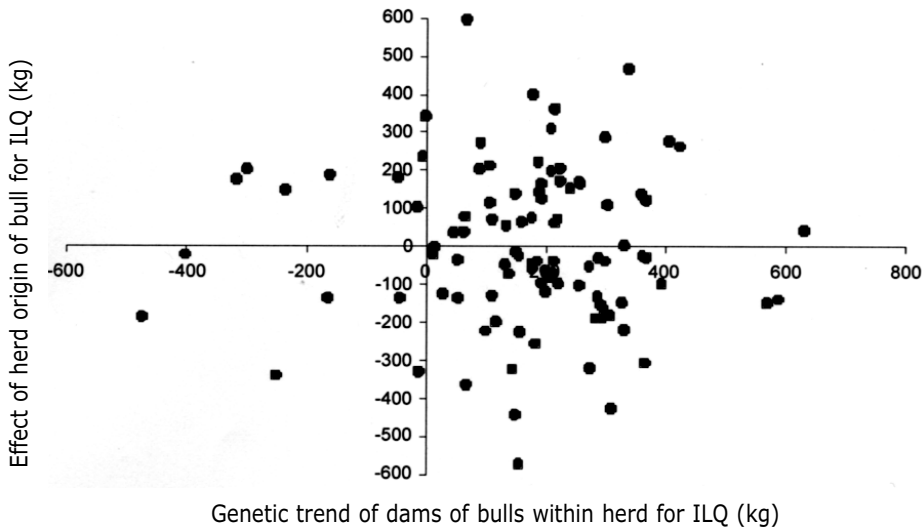
[1] ILQ = 4.5 x (-0.173 x milk yield) + fat yield + (11.3 protein yield)

based non-random Mendelian sampling due to the reduced number of bulls per herd origin. To test this hypothesis Figure 5 and Figure 6 show the results of the analyses conducted on the relation between effect of herd origin of bull with average genetic trend of dams of bulls or average genetic trend of bulls within herd for ILQ, respectively. In both cases, the linear regression coefficients and R^2 were close to zero and similar results were obtained both using all herds or only herds with more than 10 proven bulls per herd (29 herds). This simple approach did not validate the hypothesis that herd origin of bull might be assumed as an indication of non-random Mendelian sampling,

Figure 6.   Relation between effect of herd origin of bull and genetic trend of bulls within herd for ILQ. [1]

Genetic trend of bulls within herd for ILQ (kg)
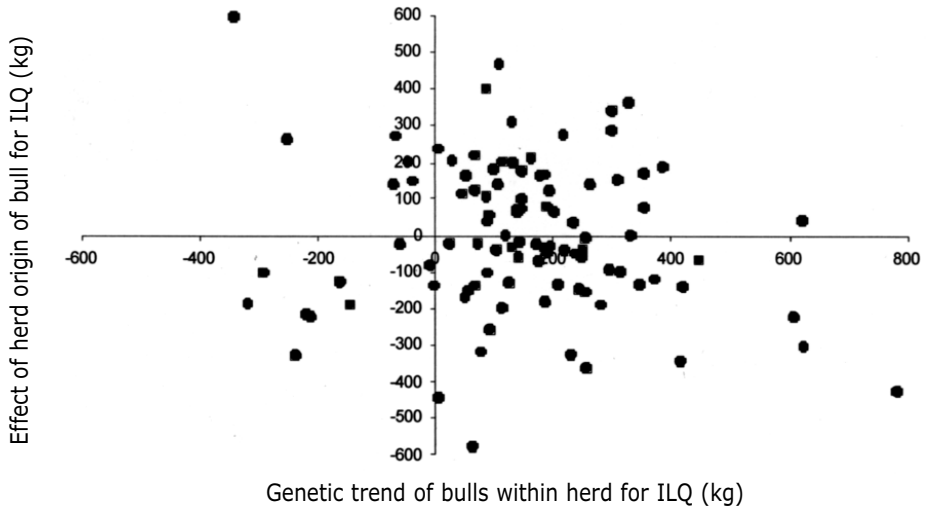
[1] *ILQ = 4.5 x (-0.173 x milk yield) + fat yield + (11.3 protein yield)*

Figure 7.   Distribution of AI center effects for classes of ILQ [1]

Classes of ILQ (kg)
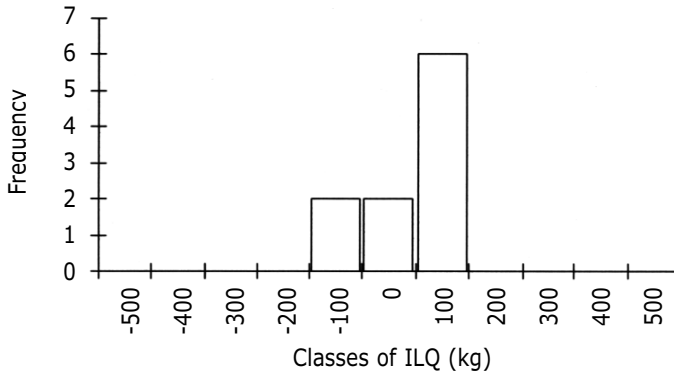
[1] *ILQ = 4.5 x (-0.173 x milk yield) + fat yield + (11.3 protein yield)*

hence, the causes of the significant effect of herd origin of bull was not clear and may be due to numerous factors, one of which might be preferential treatment of dams of bulls.

Effect of AI stud of Bull on Breeding Values

The range of effects of AI studs for ILQ trait was not significant (Figure 7). The literature provides few studies on effect of AI studs on EBV of bulls, and the few studies available that analyzed the effect of sampling status of bulls report conflict-ing results (Cassell *et al.*, 1976; Meinert and Pearson, 1992; Norman *et al.*, 1985; Powell *et al.*, 1994). Norman *et al.* (1985) found no difference due to the sampling status of bulls when comparing AI with non-AI sampled bulls. However, Meinert *et al.* (1992) compared no-AI and AI bull evaluations and concluded that no-AI evaluations were overesti-mated. Likewise, Cassell *et al.* (1976) reported that genetic evaluations of Holstein bulls with limited sampling were inflated by 119 kg relative to evalu-ations for bulls with multi-herd sampling.

Figure 8.   Distribution of sire name effects for classes of ILQ [1]
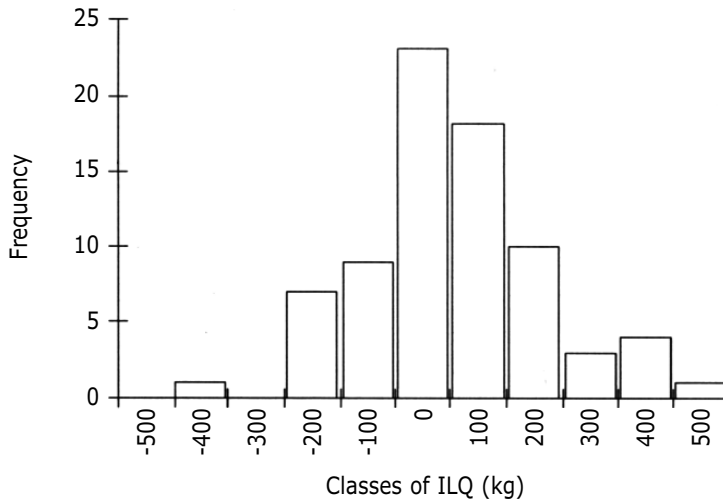
[1] ILQ = 4.5 x (-0.173 x milk yield) + fat yield + (11.3 protein yield)

In this study, the absence of a statistically significant effect of AI studs is an important result to ensure accurate and reliable genetic evaluation procedure. Indeed, in a national progeny-testing program no impact of AI studs is expected on breeding values of proven bulls when bulls are randomly distributed across the population and their breeding values are adjusted to parent average, herd origin, and birth year effect.

Effect of Sire ID of Bull on Breeding Values

The residuals of breeding values for ILQ, generated by analyses of variance above-mentioned, were analyzed as a function of sire ID, using an ANOVA method. The low R^2 (8%) indicated that sire ID did not explain a considerable amount of variation for bull EBV, after adjustment for herd origin of bull, AI stud, birth year of bull and parent average effect. Differences among sire ID for least squares means were not significant for ILQ ($P = 0.29$). The differences among sires are reported in Figure 8 and show the frequencies of sire ID effects for ILQ. The range of sire ID effect was 909 kg with a standard error deviation of 366 kg. Sires with positive effect suggest that breeding values are overestimated, whereas those with negative effect show an underestimation of their breeding value. However, potential preferential treatment cannot be assumed because a non significant effect of sire ID was detected.

On the total of 76 sires of bull, 13 were of domestic origin and 63 of foreign origin. The domestic sires evidenced an average of -5 kg of ILQ, whereas the foreign sires show an average of 36 kg. Although no bias associated with the country of bull origin was observed in this study, Cassandro *et al.* (1999) has shown that the assumption of homogeneous variance between domestic and foreign sires groups of daughters in the Italian national genetic evaluation model is not valid. Herds with a high percentage of daughters of domestic sires had a low sire and residual variance with respect to herds with a high percentage of daughters of foreign sires.

Conclusions

The effects of herd origin, AI studs and sire ID of bull on predicted breeding value for production traits in the Italian progeny test program were analyzed. The effects of herd origin of bulls was statistically significant ($P < 0.001$) for ILQ but are not clear the causes of this result, which can be due to numerous factors, one of which may be preferential

treatment. The absence of a statistically significant effect of AI studs can be viewed as favourable result, indicating that the national progeny testing scheme helps to ensure accurate and reliable official genetic evaluation procedures. However, because a clear absence of biases was not observed in this analysis, further research is recommended, firstly to understand the reasons behind the significant herd origin effect, and secondly to monitor and guarantee the greatest accuracy and reliability of genetic evaluation procedures.

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