

Genetic correlations among fertility traits and lactation persistency within and across Holstein herds with different milk production during the first three lactations

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Abstract

Genotype by environment interaction ($G \times E$) effects for lactating cows' fertility traits may differ with lactation number when accounting for herd production level. Our objective here was to investigate the genetic correlations among three fertility traits in cows and lactation persistency within and across herds with different milk-production levels by using lactation records of Japanese Holstein cows (475,446 records for first lactation, 378,540 for second, and 265,560 for third). Herds with data were categorized into three groups (**LOW**, **MID**, and **HIGH**) based on the average herd-year effects in each herd for 305-day milk yield at the first lactation. The fertility traits evaluated were conception rate at first insemination (**CR**); number of inseminations (**NI**); and days open (**DO**). Lactation persistency (**PER**) was defined as the difference between milk yields at 240 and 60 days in milk. Genetic parameters were estimated within each lactation by using a multiple-trait model that considered the traits of different herd milk-production groups (**HPGs**) as separate traits. The genetic correlations among fertility traits were estimated by using a three **HPG** \times three-trait animal model; for those between fertility traits and **PER** we used a three **HPG** \times two-trait (each fertility trait and **PER**) animal model. The genetic correlations among fertility traits were strong, whereas those between fertility traits and **PER** were weak and undesirable; most of the values did not differ significantly among **HPGs** or lactations. Some of the genetic correlations of **CR** or **NI** among different **HPGs** for the second and third lactations were lower than those for the first lactation. These findings suggest that $G \times E$ effects on a cow's ability to conceive with respect to herd production level are larger in later lactations than in the first lactation.

38 **Highlights**

- 39 • We examined G×E effects for Holstein cow fertility among herd production levels.
- 40 • Herd production level did not affect genetic correlations among fertility traits.
- 41 • Nor did it affect the genetic correlations of fertility with lactation persistency.
- 42 • G×E effects for fertility after the first lactation were relatively large.

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44 Differences in herd-average milk production affect the expression of genotype effects in terms of a

45 cow's ability to conceive after the second calving.

46

47 **Keywords**

48 Dairy cattle, fertility, genotype by environment interaction, herd milk production

Introduction

Female fertility is an important factor for improving the lifetime production of dairy cattle. Because antagonistic genetic relationships between female fertility and milk production traits have been found (e.g., Abe et al., 2009; Hagiya et al., 2013), the emphasis on fertility in the dairy cattle selection indices of many countries is greater now (Egger-Danner et al., 2015) than in the past (Miglior et al., 2017). A cow's ability to conceive is commonly evaluated by using conception rate (**CR**) or non-return rate for first insemination, and number of inseminations (**NI**). Days open (**DO**; days from calving to pregnancy) and calving interval are defined as combined traits representing a cow's abilities to recycle and to conceive after calving (ICAR, 2018). The genetic correlations among these fertility traits are strong: absolute values of more than 0.7 have been reported (e.g., Ghiasi et al., 2011; Yamazaki et al., 2014).

The existence of a genotype by environment interaction ($G \times E$) for fertility traits has been examined by considering differences in environmental descriptors such as region, herd size, temperature-humidity index, and herd-average production (Calus et al., 2005; Haile-Mariam et al., 2008; Ismael et al., 2016; Strandberg et al., 2009). Low genetic correlations among different environmental descriptors might suggest that the effect of $G \times E$ is not negligible. For traits with large $G \times E$, individual farmers could choose bulls that were more appropriate to their environments if information on bulls' genetic evaluations in different environments were available. Some $G \times E$ effects for fertility traits during first lactation have been found when production was considered (Haile-Mariam et al., 2008; Strandberg et al., 2009). However, to our knowledge there have been no reports of these effects in lactations beyond the first. According to Yamazaki et al. (2014), **CR** in later lactations is lower, and **DO** is longer, than in the first lactation. Those findings suggest the hypothesis that the strength of genotype \times herd production effects for fertility traits in later lactations may differ from those in the first lactation.

To our knowledge, there have been few studies of the genetic correlations among fertility traits and production traits such as milk yield or lactation persistency (**PER**) under different levels of herd production (Haile-Mariam et al., 2008; Togashi et al., 2016). **PER** is generally defined as the ability to maintain a high level of milk production after peak milk yield (Togashi and Lin, 2003). It has been suggested that genetic improvement of **PER** should help increase milk production without increasing mastitis susceptibility (Hagiya et al., 2014b) or somatic cell score (Yamazaki et al., 2013). However, some poor, or slightly undesirable, genetic correlations between fertility traits and **PER** have been reported (Albarrán-Portillo and Pollott, 2013; Yamazaki et al., 2014). Togashi et al. (2016) reported desirable genetic correlations between **PER** and conception until 180 days in milk (**DIM**) in a high-level reproductive management and milk-production environment. Information on genetic relationships in different environments is important for individual farmers in choosing bulls with the optimum breeding values for each trait to improve their cows' productivity.

Therefore, our objective here was to investigate the genetic relationships among three fertility traits and **PER** during the first three lactations of Holstein cows by using a multiple trait model that considered the trait values of herds with different milk-production levels as separate traits.

Materials and Methods

Data

Insemination records during the first three lactations of Holstein cows with first inseminations from 20 to 200 **DIM** recorded between 2007 and 2011 were obtained from the Livestock Improvement Association of Japan (Tokyo, Japan). Monthly test day (**TD**) milk records within 305 **DIM** were collected through the Dairy Herd Improvement program. The original data set included records for

475,446, 378,540 and 265,560 first, second, and third parity cows, respectively. Each cow had at least eight **TD** records. Age at first insemination ranged from 20 to 46 months in the first lactation (i.e., for the second calving), from 32 to 66 months in the second, and from 44 to 86 months in the third. The minimal size of the contemporary groups (herd year for first insemination and that for calving) was two cows for each data set, in accordance with the official genetic evaluation model for female fertility traits in Japan (National Livestock Breeding Center, 2017). The pedigree was traced back five generations and included 1,211,559, 1,035,440, and 798,595 animals for first-, second-, and third-parity cows, respectively.

The average milk production of each herd (**Herd production**) was defined as the average of the herd-year solution for 305-day milk yield at first lactation. Herd-year solutions for 305-day milk yield were obtained from the following single-trait animal model:

$$y_{ijkl} = HY_i + M_j + A_k + u_l + e_{ijkl},$$

where y_{ijkl} is the 305-day milk yield at first lactation of cow l ; HY_i is the fixed effect of herd year i (41,328 levels); M_j is the fixed effect of calving month j ; A_k is the fixed effect of calving age group k , with 15 levels (18 to 20, 21 to 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, and ≥ 35 months); u_l is the random additive effect of animal l ; and e_{ijkl} is a random residual effect associated with y_{ijkl} . The 305-day milk yield was estimated by using multiple-trait prediction (Schaeffer and Jamrozik, 1996) according to Wilink's function (Wilink, 1987). Solutions for fixed effects of 305-day milk yield were obtained by using the BLUPF90 program (Miszta et al., 2002), which uses the preconditioned conjugate gradient algorithm with iteration on data (Tsuruta et al. 2001). The variance components estimated by Yamazaki et al. (2014) were used to solve the fixed effects. Herds were classified into three groups based on the deviations of their **Herd production**, namely **LOW** (lower than -1 standard deviation [SD] of Herd production), **MID** (± 1 SD), and **HIGH** (higher than $+1$ SD).

The numbers of cows, herds, and means of 305-day milk yield for each **Herd production group (HPG)** in the first three lactations are shown in Table 1.

The female fertility traits were **CR**, **NI**, and **DO**. **CR** = 1 indicated that the first insemination achieved pregnancy, 0 otherwise. **NI** was classified into five levels (1, 2, 3, 4 or 5, and ≥ 6 times). **DO** greater than 365 days were set to 365 days (Oseni et al., 2004). The number of cows whose pregnancy could not be confirmed by the insemination records was 17,367, 20,721 and 17,437 in the first, second and third lactations, respectively; **DO** for these cows were treated as missing (Yamazaki et al., 2014). **PER** were estimated by using the same method as that for 305-day milk yield. **PER** was defined as the difference between milk yields at 240 and 60 **DIM** (Yamazaki et al., 2014). Summary statistics of each trait for the three **HPGs** are given in Table 2.

Models

The data were analyzed within each lactation by using a multiple-trait linear model that took into account the genetic covariance among records for the three **HPGs**. Threshold models theoretically are more appropriate for the analysis of binary (e.g., **CR**) or categorical (e.g., **NI**) data (Gianola, 1982). However, most routine national genetic evaluations of categorical fertility traits (including those in Japan) are based on linear models (Jamrozik et al., 2005; Liu et al., 2008; Mark, 2004), because analyses that use threshold models require excessive amounts of calculation time.

The model used for reproductive traits, in accordance with Japan's official genetic evaluation model (National Livestock Breeding Center, 2017), was:

$$y_{ijklmn} = FHY_i + FM_j + FA_k + s_n + u_{lm} + e_{ijklmn},$$

where y_{ijklmn} is the fertility trait of cow m ; FHY_i is the fixed effect of herd year i for first insemination (the levels were 38,906 for the first lactation, 37,464 for the second, and 34,534 for the third); FM_j is the fixed effect of region (two levels) – month j at first insemination; FA_k is the fixed

effect of age group k at first insemination, with seven levels (18, 19, 20, 21 to 25, 26 to 30, 31 to 40, and ≥ 41 months); S_n is the random effect of service sire m at first insemination (the levels were 9819 for the first lactation, 8660 for the second, and 7313 for the third); u_{lm} is **HPG** $l \times$ the random additive effect of animal m ; and e_{ijklmn} is a random residual effect associated with y_{ijklmn} . The age effect at first insemination was not considered in the third lactation record.

The model for **PER** was:

$$y_{ijklm} = HY_i + M_j + A_k + u_{lm} + e_{ijklm},$$

where y_{ijklm} is the **PER** of cow l ; HY_i is the fixed effect of herd year i (the levels for the first, second, and third lactations were 41,328, 39,405, and 35,767, respectively); M_j is the fixed effect of calving month j ; A_k is the fixed effect of calving age group k , with 30 levels (18 to 20, 21 to 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, and ≥ 35 months for first lactation; ≤ 35 , 36 to 37, 38 to 39, 40 to 41, 42 to 43, 44 to 45, 46 to 47, and 48 to 49, and ≥ 50 months for second lactation; and ≤ 45 , 46 to 50, 51 to 55, 56 to 60, 61 to 65, and ≥ 66 months for third lactation); and u_{lm} and e_{ijklm} are defined as in the previous model.

Genetic parameters for **CR**, **NI**, and **DO** were estimated by using a three-**HPG** \times three-trait animal model. Genetic correlations between fertility traits and **PER** were estimated by using a three-**HPG** \times two-trait (each fertility trait and **PER**) animal model. The covariance structure was defined as

$$\text{Var} \begin{bmatrix} \mathbf{s} \\ \mathbf{u} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{S} \otimes \mathbf{I} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G} \otimes \mathbf{A} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{R} \otimes \mathbf{I} \end{bmatrix}$$

for the three-**HLG** \times three- trait (fertility traits) animal model,

$$\mathbf{S} = \begin{bmatrix} \sigma_{s(f_1)}^2 & \sigma_{s(f_1)s(f_2)} & \sigma_{s(f_1)s(f_3)} \\ & \sigma_{s(f_2)}^2 & \sigma_{s(f_2)s(f_3)} \\ \text{Symme} & & \sigma_{s(f_3)}^2 \end{bmatrix},$$

$$163 \quad \mathbf{G} = \begin{bmatrix} \sigma_{u(Lf_1)}^2 & \sigma_{u(Lf_1)u(Lf_2)} & \sigma_{u(Lf_1)u(Lf_3)} & \sigma_{u(Lf_1)u(Mf_1)} & \sigma_{u(Lf_1)u(Mf_2)} & \sigma_{u(Lf_1)u(Mf_3)} & \sigma_{u(Lf_1)u(Hf_1)} & \sigma_{u(Lf_1)u(Hf_2)} & \sigma_{u(Lf_1)u(Hf_3)} \\ & \sigma_{u(Lf_2)}^2 & \sigma_{u(Lf_2)u(Lf_3)} & \sigma_{u(Lf_2)u(Mf_1)} & \sigma_{u(Lf_2)u(Mf_2)} & \sigma_{u(Lf_2)u(Mf_3)} & \sigma_{u(Lf_2)u(Hf_1)} & \sigma_{u(Lf_2)u(Hf_2)} & \sigma_{u(Lf_2)u(Hf_3)} \\ & & \sigma_{u(Lf_3)}^2 & \sigma_{u(Lf_3)u(Mf_1)} & \sigma_{u(Lf_3)u(Mf_2)} & \sigma_{u(Lf_3)u(Mf_3)} & \sigma_{u(Lf_3)u(Hf_1)} & \sigma_{u(Lf_3)u(Hf_2)} & \sigma_{u(Lf_3)u(Hf_3)} \\ & & & \sigma_{u(Mf_1)}^2 & \sigma_{u(Mf_1)u(Mf_2)} & \sigma_{u(Mf_1)u(Mf_3)} & \sigma_{u(Mf_1)u(Hf_1)} & \sigma_{u(Mf_1)u(Hf_2)} & \sigma_{u(Mf_1)u(Hf_3)} \\ & & & & \sigma_{u(Mf_2)}^2 & \sigma_{u(Mf_2)u(Mf_3)} & \sigma_{u(Mf_2)u(Hf_1)} & \sigma_{u(Mf_2)u(Hf_2)} & \sigma_{u(Mf_2)u(Hf_3)} \\ & & & & & \sigma_{u(Mf_3)}^2 & \sigma_{u(Mf_3)u(Hf_1)} & \sigma_{u(Mf_3)u(Hf_2)} & \sigma_{u(Mf_3)u(Hf_3)} \\ & & & & & & \sigma_{u(Hf_1)}^2 & \sigma_{u(Hf_1)u(Hf_2)} & \sigma_{u(Hf_1)u(Hf_3)} \\ & & & & & & & \sigma_{u(Hf_2)}^2 & \sigma_{u(Hf_2)u(Hf_3)} \\ & & & & & & & & \sigma_{u(Hf_3)}^2 \end{bmatrix},$$

$$164 \quad \text{and } \mathbf{R} = \begin{bmatrix} \sigma_{e(Lf_1)}^2 & \sigma_{e(Lf_1)e(Lf_2)} & \sigma_{e(Lf_1)e(Lf_3)} & 0 & 0 & 0 & 0 & 0 & 0 \\ & \sigma_{e(Lf_2)}^2 & \sigma_{e(Lf_2)e(Lf_3)} & 0 & 0 & 0 & 0 & 0 & 0 \\ & & \sigma_{e(Lf_3)}^2 & 0 & 0 & 0 & 0 & 0 & 0 \\ & & & \sigma_{e(Mf_1)}^2 & \sigma_{e(Mf_1)e(Mf_2)} & \sigma_{e(Mf_1)e(Mf_3)} & 0 & 0 & 0 \\ & & & & \sigma_{e(Mf_2)}^2 & \sigma_{e(Mf_2)e(Mf_3)} & 0 & 0 & 0 \\ & & & & & \sigma_{e(Mf_3)}^2 & 0 & 0 & 0 \\ & & & & & & \sigma_{e(Hf_1)}^2 & \sigma_{e(Hf_1)e(Hf_2)} & \sigma_{e(Hf_1)e(Hf_3)} \\ & & & & & & & \sigma_{e(Hf_2)}^2 & \sigma_{e(Hf_2)e(Hf_3)} \\ & & & & & & & & \sigma_{e(Hf_3)}^2 \end{bmatrix},$$

165 and for the three-**HPG** \times two-trait (fertility trait and **PER**) animal model,

$$166 \quad \mathbf{S} = \begin{bmatrix} \sigma_s^2 & 0 \\ 0 & 0 \end{bmatrix},$$

$$167 \quad \mathbf{G} = \begin{bmatrix} \sigma_{u(Lf)}^2 & \sigma_{u(Lf)u(Lp)} & \sigma_{u(Lf)u(Mf)} & \sigma_{u(Lf)u(Mp)} & \sigma_{u(Lf)u(Hf)} & \sigma_{u(Lf)u(Hp)} \\ & \sigma_{u(Lp)}^2 & \sigma_{u(Lp)u(Mf)} & \sigma_{u(Lp)u(Mp)} & \sigma_{u(Lp)u(Hf)} & \sigma_{u(Lp)u(Hp)} \\ & & \sigma_{u(Mf)}^2 & \sigma_{u(Mf)u(Mp)} & \sigma_{u(Mf)u(Hf)} & \sigma_{u(Mf)u(Hp)} \\ & & & \sigma_{u(Mp)}^2 & \sigma_{u(Mp)u(Hf)} & \sigma_{u(Mp)u(Hp)} \\ & & & & \sigma_{u(Hf)}^2 & \sigma_{u(Hf)u(Hp)} \\ & & & & & \sigma_{u(Hp)}^2 \end{bmatrix},$$

$$168 \quad \text{and } \mathbf{R} = \begin{bmatrix} \sigma_{e(Lf)}^2 & \sigma_{e(Lf)e(Lp)} & 0 & 0 & 0 & 0 \\ & \sigma_{e(Lp)}^2 & 0 & 0 & 0 & 0 \\ & & \sigma_{e(Mf)}^2 & \sigma_{e(Mf)e(Mp)} & 0 & 0 \\ & & & \sigma_{e(Mp)}^2 & 0 & 0 \\ & \text{Symme} & & & \sigma_{e(Hf)}^2 & \sigma_{e(Hf)e(Hp)} \\ & & & & & \sigma_{e(Hp)}^2 \end{bmatrix}$$

169 where \mathbf{S} is a (co)variance matrix of random service-sire effects for first insemination; \mathbf{G} is a
 170 (co)variance matrix of random additive genetic effects; \mathbf{R} is a residual (co)variance matrix; \mathbf{A} is the
 171 additive genetic relationship for animals; \mathbf{I} is the identity matrix; subscripts (Lf (or Lp)), (Mf (or Mp)),
 172 and (Hf (or Hp)) are the fertility traits (or **PER**) for the **LOW**, **MID**, and **HIGH HPGs**, respectively;
 173 and \otimes is the Kronecker product. The residual covariances between different **HPGs** were fixed at
 174 zero. The GIBBS3F90 program (Misztal, 2008) was used for Gibbs sampling to estimate the variance
 175 components. For Gibbs sampling, the first 300,000 samples were discarded as burn-in. The subsequent
 176 200,000 samples were saved to calculate posterior means and standard deviations for the (co)variance
 177 components. Convergence was verified through the inspection of graphical data by using the
 178 POSTGIBBSF90 program (Misztal, 2008).

179 We calculated Spearman's rank correlations for the bulls' estimated breeding values (EBVs) for
 180 each fertility trait among different **HPGs** by using our estimated variance components. EBVs were
 181 estimated by using a three-**HPG** \times one-trait animal model and a preconditioned conjugate gradient
 182 algorithm with iteration on data (Tsuruta et al. 2001) in a program developed for national evaluation
 183 in Japan by the National Livestock Breeding Center (Nishigo-mura, Japan). Bulls selected for
 184 calculating rank correlations had at least 10 daughters' records in every **HPG** for each lactation data
 185 set: 349, 319, and 273 bulls for the first, second, and third lactations, respectively. Spearman's rank
 186 correlations were calculated by using the CORR procedure of the SAS software package (SAS Institute
 187 Inc., 2015).

188

189 **Results and Discussion**

190 **CR** decreased and average **NI** increased, with increasing **HPG** level, especially in the second and third
191 lactations (Table 2); **CRs** for **HIGH HPG** were 11% lower than those for **LOW HPG** in the second
192 and third lactations. There were only small differences among the averages of **DO** in each of the
193 different **HPGs** in each lactation. Weak and undesirable phenotypic correlations between milk yield
194 traits and fertility traits have been reported in the same lactation (Hagiya et al., 2013; Yamazaki et al.,
195 2014). The differences we found here in **CR** and **NI** among the different **HPGs** may have been the
196 result of several interactions between breeding timing decision or milk production level and fertility
197 of the cows in each herd.

198 Average **PER** increased in the first lactation and decreased in the second and third lactations with
199 rising **HPG** level. The standard deviation of **PER** increased with rising **HPG** level in each lactation.
200 Weak and positive phenotypic correlations between 305-day milk yield and **PER** have been reported
201 (Yamazaki et al., 2014). These relationships thus likely affect the variance of **PER** in each **HPG**,
202 because the standard deviation of 305-day milk yield increased with increasing **HPG** level (Table 1)
203 as a result of heterogeneous variance due to differing production level.

204

205 **Heritabilities and genetic correlations within each HPG**

206 The variances of service-sire effect as proportions of the total variances were very small for fertility
207 traits and ranged from 0.0020 to 0.0042 (not shown). Most of the heritability estimates for **CR** and **NI**
208 did not differ significantly ($P \geq 0.05$) within **HPGs** among lactations or among **HPGs** for the same
209 lactation; they ranged from 0.022 to 0.044 for **CR** and from 0.035 to 0.056 for **NI** (Table 3). **CR**
210 showed significant differences between the values in **MID** (0.022) and **HIGH** (0.041) **HPG** for the
211 second lactation and between those in **LOW** (0.044) and **MID** (0.022) **HPG** for the third lactation. For

212 **NI**, the value in **MID HPG** (0.035) for the second lactation was significantly ($P < 0.05$) lower than
213 that in **HIGH HPG** for the second (0.056) and first (0.054) lactations. The heritabilities of **DO** ranged
214 from 0.065 to 0.172; the values for the third lactation (0.116 to 0.172) were significantly higher than
215 those for the first and second lactations (0.065 to 0.101) within the same **HPGs**, with the exception of
216 the difference between the first (0.084) and third (0.116) lactations in **HIGH HPG**. The heritability
217 values for **LOW HPG** tended to be higher than those for the other **HPGs** in the same lactation,
218 although the differences were not significant. Our heritability estimates for these fertility traits were in
219 line with previous findings (e.g., Abe et al., 2009; Ghiasi et al., 2011; Hagiya et al., 2013; Jamrozik et
220 al., 2005), except that those of **DO** for the third lactation were higher than in these studies. Some
221 reports have stated that the heritability estimates of **DO** for later lactations are higher than those for
222 the first lactation (Dematawewa and Berger, 1998; Menendez-Buxadera et al., 2013). Dematawewa
223 and Berger (1998) suggested that intense selection may contribute to more homogeneity (smaller
224 phenotypic variance) among cows in later parities and lead to higher heritability estimates for later
225 parities than for first parity. Our heritability estimates of fertility traits for the third lactation may have
226 been affected by selection in former lactations, because cows with poor fertility are culled.

227 The reason for the higher heritabilities of **DO** for **LOW HPG** than in the other **HPGs** in the same
228 lactations in our study was that the genetic variances were higher than those for the other **HPGs** (not
229 shown): the genetic variances of **DO** for **LOW HPG** were 37%, 38%, and 33% higher than those of
230 **MID** and also 19%, 25%, and 64% higher than those of **HIGH** for the first, second, and third lactations,
231 respectively. Ismael et al. (2016) similarly reported that the heritability and genetic variance of the
232 interval from calving to first peak estrus activity in low-producing herds were higher than those in
233 high-producing herds. Haile-Mariam et al. (2008) and Strandberg et al. (2009) also reported that the
234 heritability of the interval from calving to first insemination in low-producing herds was higher than
235 that in high-producing herds. The differences in our heritability estimates for **DO** agreed with these

236 previous findings, because **DO** is strongly genetically correlated with the interval from calving to first
237 insemination (Yamazaki et al., 2014).

238 The heritability estimates for **PER** increased significantly with rising **HPG** level in each lactation
239 (Table 3), except in the case of the difference between **MID** (0.185) and **HIGH** (0.238) in the second
240 lactation and that between **LOW** (0.115) and **MID** (0.145) in the third lactation. Those for **MID HPG**
241 were consistent with the estimates of Yamazaki et al. (2014). An increase in heritabilities for **PER** with
242 rising **Herd production** has been reported by Togashi et al. (2016). Differences in the variance of **PER**
243 among **HPGs** likely affected our heritability estimates, because the phenotypic standard deviations of
244 **PER** increased with rising **HPG** level (Table 2) as a result of heterogeneous variance due to differing
245 production level.

246 Most of the genetic correlations among fertility traits (Table 4) and those between each fertility trait
247 and **PER** (Table 5) did not differ significantly within **HPGs** among lactations or among **HPGs** for the
248 same lactation. The genetic correlations between **CR** and **NI** were the strongest (from -0.985 to $-$
249 0.903). Those of **DO** with **CR** or **NI** were also strong (from -0.885 to -0.714 and from 0.760 to 0.908 ,
250 respectively). That of **DO** with **NI** in **LOW HPG** for the first lactation (0.908) was significantly
251 stronger than that for the second lactation (0.798) (Table 4). Those of **PER** with the fertility traits were
252 weak and undesirable (Table 5), although there were large posterior standard deviations (0.033 to
253 0.100); the values of **PER** with **CR**, **NI**, and **DO** ranged from -0.266 to -0.121 , from 0.161 to 0.363 ,
254 and from 0.233 to 0.439 , respectively. The only significant difference in the genetic correlations
255 between **PER** and **DO** was for **MID HPG**, between the first (0.251) and third (0.439) lactations. Our
256 genetic correlation estimates among fertility traits were similar to previous findings (e.g., Abe et al.,
257 2009; Ghiasi et al., 2011; Kadarmideen et al., 2003; Yamazaki et al., 2014), and those between fertility
258 and **PER** were similar to the estimates of Yamazaki et al. (2014). The genetic correlation between **NI**
259 and **DO** for the second lactation was significantly weaker than that for the first lactation in **LOW HPG**

(see Table 4); however, that correlation was still moderate to strong. Our results suggest that differences in herd milk production do not affect the genetic relationships among fertility traits and lactation persistency.

Genetic correlations of each trait across different HPGs

Positive and moderate to strong genetic correlations (greater than 0.7) were estimated for each trait across different **HPGs**, except in the case of those of **CR** for the **LOW–MID** and **LOW–HIGH HPGs** in the third lactation (Table 6). The genetic correlations of **CR** for the **MID–HIGH** (0.754) and **LOW–HIGH** (0.706) **HPGs** in the second lactation, and those for the **LOW–MID** (0.527) and **LOW–HIGH** (0.509) **HPGs** in the third lactation, were significantly weaker than that for the **MID–HIGH HPG** in the first lactation (0.906). Those of **CR** for the **LOW–MID** and **LOW–HIGH HPGs** in the third lactation were also significantly weaker than that for the **LOW–MID HPG** in the first lactation (0.837). The genetic correlations of **NI** for the **LOW–HIGH** (0.808) **HPG** in the second lactation and those for the **LOW–MID** (0.821) and **LOW–HIGH** (0.733) **HPGs** in the third lactation were significantly weaker than that for the **MID–HIGH HPG** in the first lactation (0.935). Most of the genetic correlations of **DO** did not differ among **HPGs** or lactations, with the exception of the difference between the **MID–HIGH HPG** in the first lactation (0.952) and the **LOW–HIGH HPG** in the second lactation (0.830). Genetic correlations of 0.74 for calving interval between low and high herd-average production groups have been reported for the first lactation (Haile-Mariam et al., 2008; Strandberg et al., 2009). Some of our genetic correlations for **CR** in the third lactations across the different **HPGs** were lower than these previous estimates for the first lactation. Spearman's rank correlations of bulls' EBVs for each analyzed trait within each **HPG** are shown in Table 7. **CR** and **NI** showed lower correlations between different **HPGs** in the second and third lactations than in the first, suggesting that the genotype \times environment effect was not negligible.

284 Our findings indicate that differences in herd-average milk production affect the expression of
285 genotype effects in terms of a cow's ability to conceive after the second calving. These results imply
286 that the appropriate bulls for female fertility after the second calving may differ with the production
287 system (e.g., the housing management system or feeding system) related to herd production. Hagiya
288 et al. (2014a) examined the effects of housing type \times feeding system on milk yield and reported that
289 milk yield in later parity cows was more susceptible to difference in the feeding system than was milk
290 yield in first lactation cows. Here, we were unable to take these systems into account in relation to herd
291 production level. Revealing the effects of genotype \times production system on female fertility after the
292 second calving would help to inform us of the appropriate bulls for improving cow fertility in
293 individual farming systems, for example, by notifying us of those bulls with high EBVs for fertility in
294 each system.

295

296

297 **Conclusions**

298 We examined the genetic relationships among female fertility traits and lactation persistency during
299 the first three lactations of Holstein cows with regard to herd milk-production level. The genetic
300 correlations among fertility traits and those between fertility and lactation persistency did not differ
301 significantly among herd production levels. The genetic correlations and bulls' rank correlations for
302 conception rate and number of inseminations between herds with low and high milk-production levels
303 were lower in later lactations than in the first lactation. This suggests that the appropriate bulls for
304 improving a cow's ability to conceive after the second calving are different among herd milk-
305 production levels.

306

307

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311

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 393 lactations of Japanese Holstein cows. *Livest. Sci.* 168, 26-31.

394

395 Table1. Numbers of cows, herds, and average 305-day milk yield in each herd production group (**HPG**)
396 for the first three lactations

	Lactation	HPG			Overall
		LOW	MID	HIGH	
Number of cows	First	53,505	320,851	101,090	475,446
	Second	46,583	255,825	76,132	378,540
	Third	36,363	179,752	49,445	265,560
Number of herds	First	1533	6470	1407	9410
	Second	1468	6219	1353	9040
	Third	1427	6020	1292	8739
305-day milk yield (SD), kg	First	6466 (1015)	8193 (1249)	9610 (1369)	8300 (1522)
	Second	7485 (1245)	9389 (1549)	10,948 (1708)	9469 (1824)
	Third	7887 (1304)	9774 (1610)	11,393 (1784)	9817 (1885)

397 **HPG** was categorized on the basis of the milk production of each herd, i.e., the average herd-year
398 solution for 305-day milk yield in the first lactation: **LOW** (lower than –1 standard deviation (SD)
399 from the mean value), **MID** (± 1 SD from the mean value), and **HIGH** (higher than +1 SD from the
400 mean value).

401 Table 2. Summary statistics of fertility traits and lactation persistency (**PER**) in each herd production
 402 group (**HPG**) for the first three lactations

	Lactation	HPG			Overall
		LOW	MID	HIGH	
CR	First	0.38	0.38	0.37	0.38
	Second	0.37	0.34	0.33	0.34
	Third	0.36	0.34	0.32	0.34
NI (SD), times	First	2.4 (1.8)	2.5 (1.9)	2.6 (2.0)	2.5 (1.9)
	Second	2.4 (1.8)	2.6 (1.9)	2.7 (1.9)	2.6 (1.9)
	Third	2.5 (1.8)	2.6 (1.8)	2.7 (1.9)	2.6 (1.9)
DO (SD), days	First	146 (83)	144 (83)	144 (82)	144 (83)
	Second	151 (83)	151 (83)	151 (81)	151 (83)
	Third	153 (85)	154 (83)	154 (81)	154 (83)
PER (SD), kg	First	−7.2 (2.7)	−6.3 (2.9)	−5.7 (3.1)	−6.3 (2.9)
	Second	−9.3 (3.3)	−9.9 (3.7)	−10.7 (4.3)	−10.0 (3.8)
	Third	−10.1 (3.5)	−10.8 (3.9)	−11.7 (4.6)	−10.9 (4.0)

403 **HPG** is as defined in the footnote to Table 1.

404 Fertility traits: **CR**, conception rate at first insemination; **NI**, number of inseminations; and **DO**, days
 405 open. **PER** is defined as the difference between the milk yields at 240 and 60 days in milk.

406

Table 3. Posterior means (posterior SDs) of heritability for fertility traits and lactation persistency (**PER**) in each herd production group (**HPG**) for the first three lactations

	Lactation	HPG		
		LOW	MID	HIGH
CR	First	0.034 (0.006) ^{abc}	0.026 (0.002) ^{abc}	0.035 (0.003) ^{ab}
	Second	0.033 (0.005) ^{abc}	0.022 (0.002) ^c	0.041 (0.005) ^a
	Third	0.044 (0.006) ^a	0.022 (0.003) ^{bc}	0.031 (0.008) ^{abc}
NI	First	0.051 (0.007) ^{ab}	0.044 (0.003) ^{ab}	0.054 (0.005) ^a
	Second	0.041 (0.004) ^{ab}	0.035 (0.003) ^b	0.056 (0.005) ^a
	Third	0.049 (0.008) ^{ab}	0.041 (0.005) ^{ab}	0.046 (0.006) ^{ab}
DO	First	0.101 (0.008) ^{bcd}	0.073 (0.005) ^{de}	0.084 (0.007) ^{cde}
	Second	0.090 (0.008) ^{cde}	0.065 (0.004) ^e	0.074 (0.006) ^{de}
	Third	0.172 (0.016) ^a	0.136 (0.008) ^{ab}	0.116 (0.009) ^{abc}
PER	First	0.116 (0.010) ^d	0.161 (0.007) ^{bc}	0.206 (0.009) ^a
	Second	0.129 (0.009) ^{cd}	0.185 (0.008) ^{ab}	0.238 (0.016) ^a
	Third	0.115 (0.008) ^d	0.145 (0.009) ^{cd}	0.202 (0.014) ^{ab}

HPG is as defined in the footnote to Table 1.

All traits are the same as those defined in the footnote to Table 2.

Heritabilities for **PER** were estimated by using a three-**HPG** × two-trait (**CR** and **PER**) animal model.

Values with different superscript letters across rows and down columns are significantly different: $P < 0.05$ after Bonferroni correction.

414 Table 4. Posterior means (posterior SDs) of genetic correlations among fertility traits within each herd
 415 production group (**HPG**) for the first three lactations

		HPG		
	Lactation	LOW	MID	HIGH
CR - NI	First	−0.903 (0.020) ^a	−0.965 (0.005) ^{ab}	−0.939 (0.012) ^{ab}
	Second	−0.936 (0.020) ^{ab}	−0.985 (0.007) ^b	−0.943 (0.014) ^{ab}
	Third	−0.908 (0.022) ^a	−0.952 (0.013) ^{ab}	−0.922 (0.023) ^{ab}
CR - DO	First	−0.841 (0.033)	−0.885 (0.027)	−0.846 (0.024)
	Second	−0.714 (0.049)	−0.815 (0.019)	−0.798 (0.026)
	Third	−0.774 (0.046)	−0.775 (0.033)	−0.812 (0.045)
NI - DO	First	0.908 (0.012) ^a	0.859 (0.017) ^{ab}	0.864 (0.016) ^{ab}
	Second	0.798 (0.031) ^b	0.801 (0.018) ^b	0.835 (0.021) ^{ab}
	Third	0.808 (0.034) ^{ab}	0.832 (0.019) ^b	0.760 (0.041) ^b

416 **HPG** is as defined in the footnote to Table 1.

417 All traits are as defined in the footnote to Table 2.

418 Values with different superscript letters across rows and down columns are significantly different: $P <$
 419 0.05 after Bonferroni correction.

420

421 Table 5. Posterior means (posterior SDs) of genetic correlations between fertility traits and lactation
422 persistency (**PER**) within each herd production group (**HPG**) for the first three lactations

		HPG		
	Lactation	LOW	MID	HIGH
PER–CR	First	–0.121 (0.083)	–0.220 (0.045)	–0.243 (0.058)
	Second	–0.222 (0.069)	–0.180 (0.061)	–0.181 (0.081)
	Third	–0.266 (0.100)	–0.192 (0.064)	–0.189 (0.089)
PER–NI	First	0.325 (0.081)	0.187 (0.044)	0.188 (0.049)
	Second	0.208 (0.062)	0.187 (0.052)	0.251 (0.064)
	Third	0.161 (0.081)	0.363 (0.053)	0.312 (0.075)
PER–DO	First	0.387 (0.047) ^{ab}	0.251 (0.042) ^b	0.275 (0.046) ^{ab}
	Second	0.387 (0.075) ^{ab}	0.361 (0.041) ^{ab}	0.317 (0.045) ^{ab}
	Third	0.233 (0.056) ^{ab}	0.439 (0.033) ^a	0.372 (0.078) ^{ab}

423 **HPG** is as defined in the footnote to Table 1.

424 All traits are as defined in the footnote to Table 2.

425 Values with different superscript letters across rows and down columns are significantly different: $P <$
426 0.05 after Bonferroni correction.

427

Table 6. Posterior means (posterior SDs) of genetic correlations for each fertility trait and lactation persistency (**PER**) across herd production groups (**HPGs**) for the first three lactations

	Lactation	Genetic correlation between different HPGs		
		LOW–MID	MID–HIGH	LOW–HIGH
CR	First	0.837 (0.031) ^{ab}	0.906 (0.028) ^a	0.759 (0.046) ^{abc}
	Second	0.743 (0.048) ^{abc}	0.754 (0.034) ^{bc}	0.706 (0.042) ^{bc}
	Third	0.527 (0.077) ^c	0.738 (0.082) ^{abc}	0.509 (0.071) ^c
NI	First	0.875 (0.023) ^{ab}	0.935 (0.012) ^a	0.803 (0.040) ^{ab}
	Second	0.871 (0.031) ^{ab}	0.894 (0.024) ^{ab}	0.808 (0.033) ^b
	Third	0.821 (0.033) ^b	0.845 (0.029) ^{ab}	0.733 (0.057) ^b
DO	First	0.944 (0.013) ^{ab}	0.952 (0.011) ^a	0.939 (0.010) ^{ab}
	Second	0.873 (0.023) ^{ab}	0.915 (0.016) ^{ab}	0.830 (0.035) ^b
	Third	0.907 (0.018) ^{ab}	0.941 (0.013) ^{ab}	0.848 (0.040) ^{ab}
PER	First	0.940 (0.010) ^{bc}	0.974 (0.006) ^{ab}	0.906 (0.015) ^c
	Second	0.953 (0.010) ^{abc}	0.978 (0.007) ^a	0.930 (0.013) ^{bc}
	Third	0.952 (0.011) ^{abc}	0.974 (0.007) ^{ab}	0.928 (0.015) ^{abc}

HPG is as defined in the footnote to Table 1.

All traits are as defined in the footnote to Table 2.

Genetic correlations for **PER** were estimated by using the three-**HPG** × two-trait (**CR** and **PER**) animal model.

434 Values with different superscript letters across rows and down columns are significantly different; $P <$
435 0.05 after Bonferroni correction.
436

437 Table 7. Spearman's rank correlations of bulls' estimated breeding values (**EBVs**) for each fertility
438 traits across herd production groups (**HPG**) for the first three lactations

		Rank correlation of EBV between different HPGs		
	Lactation	LOW-MID	MID-HIGH	LOW-HIGH
CR	First	0.78	0.84	0.70
	Second	0.69	0.74	0.60
	Third	0.58	0.65	0.46
NI	First	0.85	0.90	0.76
	Second	0.82	0.81	0.68
	Third	0.78	0.79	0.63
DO	First	0.88	0.89	0.82
	Second	0.84	0.85	0.71
	Third	0.89	0.90	0.81

439 **HPG** is as defined in the footnote to Table 1.

440 All traits are as defined in the footnote to Table 2.

441 Bulls selected for calculating rank correlations had at least 10 daughters' records in every **HPG** for
442 each lactation data set: 349, 319, and 273 bulls for the first, second, and third lactation, respectively.

443