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Threshold analysis of indicator traits for involuntary disposal in Holstein Friesian crossbred cattle

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Incidence of culling due to involuntary causes in dairy cattle, not only affects the optimum herd structure it also causes serious loss to the ongoing selection programme in the herd. Selection programmes in the country have laid primary emphasis to production ability of the dairy cattle with little emphasis on longevity of the dairy cattle. Such selection on production traits though has increased milk yield in dairy animals, but it has also lead to an increased incidence of disease and reproductive problems. Fertility, udder and uterine problems are some of the important functional indicator traits, which are associated with higher culling rates, reduction in longevity of dairy animals, increased veterinary costs, losses due to lower production and discarded milk (Manoj *et al.* 2015). Various countries have incorporated functional traits, viz. somatic cell count (SCC) for udder health along with milk production performance in the development of selection indices or multi-trait evaluation. Presently, scanty literature is available regarding performance of the progeny of test bulls with respect to disposal causes which are vital indicators of functional performance of dairy cattle. Traits categorized under disposal causes are binary on phenotypic scale (Tokuhisa *et al.* 2011), therefore, such traits need threshold genetic analysis before inclusion of these traits in genetic evaluation of dairy cattle (Guerra *et al.* 2006).

The present study was undertaken in Karan Fries (Holstein Friesian crossbred) cattle to study the genetic parameters of disposal causes and the performance of the sires, having high breeding value (EBV) for milk production, with respect to disposal causes.

Data were collected from history sheets and disposal records of Karan Fries cows maintained at ICAR-National Dairy Research Institute (ICAR-NDRI), Karnal, Haryana. Data of 1988 Karan Fries cows, spread over a period of 34 years (1978 to 2012), were utilized for the study. The cows completing at least 1 lactation were considered in the study. Production traits considered for the present study were first lactation 305 day milk yield (F305MY), first lactation total milk yield (FTMY) and first lactation length (FLL). The culling was classified into 2 groups, viz. voluntary and involuntary culling. Voluntary culling of cows was performed on the basis of low milk production (LMP). Major reasons of involuntary culling were locomotory problem (LP), poor health and weakness (PHW), teat and udder problem (TUP) and reproductive problem (RP).

Estimation of variance components was carried out by the average information maximum likelihood method (AIREML) algorithm in WOMBAT genetic analysis tool (Meyer 2007). Numerator relationship matrix (A) was computed from pedigree information and animal model was used to predict each animal's genetic merit. The following mixed model equation for animal model was used for estimation of breeding values:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z+A^{-1}\alpha \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'Y \end{bmatrix}$$

where, $\alpha = \sigma^2_e / \sigma^2_a$; *A*, the numerator relationship matrix of all the animals, which has nonzero off-diagonals only for the animal's parents, progeny, and mates. The elements of *A* can contain additive genetic effects, non-additive genetic effects, maternal effects, and permanent environmental effects (Henderson 1988).

For heritability estimation and sire evaluation of disposal causes. Data were analyzed to estimate the heritability of disposal causes, based on one-way classification model for binary traits, with two random sources of variability i.e. among and within families (Gianola 1982). For estimation of heritability, sires having a minimum of 5 daughters were considered for analysis. The following formula was used for estimation of heritability on phenotypic scale:

$$h^2 = \frac{\left[\left\{ SSF / \pi(1-\pi) \right\} - (s-1) \right]}{r\,(k-S+1)}$$

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where, SSF, Corrected sum of square due to families; p, prevalence of character in general population; s, No. of families (sires); r, additive relationship between family members and k was calculated as follows:

$$k = \frac{\Sigma n_i - \Sigma n_i^2}{\Sigma n_i}$$

n_i, no. of individual in the i^{th} family. Standard error (SE) of heritability of binary traits was estimated by the following formula SE = $32h^2/n$; where, h^2, heritability; n, total number of animals (Pirchner 1969). The heritability estimated on phenotypic scale was transformed into underlying or continuous scale by using the following formula (Dempster and Lerner 1950):

$$h_L^2 = h_x^2 \left[\frac{p\,(p-1)}{Z^2}\right]$$

where, h^2_L , heritability of the trait on liability scale; h^2_X , heritability of the trait on binary scale; Z, height of the ordinate of standard normal density function at threshold level; p, incidence of disease in population.

Breeding value of sires was estimated for different disposal causes by using the formula:

$$a = \left[\frac{h^2(e^{-t^*t/2})}{\sqrt{2\pi\,\sigma_y^2}}\right](Y-\bar{Y})$$

where, Y, proportion of incidence of i^{th} sire; $\bar{Y}$, mean of Y; σ^2_y, variance of Y; t, threshold point of response (Gianola 1982). Further, the comparison between the rankings of the sire for disposal and production (on first lactation basis) was done on the basis of Spearman's rank correlation.

The estimates of mean were similar to Nehara *et al.* (2012) and coefficient of variation (CV%) for the production traits were moderate. AIREML heritability estimates for traits were moderate for F305MY, FTMY and low in case of FLL (Table 1). Lower heritability estimate 0.21 and 0.24 for F305MY was obtained using REML by Divya *et al.* (2012) and Toghiani (2012) in Holstein crossbred cattle, respectively. Heritability of the involuntary disposal causes, namely reproductive problem (RP), teat udder problem (TUP), locomotory problem (LP) and poor health and weakness (PHW) estimated using one-way classification model indicated low estimates for most of the disposal causes on the binary scale; however the estimates on continuous scale indicated sizeable additive genetic variance (Table 2). The heritability estimate of disposal due to teat and udder problem (TUP) was highest (0.23 on continuous scale) among all the involuntary disposal causes. Threshold analysis for the estimation of heritability, used by Lin *et al.* (1989) for reproductive problems in Holstein cattle, viz. dystocia, retained placenta, metritis and cystic ovaries, revealed very low estimates (0.002 to 0.005) for the traits. Nogalski and Piwczynski (2012) reported heritability estimates for reproductive problems such as stillbirths, placental expulsion and calving ease as 0.42, 0.16 and 0.21, respectively. In Holstein cattle, an overall heritability of 0.01 for dystocia was estimated by Martinez *et al*. (1983). Thompson (1984) reported that the heritabilities for dystocia, retained placenta, mastitis and milk fever in Holstein cows were in the range of 0.03 to 0.06. Heritability of a total udder score, considering both suspension and teat size, in Line 1 Herefords was reported as 0.23 (MacNeil and Mott 2006).

The rankings of the sire based on disposal causes were compared with their rankings based on first lactation production performance. The estimates of Spearman's rank correlation of the 3 production traits (F305MY, FTMY and FLL) with disposal causes reproductive problem (RP), locomotory problem (LP) and poor health and weakness (PHW) were negative. Though not significant, the negative estimates indicated that the sires which were selected based on the superior performance of their daughters with respect to first lactation production performance, had higher incidence of RP, TUP, LP and PHW in their daughters and thus ranked poorly with respect to these disposal causes. The rank correlation estimates were significant only in production traits with PHW (Table 3). Studies indicated that in high yielders the incidence of management or production diseases such as under nutrition (loss of BCS), hypocalcaemia, mastitis, and lameness all lead to reduced

Table 1. Mean, coefficient of variation (CV%) and heritability estimates of first production traits by AIREML methods

Trait	Number of records	Mean±SE	CV%	Heritability (AIREML)
F305MY (kg)	1553	3027.11±20.31	26.43	0.31 ± 0.09
FTMY (kg)	1596	3415.05±31.96	37.39	0.14 ± 0.06
FLL (days)	1580	335.23±2.39	28.32	0.04 ± 0.01

Table 2. Heritability estimates of involuntary disposal causes

Disposal cause	Incidence (Binary-scale)	Heritability	Heritability (Dempster -Lerner)	Standard error
RP	0.15	0.05	0.11	0.003
TUP	0.19	0.11	0.23	0.008
LP	0.13	0.04	0.11	0.003
PHW	0.08	0.02	0.06	0.001

Table 3. Rank correlations based on EBVs of first lactation production performance and involuntary disposal causes

Trait	Spearman's rank correlation			
	RP	TUP	LP	PHW
F305MY	-0.10	0.03	-0.17	-0.27**
FTMY	-0.14	-0.02	-0.09	-0.29**
FLL	-0.10	-0.001	-0.08	-0.25*

*significant at P<0.05; **highly significant at P<0.01.

reproductive performance compared to unaffected contemporaneous herd-mates (Dobson *et al.* 2007). Various reports advocated the inclusion of functional performance of the animal along with production performance in genetic selection. Unfavourable correlation was observed between breeding values for foot traits measured in first lactation with those for milk production (Boelling and Pollott 1997). Genetic correlations of production with culling for leg problems ranged from 0.20 to 0.27 and indicated that long term selection for yields probably would increase culling for impaired legs (Uribe *et al.* 1995). Oltenacu and Algers (2005) reported unfavourable correlations (0.2 to 0.4), indicating that selection for milk yield alone would lead to poorer fertility and animal health. Osteras *et al.* (2007) observed the increased incidence of clinical mastitis from 0.15 to 0.23 cows treated per cow year from 1975 to 2002 in dairy cattle of Norway.

SUMMARY

AIREML heritability estimates for production traits F305MY, FTMY and FLL were 0.31±0.09, 0.14±0.06 and 0.04±0.01, respectively. Heritability estimates for binary or threshold traits RP, TUP, LP and PHW were 0.05±0.003, 0.11±0.008, 0.04±0.003 and 0.02±0.001, respectively. Results revealed that disposal was affected to a lesser extent by additive gene action. The estimates of spearman's rank correlation of production traits with disposal causes were negative. The disposal causes studied under the above analysis can be viewed as indicator of functional performance of dairy cattle. Selection of sires based on superior production performance of its daughters was going to have a negative impact on the functional traits; which underlines the fact that sire evaluation should be inclusive of functional performance of the daughters in addition to the production performance. Such selection would lead to lesser veterinary costs and also reduce the cost of other inputs thus maximizing profits in dairying.

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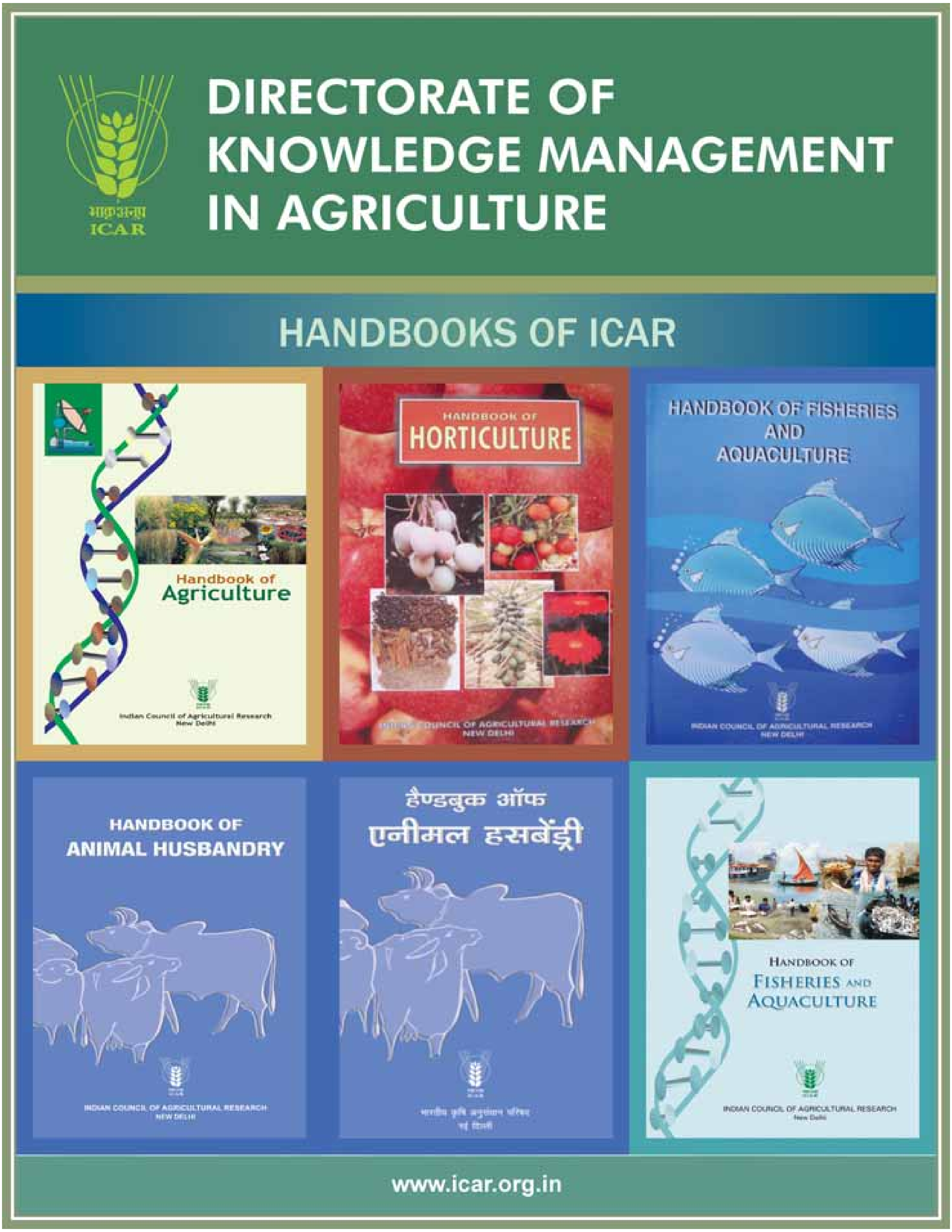
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