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Genetic Relationships between Length of Productive Life and Type Traits in a Holstein Population in Japan

Y. Terawaki¹, Y. Gotoh², S. Yamaguchi³ and V. Ducrocq⁴

Introduction

Longevity is one of the traits receiving the most interest-ability-of-attention in the Holstein cattlebreed. Obtaining a complete longevity Accomplishment-of-records on-longevity requires a relatively long observation period. In contrast, scores on type traits can be recorded in-earlier time-in-early in life-of-a-cow. When-To genetically improve longevity-would-be-genetically-improved-expecting-selection-response, it would be important-useful to identify some-the type traits which are genetically relating-related to longevity. Many results-studies on genetic relationships between longevity and type traits applied-to-linear-model have been reported, but there-is-little-reports-by-few-of-these-were-based-on survival analysis, which is the only way to properly account for the statistical characteristics of longevity.

The aim of the present study is to estimate approximate genetic relationships-correlations between longevity and type traits from-derived-from sires' predicted breeding value effect on length of productive life estimated by-using survival analysis and predicted breeding value of sire-for-on type traits estimated applied-tousiang a linear model.

Material and methods

Length of productive life (LPL) records were obtained from the-data-of the Hokkaido Dairy Cattle Milk Recording and Testing Association. The observation period was from January 1, 1984 to December 31, 1999. Records of cows still alive at the end of the observation period were considered as censored at-on December 31, 1999. LPL was defined as the number of days from first calving to culling or censoring date. Cows having a first calving before January 1984 and/or without type trait records were excluded from the analysis. For estimating genetic parameters, only the-records were-edited-for-from herds having at least 30 records and from sires having at least 20 daughters were kept. After editing, a total of 134,047 records were available in-total.

Genetic parameters for LPL were estimated using the following survival model with piecewise Weibull baselines.

-using the Survival Kit (Version 5.0) software (Ducrocq and Solkner (1998)):

¹ Rakuno Gakuen University Dairy Science Institute, 069-8501 Ebetsu, Japan

² Holstein Cattle Association of Japan, Hokkaido Branch, 001-8555 Sapporo, Japan

³ Hokkaido Dairy Cattle Milk Recording and Testing Association, 060-0004 Sapporo, Japan

⁴ INRA, UMR1313 - Génétique Animale et Biologie Intégrative, 78352 Jouy en Josas, France
INRA Station de Génétique Quantitative et Appliquée 78352 Jouy en Josas-Cédex, France

$$h(t) = h_{0n}(\tau) \exp[\text{HY}_i(t) + Y_j(t) + \text{MILK}_k(t) + \text{SIZE}_l(t) + \text{SIRE}_m] \dots \quad (1)$$

where $h(t)$ is the hazard function of the cow;

t is the number of days after ~~its~~ her first calving;

$h_{0n}(\tau)$ is the Weibull baseline for the n^{th} subclass of parity ~~and by~~ stage of lactation;

τ denotes the number of days between the most recent calving and current time t ;

$-\text{HY}_i(t)$ is the effect of the i^{th} herd-year interaction, assumed to follow a log-gamma distribution;

$Y_j(t)$ is the time-dependent fixed effect of the j^{th} year (1984, 1985, ..., 1999);

$\text{MILK}_k(t)$ is the time-dependent fixed effect of the k^{th} within-herd class of 305-d milk yield (1, 2, ..., 7);

$\text{SIZE}_l(t)$ is the time-dependent fixed effect of the l^{th} class of variation in herd size (1, 2, ..., 5);

SIRE_m is the random effect of the m^{th} sire. The sire effects ~~we~~ are assumed to be independent and to follow a normal distribution.

The analyses were performed using the Survival Kit (Version 5.0) software (Ducrocq and Sölkner (1998)):

Type trait consisted of 5 score traits and 17 linear traits. Genetic parameters ~~Predicted breeding values~~ of sires for type traits were estimated using BLUP applied to an animal model ~~in at the~~ Holstein Cattle Association of Japan, Hokkaido Branch.

Approximate genetic correlations between LPL and type traits were estimated according using the approach of ~~to~~ Blanchard et al. (1983). The precision ~~(reliability)~~ of sire effect on LPL and of the predicted breeding value of a sire ~~for~~ type traits were calculated using the following method by Roxström and Strandberg (2002) ~~usual selection index formula:~~

$$b = n / (n + (4 - h^2_0) / h^2_0) \dots \quad (2)$$

where b is precision ~~(the reliability)~~ of sire LPL ~~effect on LPL~~ and of the predicted breeding value of a sire ~~for~~ type traits; n is the number of uncensored daughters of the sire for LPL or the his total number of daughters for type traits; h^2_0 is the effective ~~heritability on the original scale, the original scale was replaced by effective heritability~~ (h^2_{eff}) for LPL (Yazdi et al. (2002)) ~~in the present study for LPL or the classical~~ heritability for type traits.

Results and discussion

Statistics ~~General statistics~~ of records and genetic parameters for LPL are shown in table 1. Rate ~~Proportion~~ of right-censored record ~~is was~~ low (30.1%). This is due to the relatively long period of observation considered in the present study compared with other reports (Caraviello et al. (2004); Ducrocq (2005); Chirinos (2007)). Average censoring time and average failure time ~~are were~~ 1125.4 and 1386.6 days. Terawaki and Ducrocq (2009) reported that corresponding values were 1005 - 1040 and 1100 - 1220 days using the ~~data~~ including cows having no type records. Also, rate ~~the proportion~~ of right-censored records were 14.3 - 27.7% in the that report. These comparisons indicate that cows having type records tend to have longer LPL than the ones without type records. Heritability of LPL (h^2_{eff}) ~~is was~~ 0.117 and in the range of other reported values.

Table 1: Summary of survival analysis for LPL

Number of herd	1674
Number of sire	418
Right-censored record (%)	30.1
Average censoring time (d)	1125.4
Average failure time (d)	1386.6
Gamma parameter of the log-gamma distribution	3.690
Herd-year variance	0.311
Sire variance	0.040
Heritability (h^2_{eff})	0.117

Table 2 shows the heritability and the mean of precision (reliability) of the predicted breeding values of a sire for type traits, the correlation coefficient ($r_{e,bv}$) between sire effect on LPL and predicted breeding values of sire for type traits, and the approximate genetic correlation coefficient (r_g) between LPL and type traits. These values in table 2 were calculated on 96 sires having at least 200 or more than 200 uncensored daughters records. The highest EBV correlation $r_{e,bv}$ and approximate genetic correlation r_g are were -0.651 and -0.679 for udder depth, followed by udder (-0.499, -0.524), feet and legs (-0.409, -0.432) and fore udder attachment (-0.402, -0.422). Larroque and Ducrocq (2001) examined relationships between type and longevity in the Holstein breed with survival analysis, and indicated large contribution to the likelihood for LPL of from phenotypes for udder depth and udder cleft on LPL. Moreover, they reported similar results about type traits genotype in same paper. Also, Buenger et al. (2001) reported high significant levers levels for phenotype and breeding value of udder depth on LPL. These results support Their results are consistent with the high negative correlation r_g for udder depth and fore udder attachment obtained in the present study.

Table 2: Heritability, precision (reliability), and correlation coefficient between EBV $r_{e,bv}$ and approximate genetic correlation r_g for type traits for and LPL

Trait	Heritability ^a	Precision- (+Reliability)	$r_{e,bv}$ ^b	r_g ^b
Frame/Capacity	0.27	0.985	-0.233	-0.244
Feet and legs	0.13	0.969	-0.409	-0.432
Dairy character	0.34	0.988	-0.071	-0.074
Udder	0.20	0.980	-0.499	-0.524
Final score	0.27	0.985	-0.364	-0.380
Stature	0.53	0.993	-0.172	-0.179
Chest width	0.30	0.987	-0.102	-0.106
Body depth	0.38	0.990	0.010	0.011
Angularity	0.25	0.984	0.084	0.088
Rump angle	0.41	0.990	-0.026	-0.027
Pin width	0.34	0.988	0.045	0.047
Rear legs set	0.20	0.980	0.143	0.150
Rear legs rear view	0.11	0.963	-0.201	-0.212

Foot angle	0.05	0.923	-0.189	-0.204
Fore udder attachment	0.21	0.981	-0.402	-0.422
Rear udder height	0.26	0.984	-0.122	-0.128
Rear udder width	0.21	0.981	0.066	0.070
Udder support	0.20	0.980	-0.173	-0.182
Udder depth	0.46	0.992	-0.651	-0.679
Front teat placement	0.38	0.990	-0.217	-0.227
Rear teat placement	0.31	0.987	-0.054	-0.056
Teat length	0.40	0.990	0.116	0.121

^a Heritability substituted in formula (2).

^b [a negative value means that higher type scores are related with lower risk of culling](#)

~~There are some reports (Kawahara et al. (1996); Suzuki et al. (1996); Fujita and Suzuki (2006)) previously reported on the genetic relationships between longevity and type traits in Holstein cattle in Japan applied using a linear model. Kawahara et al. (1996) reported that longevity traits had moderately positive genetic correlations with ~~rump~~-angle (0.42), angularity (0.40) and some udder traits (the highest one was 0.38). Suzuki et al. (1996) examined-performed a principal component analysis for 14 linear type traits and estimated a genetic correlation coefficient (of 0.42) between the second principal component and productive file. The second component was strongly related to udder support, fore udder attachment, rear udder height and rear udder width. Fujita and Suzuki (2006) estimated genetic correlation coefficients between herd-life and type traits and reported the highest coefficient (0.37) for feet and legs followed by mammary system (0.34), udder depth (0.33) and udder cleft (0.32). These results in Japan were similar to one of those presented study here in regard to as far as some udder traits are concerned. On the other hand, Longevity-longevity trait had high genetic relationship with feet and legs only in the only-present study and in Fujita and Suzuki (2006).~~

Conclusion

The results in the present study clearly show that LPL is strongly genetically very closerelated to udder depth, and overall udder and fore udder attachment. Also, feet and legs exhibits a genetically-high geneticly correlation withrelate to LPL. These type traits are very important when-to genetically improve longevity are improved through selection response in Holstein cattle in Japan.

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