Genetic Evaluation of Calving Traits for Holstein and Japanese Black (Wagyu) Bulls Including Purebred and F1 Crossbred Calvings with Holstein Heifers

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Introduction

A part of dairy farmers in Japan have produced beef calves by not only Holstein purebreds but also filial hybrids (F1) which are cross of Japanese black (Wagyu) bulls with Holstein heifers or cows. The F1 calves produced by Wagyu × Holstein is usually a small size as compared with the calves of pure Holstein. Therefore, the calvings by Wagyu-sired crossbred are increasing in Holstein heifers to avoid a calving difficulty (CD) and stillbirth (SB), and reached approximately 33 % of total calvings of Holstein heifers in Hokkaido area of Japan. The purpose of this study is to develop the genetic evaluation systems for CD and SB using a sire-maternal grandsire (S-MGS) threshold model including calvings by Holstein-sired purebred and Wagyu-sired crossbred with Holstein heifers.

Materials and methods

Data manipulations. CD and SB records for Holstein-sired purebred and Wagyu-sired crossbred calvings with Holstein heifers were extracted from the Dairy Herd Recording database of Hokkaido. The CD scores on a 1 to 5 scale were classified into three groups (group-1: score 1 and 2, group-2: score 3, group-3: score 4 and 5) and defined as a difficult birth for group-2 and -3. The SB scores were recorded as 0 (live) or 1 (stillborn or death immediately after calving). The calving records to estimate genetic parameters were 671,104 from January 1990 to Jun 2008. 759,789 records from January 1990 to December 2009 were used to calculate genetic evaluations.

Statistical analyses. The S-MGS threshold model used for these analyses :
$\mathbf{y} = \mathbf{X\beta} + \mathbf{Wh} + \mathbf{Z}_s\mathbf{a}_s + \mathbf{Z}_m\mathbf{a}_m + \mathbf{e}$, where $\mathbf{y}$ is a vector for the liabilities to CD or SB, $\boldsymbol{\beta}$ is a fixed vector including calving year-month, genetic groups of sires and MGS, and linear regressions (inbreeding depression per % inbreeding) on inbreeding coefficients of calves and dams. The model to analyze CD includes a calf's sex (female, male), calving status (twin≤, stillbirth) as fixed effect. $\mathbf{h}$, $\mathbf{a}_s$ and $\mathbf{a}_m$ are random vectors of herd-year and additive genetic effects of the sire and MGS, respectively. The elements of $\mathbf{h}$ is 78,911 for estimates of genetic parameters and 83,547 for genetic evaluations, and $\mathbf{h} \sim N(0, \sigma_h^2)$. $\mathbf{e} \sim N(0,1)$ is a random residual vector. $\mathbf{X}$, $\mathbf{W}$, $\mathbf{Z}_s$ and $\mathbf{Z}_m$ are known incidence matrices corresponding with each vector. Table 1 shows a descriptive summary of records using this analysis. If $\mathbf{a}_s = (\mathbf{a}_{s_H} \quad \mathbf{a}_{s_W})'$ where *H* and *W* show Holstein and Wagyu

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respectively, $\mathbf{a}_{s_H}$, $\mathbf{a}_{s_W}$ and $\mathbf{a}_m$ are assumed to follow a multivariate normal distribution with 0 mean and (co-) variance matrix $\mathbf{G} \otimes \mathbf{A}$ where $\mathbf{A}$ is the numerator relationship matrix among sires and $\mathbf{G} = \begin{bmatrix} \sigma^2_{s_H} & 0 & \sigma_{s_H m} \\ 0 & \sigma^2_{s_W} & \sigma_{s_W m} \\ \sigma_{s_H m} & \sigma_{s_W m} & \sigma^2_m \end{bmatrix}$. Variance components estimated from the S-MGS threshold model were transformed to direct (D_H and D_W) and maternal (M) variance components using

$$\begin{bmatrix} \sigma^2_{D_H} \\ \sigma^2_{D_W} \\ \sigma_{D_H M} \\ \sigma_{D_W M} \\ \sigma^2_M \end{bmatrix} = \begin{bmatrix} 4 & 0 & 0 & 0 & 0 \\ 0 & 4 & 0 & 0 & 0 \\ -2 & 0 & 4 & 0 & 0 \\ 0 & -2 & 0 & 4 & 0 \\ 1 & 1 & -4 & -4 & 4 \end{bmatrix} \begin{bmatrix} \sigma^2_{s_H} \\ \sigma^2_{s_W} \\ \sigma_{s_H m} \\ \sigma_{s_W m} \\ \sigma^2_m \end{bmatrix}$$

by Wiggans et al. (2003). THRGIBBS1F90 program was used for estimates of variance components (Misztal et al., 2002). CBLUPF90 program was reconstructed and extended to deal with a large dataset and used to obtain sire and MGS solutions on the underling scale as the estimated transmitting abilities (ETAs). These ETAs were converted into percentages ETA (%ETA) of CD and SB in heifers for sire (service sire) and MGS (daughter) effects using the method of Cole et al. (2005).

Table 1: A descriptive summary of calving data for statistical analysis

	Genetic parameter		Genetic evaluation	
	Holstein	Wagyu	Holstein	Wagyu
Record	455,910	215,194	506,616	253,173
Sire	4,529	303	4,892	315
Maternal grand sire	4,792	-	5,221	-
Total bull includes pedigree	5,735	497	6,257	520

Results and discussion

The phenotypic trends of CD in Holstein heifers calving from 1990 to 2009 decreased from 18.5 % to 9.1 % for Holstein-sired purebred and 11.7 % to 6.4 % for Wagyu-sired crossbred calvings as shown in Figure 1. Contrarily, the phenotypic trends of SB increased from 3.6 % to 12.0 % for Holstein-sired purebred and 2.1 % to 6.8 % for Wagyu-sired crossbred calvings. Direct heritabilites for Holstein-sired purebred and Wagyu-sired crossbred were 5.6 and 10.2 % for CD and 6.5 and 7.1 % for SB respectively (Table 2). Maternal heritabilites for CD and SB were 3.6 and 9.8 % respectively. Genetic correlations between Holstein direct and maternal were positive and very small. On the other hand, the clearly negative correlations existed between Wagyu direct and Holstein maternal (-0.642 for CD and -0.395 for SB). Means of %ETA for Holstein service sire were 10.5 % for CD and 9.8 % for SB and large as compared with 6.3 % and 6.4 % of Wagyu service sire (Table 3). Means of daughter %ETA were 9.9 % for CD and 10.2 % for SB and were similar to means of %ETA for Holstein service sire respectively. Standard deviations of %ETA for daughter were 2.4 % and 4.5 %

and obvious large as compared with standard deviations of %ETA for Holstein service sire, 1.8 % and 1.3 % for CD and SB respectively. The annual average genetic progress on CD during the period 1990 to 2006 was -0.21 %ETA/yr for Holstein service sire and +0.23 %ETA/yr for Wagyu service sire. It was suggested that the selection response of CD in Holstein population has progressed in a negative direction with selection intensity to Holstein service sires, because the official proofs of CD for Holstein service sire has been already published in Japan. The annual average genetic progress on SB was -0.04 %ETA and very small for Holstein service sire, +0.26 %ETA/yr for Wagyu service sire and +0.25 %ETA/yr for Holstein daughter. It may be assumed that Wagyu service sires and Holstein daughter have accumulated many lethal genes during a long term. The inbreeding depressions per % inbreeding of CD and SB were +0.02 % and +0.17 % for pure Holstein calf and +0.08 % and +0.14 % for Holstein dam respectively.

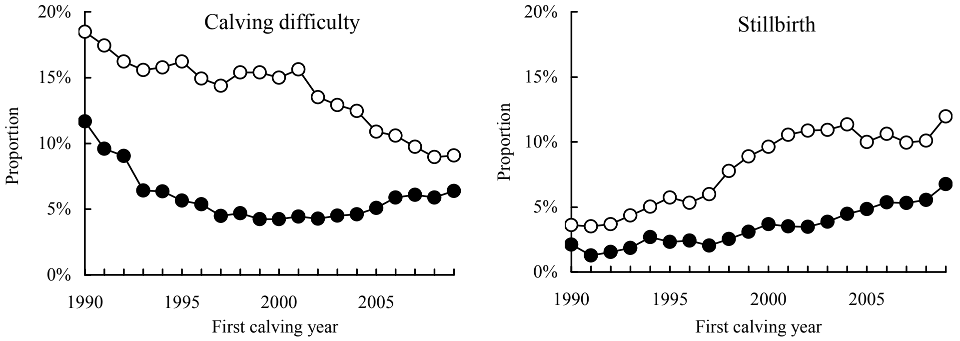

Figure 1: Changes for means of proportions of calving difficulty and stillbirth for Holstein-sired purebred (○) and Wagyu-sired crossbred calvings (●) with heifer's calving year

Table 2: Heritabilities (%) and genetic correlations for direct and maternal calving difficulty and stillbirth effects respectively

	h^2_{dirH}	h^2_{dirW}	h^2_{mat}	$r_{dirH-mat}$	$r_{dirW-mat}$
Calving difficulty	5.6	10.2	3.6	0.022	-0.642
Stillbirth	6.5	7.1	9.8	0.021	-0.395

h^2: heritability, *r*: genetic correlation, *dirH*: direct effect by Holstein-sired purebred, *dirW*: direct effect by Japanese black beef (Wagyu) cattle-sired crossbred, *mat*: maternal effect (only Holstein)

Conclusion

The joint evaluation of calving traits (CD and SB) for Holstein and Wagyu bulls was developed using a S-MGS threshold model. This evaluation utilizes information from F1 crossbred calvings of Wagyu bulls with Holstein heifers, as well as purebred calvings of Holstein. The genetic trends of CD decreased by -0.21 %ETA/yr for Holstein service sires and increased by +0.23 %ETA/yr for Wagyu service sires. The estimates of annual genetic changes of SB increased for Wagyu service sires (+0.26 %ETA/yr) and Holstein daughters (+0.25 %ETA/yr).

Table 3: Means, standard deviations (SD), minimums and maximums of %ETA for service sire and daughter

	Holstein				Wagyu			
	Mean	SD	Min.	Max.	Mean	SD	Min.	Max.
Calving difficulty								
Service sire	10.5	1.8	4.9	19.7	6.3	2.2	2.9	16.7
Daughter	9.9	2.4	3.2	32.6	-	-	-	-
Stillbirth								
Service sire	9.8	1.3	5.5	16.9	6.4	1.6	3.5	12.2
Daughter	10.2	4.5	1.4	52.9	-	-	-	-

Wagyu : Japanese black beef cattle

Table 4: Genetic gains per year of calving difficulty and stillbirth using %ETA

	Calving difficulty, %ETA		Stillbirth, %ETA	
	Holstein	Wagyu	Holstein	Wagyu
Service sire	-0.21	0.23	-0.04	0.26
Daughter	-0.09		0.25	

Wagyu : Japanese black beef cattle

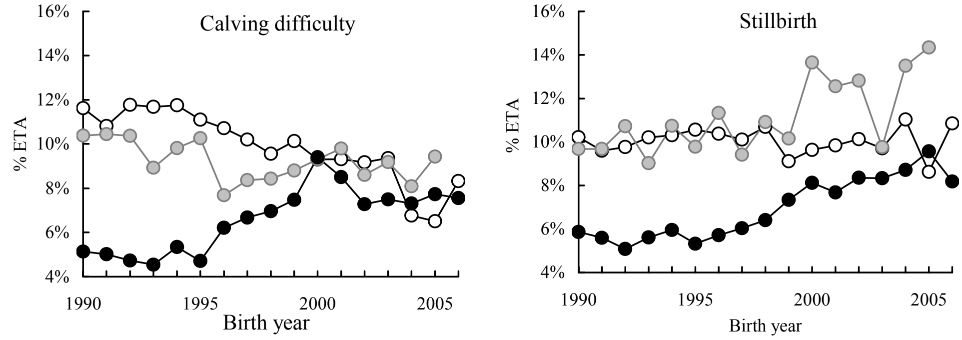

Figure 2: Means of %ETA of calving difficulty and stillbirth for Holstein (○) and Wagyu service sires (●), and Holstein daughter (◍) with birth year

References

Cole, J. B., Goodling, Jr., R. C., Wiggans, G. R., VanRaden, P. M. (2005). *J. Dairy Sci.*, 88:1529–1539.

Misztal, I., Tsuruta, S., Strabel, T., Auvray, T. and Lee, T. (2002) *Proc 6th WCGALP* 28:7.

Wiggans, G. R., Misztal, I., Van Tassell, C. P. (2003). *J. Dairy Sci.*, 86:1845–1848.