



Genetic and genomic evaluation of age at first calving in Italian Holsteins

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ABSTRACT

Age at first calving (AFC) represents the nonproductive period of ~2 yr in Holstein cows, and thus, it has a relevant effect on the cost of rearing replacements in the dairy herd. In the present study, we aimed to evaluate genetic and genomic aspects of AFC in the Italian Holstein population. Data of 4,206,218 heifers with first calving between 1996 and 2020 were used. Age at first calving averaged 26.09 ± 3.07 mo and decreased across years. Heritability was estimated using a linear animal model which included the fixed effects of herd-year-season of birth and classes of gestation length, and the random animal additive genetic effect fitted to a pedigree-based relationship matrix. The EBV and genomically EBV (GEBV) were obtained, and they were standardized to mean 100 and standard deviation 5, where animals above the mean are those contributing to reduce AFC. Heritability estimates of AFC ranged from 0.031 to 0.045. The trend of sires' GEBV was favorable and indicated a reduced AFC across years. Approximate genetic correlations between GEBV of AFC and GEBV of other economically important traits were calculated on a subset of genotyped females born after 2015. Moderate favorable associations of AFC with production traits (0.39–0.51), udder depth (0.40), interval from first to last insemination in heifer (–0.43), and longevity (0.34) were assessed. Overall, the greatest lifetime productive performances and most favorable days open in first lactation were observed when heifers calved at 22 to 23 mo. In contrast, progeny of sires with GEBV of AFC above the mean yielded more milk, fat, and protein in first lactation, and had shorter days open than progeny of sires with GEBV of AFC below the mean. Results suggested that breeding strategies to improve AFC should be pursued, also considering genetic correlations between AFC and traits which are already part of the Italian Holstein breeding objective.

The inclusion of AFC in an aggregate index is expected to contribute to enhance farm income.

Key words: dairy cattle, heifer, heritability, longevity, profit

INTRODUCTION

Age at first calving (AFC) is the period from birth to the onset of the productive career of the dairy cow. The AFC is a relevant contributor to the costs of rearing replacement heifers on the farm and thus, to total milk production costs. Interest exists to shorten AFC and therefore breed heifers with proper growth rate at an earlier age. In Italy, the average daily rearing cost of a heifer has been estimated to increase from €3.20 to €3.30 moving from 24 to 30 mo of AFC, respectively (Paganini, 2023). In the United Kingdom, an average daily cost of £2.31 (\$2.93) for rearing a heifer to calving has been reported (Boulton et al., 2017), and in the United States this cost has been estimated to vary from \$2.46 to \$3.55 (Tranel, 2019; Cabrera, 2023). Differences in costs, especially those related to more recent estimates, are likely due to the strong increase of feed costs. Hence, the direct economic advantage of reducing AFC is immediately derived. The effects of AFC reduction on lifetime performances have been extensively evaluated. Eastham et al. (2018) observed that heifers with AFC to 22 to 23 mo had, on average, the greatest lifetime milk yield, the lowest SCC, and the shortest calving interval. Accordingly, an average AFC between 22 and 24 mo concurrently with an average daily gain between 0.7 and 0.8 kg have been recommended to achieve a first-calving size adequate to maximize milk production and reduce rearing costs (Abeni et al., 2000; Tozer and Heinrichs, 2001). Furthermore, AFC to 22 to 23 mo has resulted in shorter days open and calving interval, and greater conception rate in first-lactation cows (Ettema and Santos, 2004; Krpálková et al., 2014). Nevertheless, AFC <22 mo has been associated with increased calving difficulty, stillborn, perinatal mortality, and risk of dystocia (Ettema and Santos, 2004; Berry and Cromie, 2009).

Received March 15, 2023.

Accepted November 24, 2023.

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The AFC depends on a plethora of factors, including management, genetics (Mourits et al., 1999), nutrition, and growth rate (Wathes et al., 2008). Given that AFC depends on both BW and size, AFC is the result of a proper growth rate within an optimal time interval (Le Cozler et al., 2008). Fertility is characterized by lower heritability compared with production or type traits, however exploitable additive genetic variation has been reported for AFC, along with its genetic correlations with other nonproduction traits such as calving interval, calving ease, and conception rate (Berry et al., 2014; Heise et al., 2018; Brzáková et al., 2020). Although BW is more representative of heifer growth rate, its monitoring on a routine cost-effective basis is hardly feasible, whereas information on AFC can be quickly retrieved from herdbook information or easily recorded on-farm. In Italian Holsteins, AFC has been stored in national database since the early 1990s, but information on genetic variation of this trait and its potential use for breeding purposes has not been explored so far. Genetic and genomic proof for AFC could be exploited to support farmers to maximize the profit, which is achievable by reducing heifer rearing costs and maximizing yield output. Hence, the aim of the present study was to investigate genetic and genomic aspects of AFC in Italian Holstein population.

MATERIALS AND METHODS

Data

This study did not involve animals and thus prior ethical approval was deemed not to be required. Data stored in the national database of the Italian Holstein, Brown Swiss and Jersey Association (ANAFIBJ, Cremona, Italy), including AFC of 5,650,513 Holsteins born since 1993 and with first-calving date between 1996 and 2020, were used. Animals with unknown parents, AFC outside the range 18 to 36 mo, and gestation length outside the range 240 to 305 d were discarded from the dataset. Contemporary groups were defined as cows born in the same herd-year-season (**HYS**), and HYS with less than 10 individuals were removed. Two seasons of birth were defined, the first from October to April and the second from May to September. After all edits, 4,206,218 Holsteins distributed across 11,528 herds remained for subsequent statistical analyses.

Statistical Analyses

Fixed Effects. Numerous fixed effects were tested (HYS of birth and calving; herd-year of birth and calving; year-month of first insemination; month of first insemination; gestation length) and those to be

included in the analysis of AFC were identified through a forward stepwise approach based on Akaike Information Criterion, root mean square error, and coefficient of determination in R software version 4.0.3 (R Core Team, 2020). The final model was:

$$y_{ijk} = \mu + \text{HYS}_i + \text{GL}_j + e_{ijk},$$

where y_{ijk} is AFC; μ is the overall intercept of the model; HYS_i is the fixed effect of the i th herd-year-season of birth ($i = 168,135$ classes); GL_j is the fixed effect of the j th gestation length class ($j = 4$ classes: 240–260, 261–280, 281–290, and 291–305 d); and e_{ijk} is the random error.

Variance Component Estimation. The pedigree of cows with phenotypic information was traced back to at least 4 generations. Unknown ancestors were assigned to phantom parent groups based on animal origin and year of birth (296 genetic groups). Variance components were estimated with the Gibbs sampler THRGIBBS1F90 (Misztal et al., 2002; Misztal, 2008) with 160,000 iterations, a burn-in of 10,000, and a thinning rate of 10. The post-Gibbs analysis was carried out with the software POSTGIBBSF90 (Misztal et al., 2002) using the last 150,000 samples. The animal model used to estimate variance components accounted for the fixed effects previously identified; the animal additive genetic effect, fitted to the pedigree-based relationship matrix (**A**), was included as a random term. To reduce computational time, variance components of AFC were assessed in 3 different subsets each including data of animals from 300 herds randomly selected from the whole edited data. Estimated variance components of the 3 subsets were then averaged and the heritability (h^2) was calculated as

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2},$$

where σ_a^2 is the additive genetic variance, and σ_e^2 is the residual variance.

Breeding Value Estimation. Estimated breeding values were obtained with MiX99 software (Lidauer et al., 2019) using average variance components estimated in the previous step and the same aforementioned animal model, and were standardized to mean 100 and standard deviation (**SD**) 5 as undertaken for EBV of other functional traits published by ANAFIBJ. An EBV >100 identifies animals whose progeny are characterized by shorter AFC.

Genomic Prediction and Validation. Genomic validation was performed according to Finocchiaro et al. (2012). Estimated deregressed proofs (**EDP**) were obtained for 2 datasets: the full dataset with all re-

corded phenotypes in routine evaluation run (December 2021) and the reduced dataset (cut-off set to the year 2017). The SNP genotypes were collected using different DNA chip and missing SNP genotypes were imputed with PedImpute software (Nicolazzi et al., 2013) to a standard SNP panel of 69,084 markers. The EDP of the reduced dataset were the response variables to perform genomic evaluation and simultaneously estimate the effects of all SNP ($n = 69,084$) using the SNPblup model. The SNP effects were used to compute the direct genomic values (**DGV**) of 6,731 genotyped sires with daughters in the full dataset but without daughters in the reduced dataset (4,811 sires, validation set). Finally, current EDP were linearly regressed on DGV of validation sires and the coefficient of determination of this linear regression was the reliability of the DGV of validation sires (Galluzzo et al., 2022). Then, genomically EBV (**GEBV**) were estimated by blending DGV and EBV of the full run according to the following formula:

$$GEBV = \frac{EDC_C \times EBV + EDC_G \times DGV}{EDC_C + EDC_G},$$

where EDC_C is the conventional effective daughter contribution (Fikse and Banos, 2001), and EDC_G is the genomic effective daughter contribution (Petry and Ducrocq, 2011).

Approximate Genetic Correlations. Approximate genetic correlations of AFC with other production and functional traits evaluated by ANAFIBJ were estimated using Pearson correlations on a subset of GEBV of genotyped females born after 2015:

$$r_{AFC,y} = \frac{cov_{AFC,y}}{\sqrt{var_{AFC}var_y}},$$

where $cov_{AFC,y}$ is the covariance between GEBV of AFC and trait y , and var_{AFC} and var_y are the variances of GEBV of AFC and trait y , respectively. Proof for the traits investigated are expressed on a different scale based on conventional ANAFIBJ genetic and genomic evaluation. Before any standardization, proofs are subtracted to the average of base population, represented by individuals born in the previous 6 to 8 yr, inclusive. Production traits (i.e., milk, fat, and protein yield) are expressed in kilograms per lactation and higher values are desired. Linear traits proofs, including those considered in the present study (i.e., locomotion and udder depth), are standardized to mean 0 and SD 1, with higher proofs desired. Similar to production traits, fertility proofs are expressed on their original scale.

In particular, proofs for heifer and cow interval from first to last insemination are expressed in days, and proofs for heifer age at first insemination are expressed in months; in all instances, smaller values are desired. The GEBV of heifer and cow nonreturn rate at 56 d from the first insemination (binary traits) are unitless and higher values are desired. Finally, GEBV of the other functional traits, including dystocia, BCS, SCS, mastitis resistance, longevity (defined, in the present paper, as productive longevity, i.e., from first calving to culling), and direct and maternal gestation length are standardized to mean 100 and SD 5; in all instance proofs greater than 100 indicate individuals whose daughters will perform better than the average, except for direct and maternal gestation length for which intermediate proofs are the optimum.

Effect of Cow AFC and Sire EBV for AFC on Production and Functional Traits. The effect of AFC on first-lactation milk, fat, and protein yield, lifetime milk, fat, and protein yield, days open in first lactation, and longevity was quantified through ANOVA based on the following linear mixed model:

$$y_{ijk} = \mu + AFC_i + HYS_j + e_{ijk},$$

where y_{ijk} is the studied trait; μ is the overall intercept of the model; AFC_i is the fixed effect of the i th AFC class of the cow ($i = 16$ classes, with the first being a class from 18 to 21 mo, followed by 15 monthly classes); HYS_j is the random effect of the j th herd-year-season of birth group ($j = 17,989$ classes); and e_{ijk} is the random residual term. The best AFC class was the one that maximized first-lactation milk, fat, and protein yield, lifetime milk, fat, and protein yield, and longevity, and that minimized days open.

Subsequently, a second ANOVA was performed to investigate the effect of sire EBV for AFC on daughters' performance, namely first-lactation milk, fat, and protein yield, lifetime milk, fat, and protein yield, days open in first lactation, and longevity. For this purpose, only sires with an officially releasable EBV for the national genetic and genomic evaluation run were considered (i.e., sires with at least 30 daughters in at least 30 herds, and with EBV reliability $\geq 50\%$). Sire EBV for AFC were grouped in 7 classes: $-3: 83 \leq x \leq 87$; $-2: 88 \leq x \leq 92$; $-1: 93 \leq x \leq 97$; $0: 98 \leq x \leq 102$; $1: 103 \leq x \leq 107$; $2: 108 \leq x \leq 112$; $3: 113 \leq x \leq 117$, where x is the standardized sire EBV for AFC. Values above and below 0 identify sires that transmit lower and higher AFC to their progeny, respectively. The linear mixed model was as follows:

$$y_{ijk} = \mu + EBV_AFC_i + HYS_j + e_{ijk},$$

where y_{ijk} is the studied trait; μ is the overall intercept of the model; EBV_AFC_i is the fixed effect of the i th class of sire EBV for AFC ($i = 7$ classes); HYS_j is the random effect of the j th herd-year-season of birth group ($j = 17,989$ classes); and e_{ijk} is the random residual term. The analyses were performed using the software Echidna (Gilmour, 2018).

RESULTS AND DISCUSSION

Age at first calving decreased by 2 mo from 1996 to 2020, from 28.1 ± 2.9 to 26.1 ± 3.1 mo. The frequency (%) of heifers across monthly classes of AFC in 1996 and 2020 are presented in Table 1. When considering heifers calving in 1996, the highest frequency was observed for AFC between 26 and 27 mo, whereas in 2020 the highest frequency was observed between 24 and 25 mo. This trend followed the reduction of age at first insemination reported by Ferrari et al. (2023). Also, a similar trend has been reported by Hutchison et al. (2017), suggesting that both higher selection intensity for productive and reproductive traits, and improved management practices have indirectly enhanced AFC, allowing farmers to breed animals earlier.

Heritability and Approximate Genetic Correlations

Posterior mean of heritability of AFC, its lower and upper bounds of the 95% highest posterior density (HPD95), and the coefficient of additive genetic variation in the 3 subsets are reported in Table 2. Posterior mean of heritability ranged from 0.031 (subset 3) to 0.045 (subset 2), with the lowest estimate included in the HPD95 of subset 3 (0.020) and the greatest in the HPD95 of subset 2 (0.056). Coefficient of additive genetic variation ranged from 1.30% (subset 3) to 1.56% (subset 2), suggesting a genetic potential to reduce AFC

by 10 to 12 d relative to the population mean. Heritability estimates from the current study are in agreement with those of Heise et al. (2018) and Brzáková et al. (2019) in Holstein populations (0.10 and 0.031, respectively). In beef breeds, heritability of AFC has been estimated to be 0.18 and 0.23 in Aberdeen Angus and Charolais, respectively (Brzáková et al., 2020), i.e., higher than that reported for dairy breeds.

Approximate genetic correlations between cow GEBV of AFC and cow GEBV of production and functional traits are presented in Table 3. The AFC was positively and moderately correlated with production traits (from 0.39 with milk yield to 0.51 with protein yield), which is favorable considering that high GEBV of AFC are desirable. Similarly, Hutchison et al. (2017) assessed significant positive and favorable genetic correlations between AFC and milk, fat, and protein yield. Weak and moderate approximate genetic correlations were estimated between AFC and locomotion (0.13), and AFC and udder depth (0.40; Table 3), respectively, suggesting that, on average, AFC has an almost negligible effect on locomotion and a more pronounced effect on udder morphology. The approximate genetic correlations between GEBV of AFC and GEBV of fertility traits were favorable, being -0.17 between AFC and cow interval from first to last insemination, -0.43 between AFC and heifer interval from first to last insemination, and -0.73 between AFC and age at first insemination. These associations agree, in both direction and magnitude, with those reported by Brzáková et al. (2019) who assessed the genetic correlations between AFC and cow and heifer interval from first to last insemination in Czech Holsteins. The correlations of AFC with non-return rate at 56 d in heifers (0.23; Table 3) and age at first service in heifers corroborate with Muir et al. (2004). Because interest exists for farmers to shorten to some extent AFC, the aforementioned correlations indicate that genetic selection for AFC can actually improve interval fertility traits, thus resulting in favorable indirect response to selection. Therefore, proper emphasis should be placed to AFC and fertility in the national total merit selection index to achieve desired gains for all these traits, which could be achievable given the nonunity genetic correlations among them. Approximate genetic correlations between GEBV of AFC and GEBV of functional traits other than fertility were favorable and moderate to weak, with values from 0.14 (AFC and mastitis resistance) to 0.34 (AFC and longevity), except for the correlation between AFC and direct gestation length and BCS which was unfavorable, despite weak (-0.26 and -0.07 , respectively). These correlations agree with those retrieved from the literature (Berry and Cromie, 2009; Zavadilová and Štípková, 2013; Eastham et al., 2018), which reported

Table 1. Frequency (%) of heifers across age at first calving (AFC) in 1996 and 2020

AFC, mo	1996	2020
18–20	0.09	1.08
21	0.30	3.02
22	1.04	8.05
23	3.49	14.30
24	7.53	15.19
25	12.24	14.39
26	13.86	11.19
27	14.35	9.07
28	12.12	6.61
29	9.87	5.02
30	7.35	3.57
31	5.74	2.80
32	4.16	2.00
33–36	7.86	3.71

Table 2. Posterior mean of h^2 of age at first calving, lower and upper bounds of the 95% highest posterior density (HPD95), and genetic CV estimated in the 3 randomly selected subsets

Item	Herd, n	Animal, n	h^2	HPD95	CV (%)
Subset 1	300	101,110	0.037	0.028; 0.046	1.409
Subset 2	300	101,659	0.045	0.034; 0.056	1.563
Subset 3	300	103,000	0.031	0.020; 0.042	1.298

a favorable association between genetic selection to reduce AFC and animal functionality. These findings support the common choice of farmers to anticipate AFC, as this can lead to lower probability of subclinical mastitis after calving and greater survival to higher parities (Eastham et al., 2018). Shortening AFC by genetic selection could slowly worsen animal body condition, resulting in a noncomplete maturation at first calving. To handle this point, at farm level, the time at first insemination should be carefully evaluated along with growth rate and maturation state.

Maximizing Phenotypic Performances with AFC

Figures 1 and 2 depict the least squares means of first-lactation and lifetime milk, fat, and protein yield, days open in first lactation, and longevity across monthly classes of AFC. Cows with lower AFC produced less milk, fat, and protein in first lactation compared with animals calving at older age, in agreement with previous studies (Berry and Cromie, 2009; Mohd Nor et al., 2013; Eastham et al., 2018). Cows calving at 36 mo yielded 735 kg more milk, in first lactation, compared with cows whose AFC was from 18 to 21 mo. The same trend was observed for first-lactation protein and fat yield, which increased by ~25 and 33 kg, respectively, moving from 18 to 21 to 36 mo of AFC (Figure 1). This

trend is likely due to the fact that heifers calving at an earlier age might not have reached a proper body size and maturity, and thus an important amount of the ingested energy during first lactation is partitioned into growth rather than into milk production (Sejrsen et al., 2000; Hutchison et al., 2017). Days open in first lactation increased by ~13 d moving from 22 to 32 to 35 mo of AFC (Figure 1), in accordance with the trends reported by Ettema and Santos (2004) and Zavadilová and Štípková (2013). Moreover, Eastham et al. (2018) reported that the shortest calving interval between first and second lactation was observed when AFC occurred at 23 mo. Days open reduction reflects pregnancy rate improvement.

However, when considering lifetime performances, milk, fat, and protein yields were greater in heifers that first calved at lower age (22–24 mo) than heifers that calved later (35–36 mo). In particular, lifetime milk yield, protein yield, and fat yield decreased by 3,400, 105, and 128 kg, respectively, when AFC moved from 22 to 36 mo (Figure 2). Accordingly, Froidmont et al. (2013) reported the greatest lifetime milk, fat, and protein yield for cows with AFC from 22 to 26 mo than cows with later AFC. This favorable association can be mainly attributed to the longer productive life of cows with earlier AFC, as suggested by longevity in Figure 2d. Indeed, longevity decreased by ~140 d moving from

Table 3. Approximate genetic correlations of cow genomically enhanced breeding values for age at first calving with those for production and functional traits

Trait	Age at first calving	Interpretation
Milk yield	0.39	Favorable
Fat yield	0.40	Favorable
Protein yield	0.51	Favorable
Locomotion	0.13	Favorable
Udder depth	0.40	Favorable
Nonreturn rate at 56 d (cow)	0.18	Favorable
Nonreturn rate at 56 d (heifer)	0.23	Favorable
Interval from first to last insemination (cow)	-0.17	Favorable
Interval from first to last insemination (heifer)	-0.43	Favorable
Age at first service (heifer)	-0.73	Favorable
Dystocia maternal	0.25	Favorable
BCS	-0.07	Unfavorable
SCS	0.20	Favorable
Mastitis resistance	0.14	Favorable
Longevity	0.34	Favorable
Direct gestation length	-0.26	Unfavorable
Maternal gestation length	0.30	Unfavorable

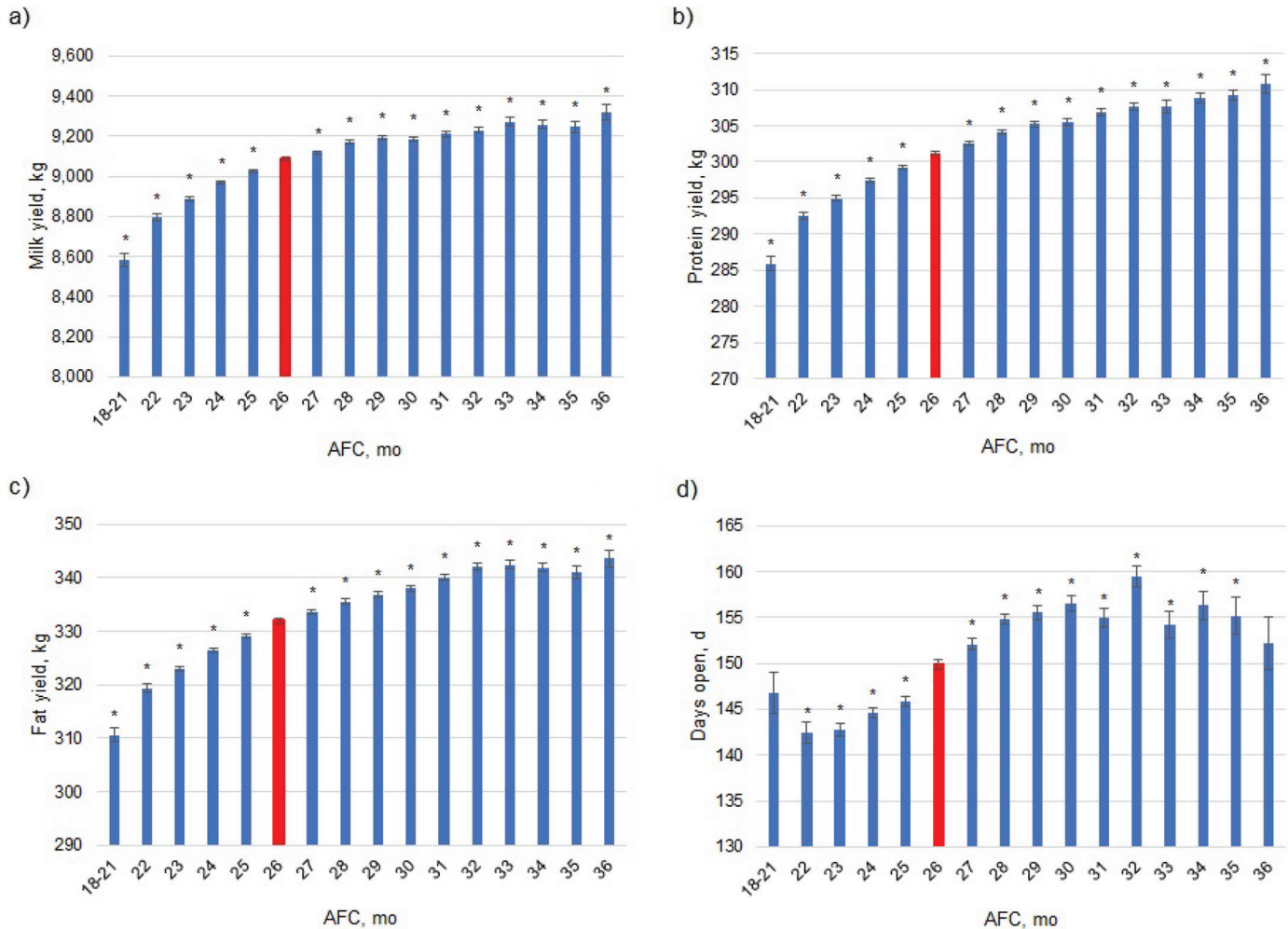


Figure 1. Least squares means and standard error of first-lactation (a) milk yield, (b) protein yield, (c) fat yield, and (d) days open for each class of age at first calving (AFC). Red bars represent the actual population mean class. Asterisks indicate the significance of the class with respect to the mean class ($P < 0.05$).

18 to 21 to 36 mo of AFC, and this trend agrees with findings of Hutchison et al. (2017). Similarly, Berry and Cromie (2009) observed that animals that first calved at 24 mo have greater survival probability to higher lactations than animals calving at 36 mo.

Maximizing Sires’ Genetic Potential with AFC

Figure 3 depicts the trend of sires’ GEBV for AFC by year of birth. Overall, AFC improved over years, suggesting that indirect selection for this trait occurred, in accordance with results of Amimo et al. (2006) and Hutchison et al. (2017).

Figures 4 and 5 show the trend of first-lactation and lifetime milk yield, fat yield, protein yield, longevity, and days open in first lactation across classes of sire EBV for AFC, where sires above 100 transmit lower

AFC. Considering first-lactation milk, fat, and protein yield (Figure 4), sires in class –3 had the lowest production, whereas sires in classes 1 or higher had the highest milk, fat, and protein yield, except for class 2 for milk and fat yield, and class 3 for milk and protein yield which did not differ significantly from the mean. This corroborates with the favorable genetic correlation between production traits and EBV for AFC (Table 3). The trend of days open across classes of sire EBV for AFC depicted in Figure 4 supports the moderate genetic association between AFC and other fertility traits, as indicated by Berry et al. (2014). Indeed, daughters’ fertility performances, in terms of days open in first lactation, deteriorates as bulls EBV for AFC decrease, with the exception of daughters of sires in class 3. Overall, it is worth noting that least squares means of production traits, days open in first lactation,

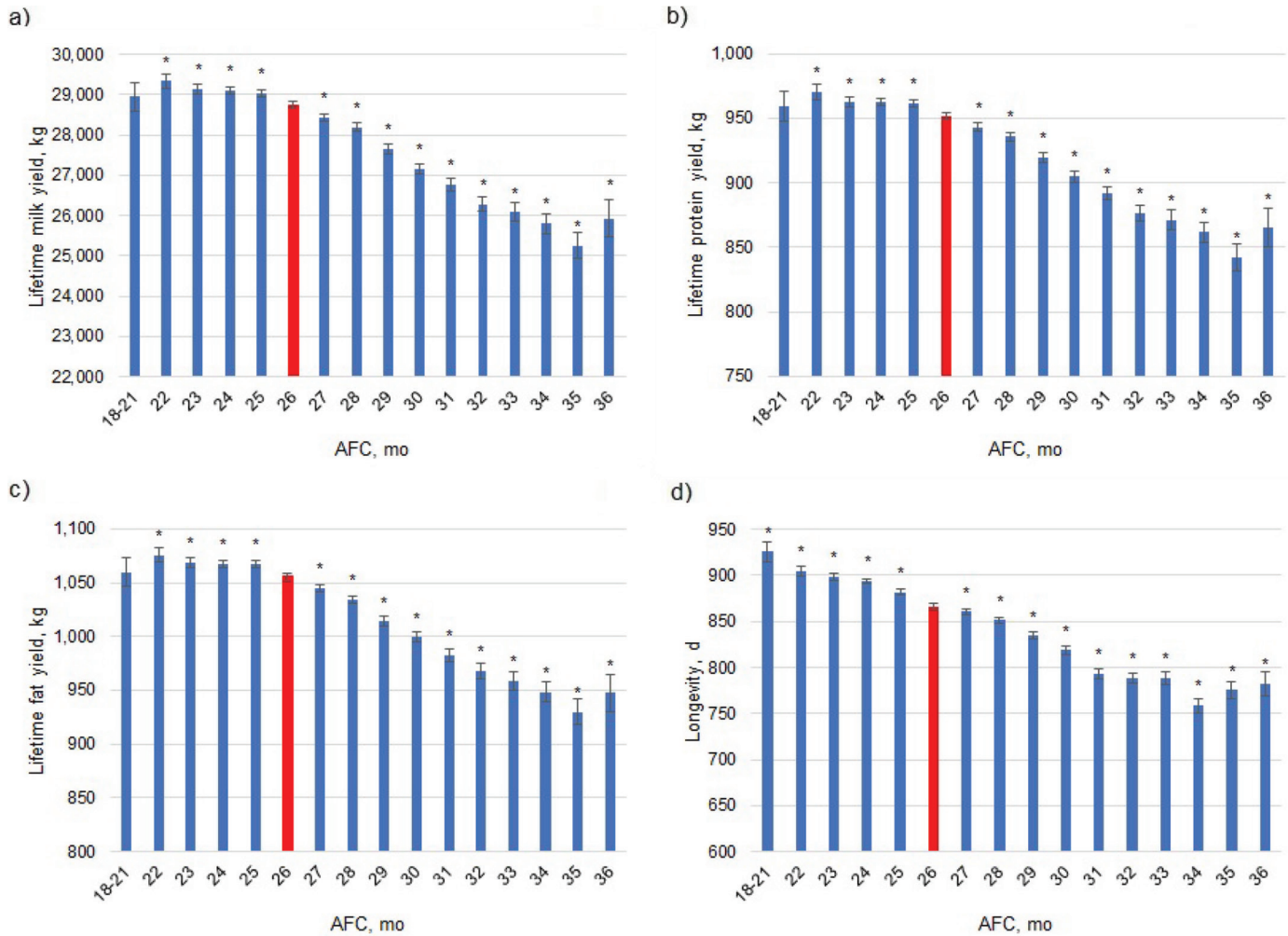


Figure 2. Least squares means and standard error of lifetime (a) milk yield, (b) protein yield, (c) fat yield, and (d) longevity for each class of age at first calving (AFC). Red bars represent the actual population mean class. Asterisks indicate the significance of the class with respect to the mean class ($P < 0.05$).

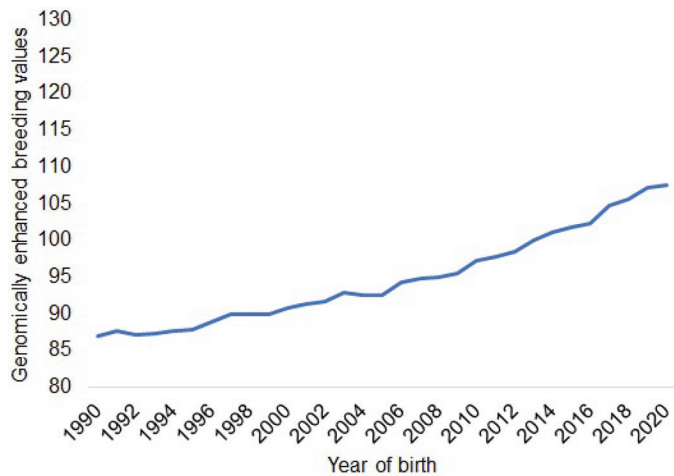


Figure 3. Trend of average sires' genomically enhanced breeding values for age at first calving by year of birth.

and longevity in class 3 (Figures 4 and 5) should be considered with caution due to the low number of sires in this class, which resulted in larger standard errors compared with the other sires EBV classes. The pattern of lifetime milk, protein, and fat yield across sires EBV classes for AFC appeared opposite to the trend observed in first lactation (Figure 5). Nevertheless, the biological effect of the differences among least squares means of production traits across classes of sires EBV for AFC was negligible, again with the exception of the last EBV class, which however has to be considered with caution due to the large standard error. For example, by excluding such class, the differences between the greatest and the lowest least squares means for lifetime protein and fat yield was less than 40 kg. Also, in terms of longevity (Figure 5d) the differences among least squares were small (less than 2 wk) and in many cases

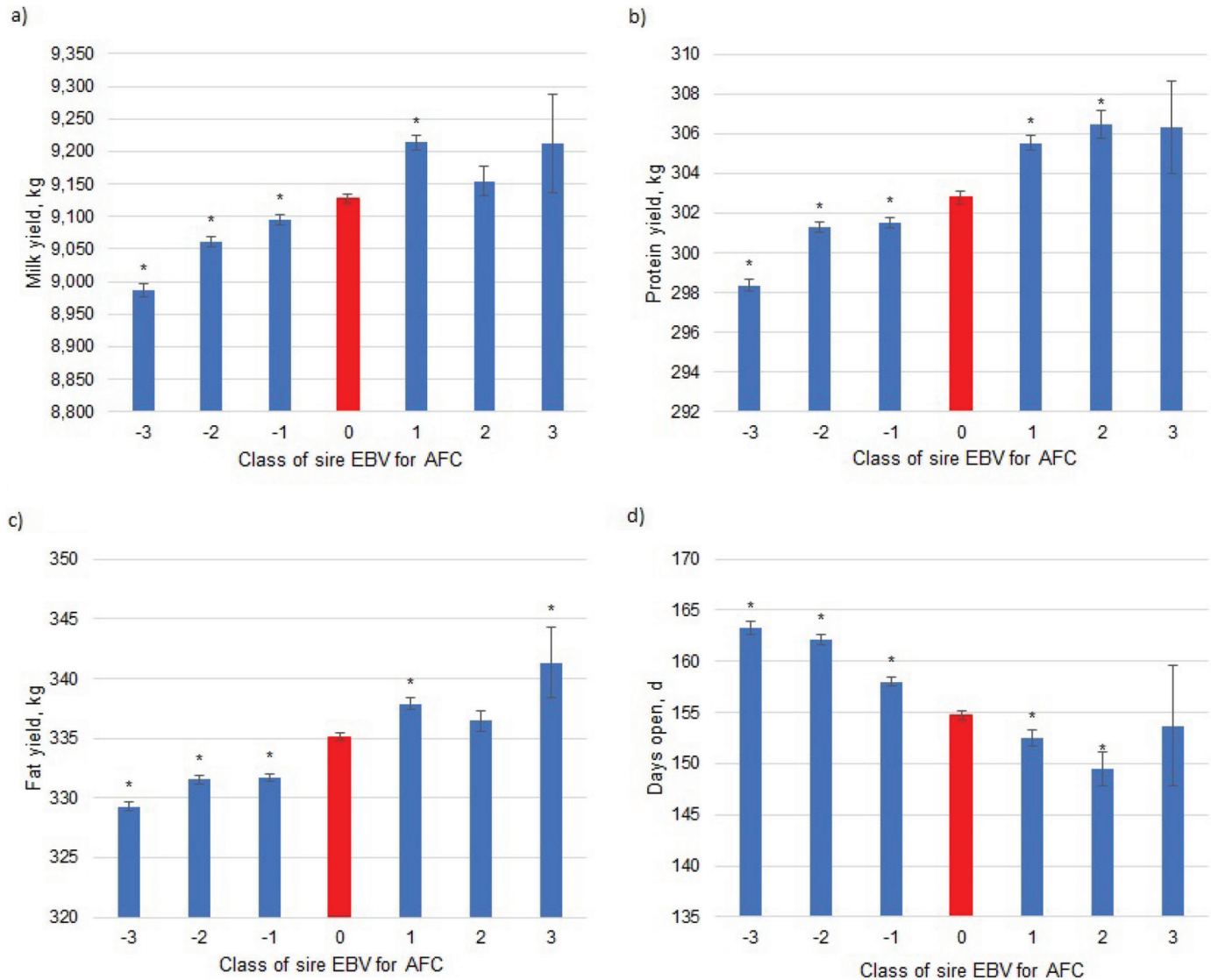


Figure 4. Least squares means and standard error of first-lactation (a) milk yield, (b) protein yield, (c) fat yield, and (d) days open across classes of sire EBV for age at first calving (AFC) standardized to mean 100 and SD 5. Classes are: -3: $83 \leq x \leq 87$; -2: $88 \leq x \leq 92$; -1: $93 \leq x \leq 97$; 0: $98 \leq x \leq 102$; 1: $103 \leq x \leq 107$; 2: $108 \leq x \leq 112$; 3: $113 \leq x \leq 117$. Red bars represent the standardized population mean class. Asterisks indicate the significance of the class with respect to the mean class ($P < 0.05$).

did not differ significantly from least squares means of the reference class of sires EBV for AFC.

CONCLUSIONS

Our results suggested that there is room to lower actual phenotypic mean of AFC in Italian Holstein population to maximize production performances, without negatively affecting fertility. Although relatively small, additive genetic variation exists for AFC, allowing the potential identification of elite sires for this trait. Any possible breeding strategies to improve AFC should be pursued, also considering the genetic

correlations between AFC and the other traits included in the national breeding objective. Indeed, approximate genetic correlations of AFC with milk, fat, and protein yield, and fertility traits were favorable. Finally, sires transmitting shorter AFC transmit also improved daughters' production performances in first lactation, yet the effect on lifetime productive lifetime length is small.

ACKNOWLEDGMENTS

This study was supported by "Latteco2 project, sotomisura 10.2 of the PSRN-Biodiversity 2020-2023"

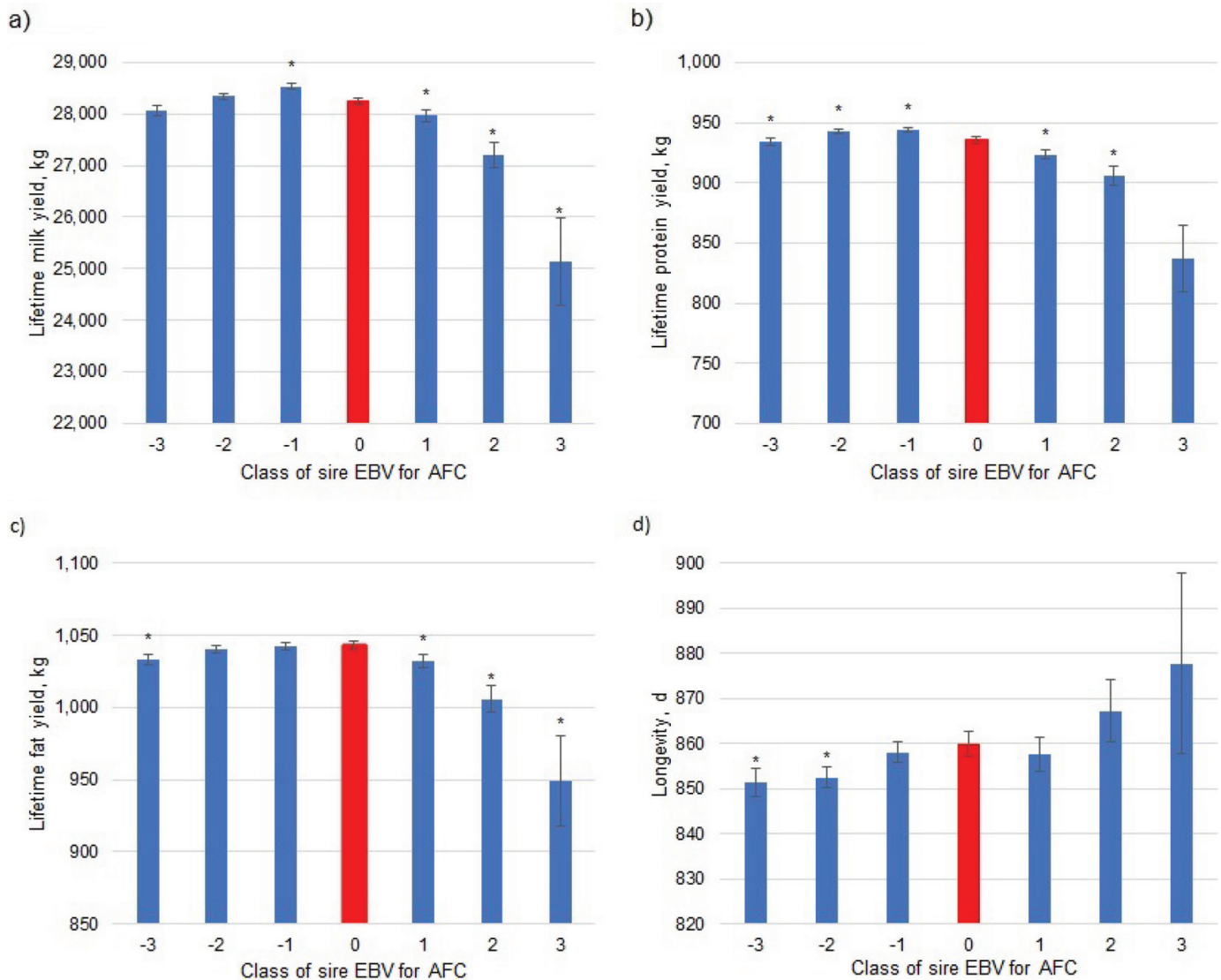


Figure 5. Least squares means and standard error of lifetime (a) milk yield, (b) fat yield, (c) protein yield, and (d) longevity across classes of sire EBV for age at first calving (AFC) standardized to mean 0 and SD 1. Classes are: -3: $83 \leq x \leq 87$; -2: $88 \leq x \leq 92$; -1: $93 \leq x \leq 97$; 0: $98 \leq x \leq 102$; 1: $103 \leq x \leq 107$; 2: $108 \leq x \leq 112$; 3: $113 \leq x \leq 117$. Red bars represent the standardized population mean class. Asterisks indicate the significance of the class with respect to the mean class ($P < 0.05$).








(MIPAAF, Rome, Italy; D.M. no. 465907 del 24/09/2021, project unique code J12C21004080005). Moreover, this study was carried out within the Agritech National Research Center and received funding from the European Union Next-GenerationEU (piano nazionale di ripresa e resilienza—missione 4 componente 2, investimento 1.4—D.D. 1032 17/06/2022, CN00000022). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them. The authors have not stated any conflicts of interest.

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