



Development of genetic evaluation for milk production traits of Holsteins in Japan

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2 **Development of genetic evaluation for milk production traits of**
3 **Holsteins in Japan**

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10 Running head: Genetic evaluation of Holsteins in Japan

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14

1 **Abstract**

2 The procedure used for the genetic evaluation of dairy cattle in Japan
3 has developed from a lactation sire-MGS model to a multiple-lactation random
4 regression test-day animal model. Genetic evaluation of Holstein bulls in Japan
5 began in 1989 with the use of field-style progeny testing; dairy herd improvement
6 program data from all over Japan were used, along with a sire and maternal
7 grandsire model. In 1993, an animal model was introduced to estimate breeding
8 values for yield and type traits. A random regression test-day model was first
9 applied in 2010. In the business of breeding dairy cattle, it is very important to
10 users that estimated breeding values are reliable and stable among subsequent
11 routine evaluations. With experience in the genetic evaluation of dairy cattle in
12 Japan, Japanese researchers have found ways to improve the stability of
13 estimated breeding values. These modifications involve changes in data editing,
14 development of evaluation models, changes to the structures of unknown-parent
15 groups, awareness of the problems of predicting lactation yield from partial
16 test-day records, and adjustment for heterogeneity within herd variances. Here, I
17 introduce developments in, and our experiences with, the genetic evaluation of
18 yield traits of Holstein cattle in Japan.

19 **Keywords:** Dairy cattle, genetic evaluation, Holstein, test-day model,
20 heterogeneity within herd variance

21

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1 **1 Introduction**

2 In Japan, 99% of dairy cattle are Holsteins. Genetic evaluation of
3 Holstein bulls began to be published in 1989 with the use of field-style progeny
4 testing (PT); dairy herd improvement (DHI) program data from all over Japan
5 were used, along with a sire and maternal grandsire (MGS) model (National
6 Livestock Breeding Center, 1999). Estimated transmitting abilities were obtained
7 for yield traits, including milk, fat, protein, and solid-non-fat (SNF) yields, as well
8 as fat, protein, and SNF percentages, in cow's milk. Sires were ranked according
9 to an economic index calculated by using milk prices.

10 In 1993, an animal model was introduced to estimate breeding values for
11 yield and type traits (National Livestock Breeding Center, 1993). Details of the
12 top cows in Japan, as ranked by the economic index, were published in the
13 same way as for the bulls. Farmers and artificial insemination (AI) technicians
14 became able to select bulls by using the estimated breeding values (EBVs) of
15 yield traits and conformation traits (Table 1). Management traits—milking speed,
16 temperament, and calving ease—began to be evaluated and published in 1997
17 (Table 1). These traits were estimated by using a threshold sire–MGS model. In
18 1998, bulls were ranked for the first time by the Nippon total profit index (NTP) as
19 a total merit index. The first NTP contained EBVs for fat and protein contents
20 and for conformation traits such as mammary system, udder depth, and
21 fore-udder attachment.

22 An EBV for somatic cell score was published in 2003. At the same time,

1 bulls in Japan attended a MACE (multiple-trait across-country evaluation)
2 conducted by INTERBULL (Interbull, 2018). In 2006, herd life published as a
3 longevity trait (Hagiya et al., 2012), and in 2008 a model that included lactation
4 persistency (LP) as a new health trait was published (Table 1). The EBV of herd
5 life was estimated by using a multiple-trait animal model. Multiple trait prediction
6 (Schaeffer & Jamrozik, 1996) was used to estimate LP for each lactation, and a
7 single-trait animal model was used to estimate the EBV of LP. A random
8 regression test-day model (RR-TDM) was first applied to yield traits in 2010. The
9 estimation of LP was then updated by using the RR-TDM. Stillbirth modeling
10 began to be published in 2011 (Table 1). The EBV of conception rate and days
11 open associated with female fertility traits were published in 2014 (Atagi and
12 Hagiya, 2005; Hagiya et al., 2014). The RR-TDM was updated to a
13 multiple-lactation model in 2015. Genomic EBVs were published in Japan for
14 heifers in 2013 and for bulls in 2017.

15 Here, I introduce the developments in, and our experiences of, the
16 genetic evaluation of yield traits in Holstein cattle in Japan.

17

18 **2 Data collection system**

19 Most dairy cattle in Japan are bred through AI using frozen semen. In
20 1969, PT was started in 180 young Holstein bulls in Japan to evaluate dairy bulls'
21 genetic performance on the basis of their daughters' records (National Livestock
22 Breeding Center, 1993). Daughters of the bulls were tested for milk, fat, protein,

1 and SNF yields at PT stations run by the National Livestock Breeding Station.
2 The Japanese system of PT differed from those in other countries, because in
3 Japan the testing stations were run by the government. This system of PT was
4 the only choice then available, because no DHI program existed at the time in
5 Japan (Abe, 1993). Selected bulls were used throughout Japan through AI.
6 Genetic evaluations of bulls were made by using herdmate comparisons
7 (Mitsumoto, 1980). However, PT stations had the disadvantage of being
8 expensive, and testing facilities were therefore limited (Touchberry, Rottensten,
9 & Andersen, 1959).

10 Japan's DHI program started in 1974. The traditional DHI collected
11 monthly records of milk production, milk fat, milk protein, and SNF yields and
12 percentages, along with such characteristics as animal ID, birth date, calving
13 date, parity, and days in milk (DIM). The DHI program service has expanded
14 over the years, and the number of licensed herds and cows has increased. In
15 1984, by which time about 34% of all cows were DHI licensed (Livestock
16 Improvement Association of Japan, 2018), new PT using farmers' herds—called
17 field testing—was introduced in Japan. As part of this field testing, bull semen
18 was distributed to licensed DHI dairy farms throughout Japan. Daughters of PT
19 bulls were produced in farmers' herds and their data recorded with those of their
20 contemporaries from calving to at least 240 DIM. For the first few years, data on
21 daughters were collected from both PT stations and farmers' herds, but
22 collection gradually shifted toward field testing.

1 Classification records were collected from daughters in herds
2 participating in PT. The conformation traits of bulls' daughters and their
3 contemporaries were recorded by professional classifiers from the Holstein
4 Association of Japan. Conformation traits were evaluated by using the
5 recommended standard linear traits and definitions of type traits published by the
6 World Holstein Friesian Federation (2016).

7 Genetic evaluation of Holstein bulls using records from all over Japan
8 began in 1989 by using a sire–MGS model, with data from DHI, and
9 classification and pedigree records from the Holstein Association of Japan.
10 Thereafter, AI bulls were generally selected by genetic evaluation.

11

12 **3 Lactation model**

13 In 1993, the first EBVs in Japan, of 2.1 million dairy cattle were
14 estimated by using an animal model (Abe, 1993). The EBVs were published for
15 all PT bulls and top-ranked cows. Data contained in the animal model for milk
16 yield traits were records of milk yields and conformation traits on Holstein cows
17 aged from 22 to 35 months at first calving, and lactation records from the first to
18 fifth parities, obtained from two milkings a day. The sum of the daily milk yields
19 from calving to 305 DIM was calculated for each cow as the 305-day lactation
20 yield. When a cow had test-day records for fewer than 305 DIM, the lactation
21 records were expanded from monthly milk records to a 305-day yield by using
22 Method P (Miller, Pearson, Fohrman, & Creegan, 1972). A record was treated as

1 a missing value when the lactation period finished with fewer than 240 DIM
 2 (National Livestock Breeding Center, 1993). EBV was estimated by using a
 3 single-trait animal model, as follows:

$$4 \quad y_{ijklmn} = HY_i + C_j + M_k + A_l + u_m + pe_m + e_{ijklmn}, \quad [1]$$

5 where y_{ijklmn} is lactation yield, HY_i is the fixed effect of herd-year i , C_j is the
 6 fixed effect of country j of the cow's bull, M_k is the fixed effect of calving month
 7 k (12 calendar months) within area (Hokkaido or Honshu), A_l is the fixed effect
 8 of calving age l , u_m is the random additive genetic effect of animal m , pe_m is
 9 the random permanent environmental effect on animal m , and e_{ijklmn} is the
 10 random residual effect associated with lactation yield. In the early 1990s, frozen
 11 semen imported from foreign countries was generally very expensive and
 12 tended to be used only on superior cows or heifers. The effect of bull's country
 13 represents the effect of cow selection in the case of cows mated by using
 14 imported frozen semen. The impact of the first EBVs estimated for cows by using
 15 the above animal model was great, and we found many new, superior lines.

16 The statistical model for yield traits was changed in 1996, as follows
 17 (National Livestock Breeding Center, 1996):

$$18 \quad y_{ijkl} = HYP_i + M_j + u_k + pe_k + e_{ijkl} \quad [2]$$

19 where y_{ijkl} is the lactation yield pre-adjusted for the effect of parity and age at
 20 calving, HYP_i is the fixed effect of herd-year-parity i , and M_j , u_k , pe_k , and e_{ijkl}
 21 are the same as in equation [1]. This model worked well, but in 1999 it was
 22 modified to include a term related to year effect (National Livestock Breeding

1 Center, 1999):

$$2 \quad y_{ijkl} = HYP_i + MY_j + u_k + pe_k + e_{ijkl} \quad [3]$$

3 where MY_j is the fixed effect of month-year j and the other terms are the same
 4 as in equation [2]. This modification accounted for the differences in seasonal
 5 effects from year to year. In this model, year effects were included in both HYP_i
 6 and MY_j ; therefore, the total effect, as shown by $HYP_i + MY_j$, was stable among
 7 subsequent routine evaluations. However, the estimated effects of each of HYP_i
 8 and MY_j separately sometimes differed among routine evaluations, and this
 9 caused confusion in the description of the fixed effect. This problem suggested
 10 that a simple model would be preferable for routine genetic evaluation in dairy
 11 cattle.

12

13 **4 Impact of the drop in bull EBVs**

14 In the early 1990s, semen from one of the highest-ranking bulls in
 15 Canada, Ronnybrook Prelude ET (HOCANM0000392457), born in 1986, was
 16 used for AI worldwide. In the business of breeding dairy cattle, the substantial
 17 drop in this bull's EBVs was a shocking fact (Lohuis & Schaeffer, 1995). Also, in
 18 Japan, bull EBVs sometimes changed considerably between two subsequent
 19 routine evaluations. We found three reasons as to why a bull's EBV stability
 20 could be compromised.

21 The first reason why two subsequent EBVs different from each other
 22 was related to data editing. When a cow with fewer than 305 DIM was still in milk,

1 her lactation yield was estimated by using test-day yields and was included in
2 the genetic evaluation. However, when a cow's lactation finished after fewer than
3 240 DIM, her lactation record was deleted from the files used for the genetic
4 evaluation. The EBV of the bull changed when his daughter's records, which had
5 been used in the previous genetic evaluation, were then deleted from the current
6 genetic evaluation. This situation should have been avoided in our data editing.

7 Second, we used genetic groups (Quaas & Pollak, 1981) to represent
8 unknown-parent groups (UPGs) of animals in the pedigree to account for genetic
9 trends. Group solutions represent the average EBVs of unknown (unidentified or
10 represented by only one descendant) animals selected to be parents without
11 records (Westell, Wuaas, & Van Vleck, 1988). We made phantom parent groups
12 (i.e., UPGs) according to birth year, as estimated by using those of the progeny.
13 For example, we assumed that UPGs were made up of groups of animals from
14 younger to older and contained an unknown parent every 5 years. The UPG for
15 younger animals therefore contained the most recent unknown parents (i.e.
16 those within the 5 most recent years). The members of the youngest UPG
17 changed from year to year. The EBV estimates of a bull that had only a few
18 daughters were thus affected when the unknown parents in his pedigree
19 changed. This is the second reason why two subsequent EBVs could change.
20 We learned that we should therefore not change the members of the current
21 UPG and those of the previous UPG. In other words, UPG members should be
22 fixed based on animal's birth year.

1 The third reason was prediction error, caused mainly by the prediction of
2 lactation yields from partial test-day records in early DIM. Method P can predict
3 future yields by using the latest test-day records and assumes a standard
4 lactation curve (Miller, Pearson, Fohrman, & Creegan, 1972). In other words, it
5 cannot adjust for differences in the shapes of the lactation curves of particular
6 individual cows. Therefore, when a bull had extremely high or low lactation
7 persistency, the estimated lactation yield was not similar to the observed yield.
8 The lactation yields estimated by Multiple-trait prediction (Schaeffer & Jamrozik,
9 1996) or best prediction (VanRaden, 1997) are better than those of method P,
10 however problems still might not be solved completely. In the case of the
11 lactation model, records of lactation yield were used, therefore it would be
12 difficult to avoid this problem. The remaining problems associated with the
13 prediction of lactation yields were solved when an RR-TDM was used.

14

15 **5 Random regression test-day model**

16 A practical test-day model using a random regression in dairy cattle was
17 introduced by Schaeffer, Jamrozik, and Dekkers (1994). In Canada, official EBVs
18 were estimated for the first time in the world by using an RR-TDM, published in
19 1999, and were used to replace EBVs determined by using an animal lactation
20 model (Schaeffer, Jamrozik, Kistemaker, and Van Doormaal, 2000). The
21 RR-TDM was superior from both a theoretical and a practical perspective. For
22 example, it could use all test-day records without predicting lactation yields, and

1 it could consider various lactation curves for each cow. In the 2000s, many
 2 countries followed Canada's lead and introduced the RR-TDM.

3 In 2010, we introduced an repeatability RR-TDM introduced in Japan
 4 was follows:

$$5 \quad y_{ijkl} = (HTD_i + \sum_{m=0}^5 b_{jm} w(t)_{klm} + \sum_{n=0}^2 u_{kn} z(t)_{kln} + \sum_{n=0}^2 p_{kn} z(t)_{kln} + e_{ijkl})^{\exp(\gamma_i/2)},$$

6 where y_{ijkl} is test-day yield, HTD_i is the fixed effect of herd-test-day i , b_{jm} is
 7 the m th fixed regression coefficient specific to subclass j of the region
 8 (Hokkaido and Honshu) – calendar month – age group at calving, u_{kn} and p_{kn}
 9 are the n th random regression coefficients specific to cow k for additive genetic
 10 and permanent environmental effects, respectively, $w(t)_{klm}$ and $z(t)_{kln}$ are
 11 covariates for fixed and random regressions, respectively, associated with DIM t
 12 for test-day record l of cow $k(t_{kl})$, and e_{ijkl} is the random residuals associated
 13 with each record. The covariates of regression are fourth-order Legendre
 14 polynomials with the exponential term of the Wilmink function (Schaeffer *et al.*,
 15 2000) for the fixed lactation curves and second-order Legendre polynomials for
 16 random terms (Kistemaker, 2003). γ_i takes into account the autoregressive
 17 model (Kachman & Everett, 1993).

18 The new RR-TDM avoided the problem of extension from test-day
 19 record to lactation record. Moreover, additional information such as lactation
 20 persistency could now be calculated easily (Togashi *et al.*, 2008). In Japan, the
 21 second-order Legendre polynomial was used to show genetic lactation curves
 22 for bulls (Figure 1). In many countries, in contrast, third- or fourth-order

1 polynomial functions are used to estimate genetic lactation curves for particular
2 animals in RR-TDMs (Interbull, 2018). In our preliminary analysis, we found that
3 a quadratic polynomial was preferable to the others in showing the genetic
4 lactation curves of bulls.

5

6 **6 Adjustment for heterogeneity within herd variance**

7 Heterogeneity of genetic and residual variances within herds exists for
8 milk production and other traits (e.g., De Veer & Van Vleck, 1987; Everett,
9 Keown, & Taylor, 1982). Variance components of milk yield have been estimated
10 from herds grouped by production level, revealing a positive correlation between
11 production level and these variance components (Boldman & Freeman 1990).
12 Everett, Keown and Taylor (1982) proposed a method of adjusting for
13 heterogeneous phenotypic variances across contemporary animals by applying
14 a log transformation. A procedure for adjustment of heterogeneous phenotypic
15 variances was also developed by using an empirical Bayes method (Wiggans &
16 VanRaden, 1991; Wigel & Gianola, 1992). When the heterogeneity is not
17 adjusted in a genetic evaluation, differences within herd subclass variances
18 result in biased EBV estimates (Weigel & Gianola, 1992). Meuwissen, De Jong,
19 and Engel (1996) reported a method of estimating breeding values and
20 correcting for heterogeneous phenotypic variances by applying an
21 autoregressive model. Their procedure considered covariance across genetic
22 relationships and the reduction of variance caused by selection. In 2003,

1 adjustment of heterogeneous variances by using the autoregressive model of
 2 Meuwissen et al. was applied to a lactation animal model in Japan (Hagiya, Atagi,
 3 Shirai, & Suzuki, 2005):

$$4 \quad y_{ijklm} = (HYPF_i + RMY_j + A_k + u_l + p_l + e_{ijklm})^{\exp(\gamma_i/2)},$$

5 where y_{ijklm} is lactation yield, $HYPF_i$ is the fixed effect of herd – year – parity –
 6 milking frequency in a day i , RMY_j is the fixed effect of age group j , A_k is the
 7 fixed effect of age group at calving k , u_l and p_l are random effects for cow k
 8 for additive genetic and permanent environmental effects, respectively, and
 9 e_{ijklm} is the random residuals associated with each record. γ_i takes into
 10 account an autoregressive model containing fixed and random effects (Kachman
 11 & Everett, 1993). This autoregressive model was used even after the evaluation
 12 method was changed to a RR-TDM.

13 The use of an autoregressive model in our genetic evaluation seems to
 14 be more appropriate than pre-adjustment from the perspective of theoretical
 15 prediction. When the autoregressive model was applied to our genetic
 16 evaluations, the estimated values of γ_i were expected to be close to 1.0.
 17 However, they were sometimes far from 1 when the herd size was small.
 18 Therefore, the range of possible values of γ_i was restricted—e.g., ranging from
 19 0.5 to 2.0. In addition, when the average value of γ_i was larger (or smaller) than
 20 1, the genetic and phenotypic trends tended to have excessively high or low
 21 values. The procedure for adjusting heterogeneous phenotypic variances was
 22 changed to pre-adjustment (Kistmaker & Shaeffer, 1998) in 2015. If the

1 autoregressive model were to be reintroduced, we would have to control the
2 average γ_i value to make it equal to 1.

3

4 **7 Conclusions**

5 The procedure used for the genetic evaluation of dairy cattle in Japan
6 has developed from a lactation sire-MGS model to a multiple-lactation RR-TDM.
7 The data-collection system has also developed in response to the efforts of
8 those involved. In genetic evaluation in Japan, we need to improve the stability
9 of EBVs between two subsequent routine evaluations; that is, we need to
10 improve the durability of the model, further develop the data collection system,
11 and learn from past failures. I hope that this review will help those who have just
12 begun to work in our genetic evaluation system, as well as young researchers in
13 the field of dairy cattle breeding.

14

15 **References**

- 16 Abe T 1993 Recent developments in the progeny testing of dairy bulls in Japan. Interbull
17 Bulletin, 8.
- 18 Atagi Y and Hagiya K 2005. Preliminary study of genetic evaluation for female fertility in
19 Japan. Interbull Bulletin 33, 51–54.
- 20 Boldman KG and Freeman AE 1990. Adjustment for heterogeneity of variances by herd
21 production level in dairy cow and sire evaluation. Journal of Dairy Science, 73,
22 503–512.

- 1 De Veer JC and Van Vleck LD 1987. Genetic parameters for first lactation milk yields at
2 three levels of herd production. *Journal of Dairy Science*, 55, 1602–1606.
- 3 Everett RW, Keown JF and Taylor JF 1982. The problem of heterogeneous within herd
4 error variances when identifying elite cows. *Journal of Dairy Science*, 65
5 (Supplement 1), 100.
- 6 Hagiya K, Atagi A, Shirai T and Suzuki M 2005. Simultaneous estimation of genetic
7 parameters and heterogeneous variance for production traits of Holstein cattle in
8 Japan. *Interbull Bulletin* 33, 155–159.
- 9 Hagiya K, Osawa T, Masuda Y, Suzuki M, Yamazaki T, Nagamine Y, Togashi K 2012.
10 Optimal combination of traits to estimate the breeding value of herd life using multiple
11 trait model. *Nihon Chikusan Gakkaiho* 83, 117–123. (In Japanese)
- 12 Hagiya K, Osawa T, Shirai T, Terawaki Y, Yamazaki T, Nagamine Y, Itoh F, Kawahara T,
13 Masuda Y and Suzuki M 2014. Reliability of estimated breeding value of conception
14 rate for Holstein female using multiple-trait animal model. *Nihon Chikusan Gakkaiho*
15 85, 131–138. (In Japanese)
- 16 Interbull 2018. MACE explained. Retrieved on 27 December 2018 from
17 <http://www.interbull.org/ib/interbullactivities>
- 18 Kachman SD and Everett RW 1993. A multiplicative mixed model when the variances
19 are heterogeneous. *Journal of Dairy Science*, 76, 859–867.
- 20 Kistemaker GJ 2003. The Canadian test day model using Legendre polynomials.
21 *Interbull Bulletin* 31, 202–204.
- 22 Kistemaker GJ and Schaeffer LR 1998. Adjustment for heterogeneous herd-test-day

- 1 variances. *Interbull Bulletin* 17, 100–104.
- 2 Livestock Improvement Association of Japan 2018. Preliminary report on the results of
3 the test for dairy cattle in Heisei 28. Retrieved on 27 December 2018 from
4 <http://liaj.lin.gr.jp/japanese/newmilk/17/H28gaikyou.pdf> (In Japanese)
- 5 Lohuis M and Schaeffer LR 1995. Prelude's type evaluation: Facts. Retrieved on 30
6 December 2018 from <http://cgil.uoguelph.ca/pub/articles/prelude2.html>
- 7 Meuwissen THE, De Jong G and Engel B 1996. Joint estimation of breeding values and
8 heterogeneous variances of large data files. *Journal of Dairy Science*, 79, 310–318.
- 9 Miller RH, Pearson RE, Fohrman MH, Creegan ME 1972. Method of projecting
10 complete lactation production from part-lactation yield. *Journal of Dairy Science*, 55,
11 1602–1606.
- 12 Mitsumoto T 1980. Strategy and organization for dairy cattle breeding. Report of the
13 Hokkaido Branch Japanese Society of Zootechnical Science. 22(2), 5–15. (In
14 Japanese)
- 15 National Livestock Breeding Center (NLBC) 1993. National livestock breeding center
16 dairy sire evaluation report 1993–I. National Livestock Breeding Center, Ministry
17 Agriculture, Forestry and Fisheries. Nishigo, Fukushima, Japan. (In Japanese)
- 18 National Livestock Breeding Center (NLBC) 1996. National livestock breeding center
19 dairy sire evaluation report 1996–I. National Livestock Breeding Center, Ministry
20 Agriculture, Forestry and Fisheries. Nishigo, Fukushima, Japan. (In Japanese)
- 21 National Livestock Breeding Center (NLBC) 1999. National livestock breeding center
22 dairy sire evaluation report 1999–II. National Livestock Breeding Center, Ministry

- 1 Agriculture, Forestry and Fisheries. Nishigo, Fukushima, Japan. (In Japanese)
- 2 Quaas RL and Pollak EJ 1981. Modified equations for sire model with groups. *Journal of*
3 *Dairy Science*, 64, 1868–1872.
- 4 Schaeffer LR and Jamrozik J 1996. Multiple-trait prediction of lactation yields for dairy
5 cows. *Journal of Dairy Science*, 79, 2044–2055.
- 6 Schaeffer LR, Jamrozik J and Dekkers JCM 1994. Random regressions in animal model
7 for test-day production in dairy cattle. *Proceedings of the 5th World Congress on*
8 *Genetic Applied to Livestock Production*, Guelph, 18, 443.
- 9 Schaeffer LR, Jamrozik J, Kistemaker GJ and Van Doormaal BJ 2000. Experience with
10 a test-day model. *Journal of Dairy Science*, 83, 1135–1144.
- 11 Togashi K, Lin CY, Atagi Y, Hagiya K, Sato J and Nakanishi T 2008. Genetic
12 characteristics of Japanese Holstein cows based on multiple-lactation random
13 regression test-day animal models. *Livestock Science*, 114, 194–201.
- 14 Touchberry RW, Rottensten K and Andersen H 1959. A comparison of dairy sire
15 progeny tests made at special Danish testing stations with tests made in farmer
16 herds. *Journal of Dairy Science*, 43, 529–545.
- 17 VanRaden PM 1997. Lactation yields and accuracies computed from test day yields and
18 (co)variances by best prediction. *Journal of Dairy Science*, 80, 3015–3022.
- 19 Weigel KA and Gianola D 1992. Estimation of heterogeneous within herd variance
20 components using empirical Bayes methods: A simulation study. *Journal of Dairy*
21 *Science*, 75, 2824–2833.
- 22 Westell RA, Wuaas RL and Van Vleck LD 1988. Genetic groups in an Animal Model.

- 1 Journal of Dairy Science, 71, 1310–1318.
- 2 Wiggins GR and VanRaden PM 1991. Method and effect of adjustment for
- 3 heterogeneous variance. Journal of Dairy Science, 74, 4350–4357.
- 4 World Holstein Friesian Federation 2016. Progress of type harmonization. Retrieved on
- 5 27 December 2018 from
- 6 <http://www.whff.info/documentation/documents/progressoftypeharmonisationversion>
- 7 [afterBuenosAiresv2.pdf](#)
- 8
- 9

1

Table 1 Timeline of the introduction of genetic evaluations in Japan and related events

Year	Event
1993	Animal model for production and conformation traits
1997	Liability sire and maternal grandsire (MGS) model for temperament, milking speed, and calving ease
2003	Animal model for somatic cell score and adjustment for heterogeneity of herd variance for yield traits
2006	Multiple trait animal model for herd life
2008	Animal model for lactation persistency
2010	Random regression repeatability test-day model for yield traits and lactation persistency
2011	Liability sire and MGS model for stillbirth
2013	Genomic enhanced breeding value (GEBV) published for heifers
2014	Animal model for conception rate and days open
2015	Multiple-lactation random regression test-day model for yields and lactation persistency
2017	GEBV for bulls and cows

2

1

2 Figure captions

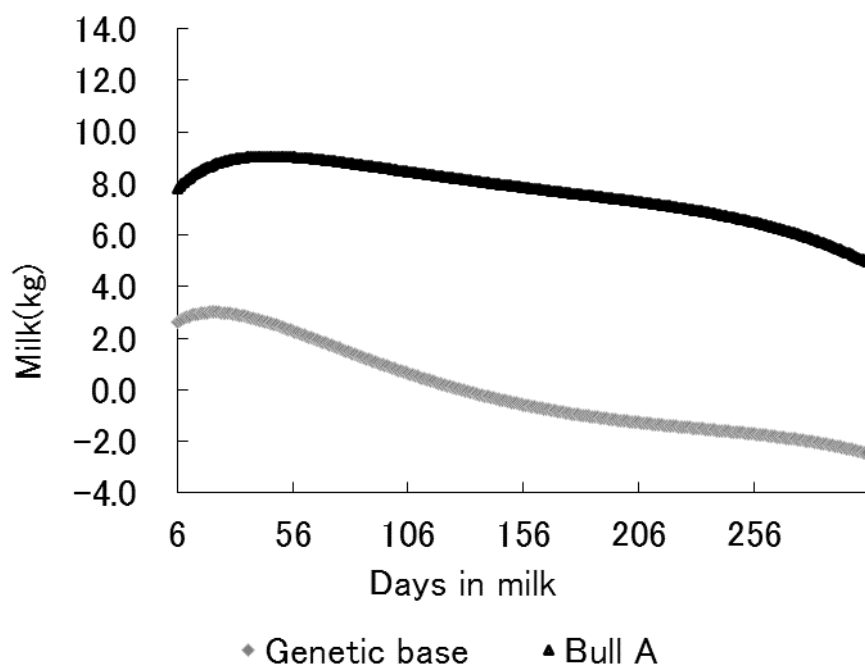
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4 Figure 1 An example of the genetic lactation curve of a bull and lactation curve
5 for genetic base

6

7

1 Figure 1
2



3
4
5

1 表題： 国内ホルスタイン種の泌乳形質に関する遺伝的能力評価の発展

2

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6

7

8 日本の乳用牛遺伝的能力評価に使用される数学モデルは，乳期サイアーMGS モ
9 デルから多産次変量回帰検定日アニマルモデルへと発展した．日本全国のホル
10 スタイン種雄牛評価は，1989年にフィールド型後代検定および牛群検定記録を
11 使用して開始された．1993年，泌乳および体型形質に関するアニマルモデルが
12 導入された．2010年，変量回帰検定日モデルが採用された．酪農における育種
13 産業において，推定育種価は，信頼性が高く，なおかつ継続した評価回次間で
14 安定していることが重要である．日本の乳用牛遺伝的能力評価における経験か
15 ら，国内の研究者らは，推定育種価の安定性を改善する方法を見出した．これ
16 らの改善は，データ編集方法の変更，評価モデルの開発，未知の両親グループ
17 構造の変更，検定日記録から乳期記録を予測する際の問題点，および不均一な
18 牛群内分散の補正を含む．ここでは，日本のホルスタイン種における泌乳形質
19 の遺伝的能力評価の発展および経験を紹介する．

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