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Genomic prediction for latent variables related to milk fatty acid composition in Holstein, Simmental and Brown Swiss dairy cattle breeds

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Abstract

Genomic selection (GS) reports on milk fatty acid (FA) profiles have been published quite recently and are still few despite this trait represents the most important aspect of milk nutritional and sensory quality. Reasons for this can be found in the high costs of phenotype recording but also in issues related to its nature of complex trait constituted by multiple genetically correlated variables with low heritabilities. One possible strategy to deal with such constraint is represented by the use of dimension reduction methods. We analysed 40 individual FAs from Italian Brown Swiss, Holstein and Simmental milk through multivariate factor analysis (MFA) to study the genetics of milk FA-related latent variables (factors) and assess their potential use in breeding. A total of nine factors were obtained, and their genetic parameters were inferred under a Bayesian framework using two statistical approaches: the classical pedigree best linear unbiased prediction (ABLUP) and the single-step genomic BLUP (ssGBLUP). The resulting factorial solutions were able to represent groups of FAs with common origin and function and can be considered concise pathway-level phenotypes. The heritability (h^2) values showed relevant variations across different factors in each breed ($0.03 \leq h^2 \leq 0.38$). The accuracies of breeding values predicted were low to high, ranging from 0.13 to 0.72 and from 0.18 to 0.74 considering the pedigree and the genomic model, respectively. The gain in accuracy in genetic prediction due to the addition of genomic information was ~30% and ~5% in validation and training groups respectively, confirming the contribution of genomic information in yielding more accurate predictions compared to the traditional ABLUP methodology. Our results suggest that MFA in combination with GS can be a valuable tool in dairy cattle breeding and deserves to be further investigated for use in future breeding programs to improve cow's milk FA-related traits.

KEYWORDS

dairy cattle, genomic selection, milk fatty acids, multivariate factor analysis

1 | INTRODUCTION

The rationale for using DNA markers to improve the rate of genetic gain in livestock species was developed decades ago (Fernando & Grossman, 1989; Hayes, Bowman, Chamberlain, & Goddard, 2009; Smith, 1967; Soller & Beckmann, 1983), but the adoption of marker-assisted selection (MAS) by the industry has been limited for many years. Reasons can be found in the genotyping costs and the theoretical complexity of calculating breeding values incorporating multiple marker information (Hayes, Bowman, Chamberlain, & Goddard, 2009). Nowadays, these limitations are completely overcome. The development of efficient and cost-effective high-throughput genotyping analyses has made whole-herd genotyping common (Wiggans et al., 2017). At the same time, the possibility to make very accurate selection decisions when breeding values are early predicted from dense marker data (Meuwissen et al., 2001) has revolutionized the use of marker information in the breeding selection and it has decreed the birth of genomic selection (GS) concept (Meuwissen et al., 2001). Today the genomic evaluation is officially accepted and widely used in the dairy cattle industry (Hayes, Bowman, Chamberlain, & Goddard, 2009; Wiggans et al., 2017). Compared with the traditional BLUP, the use of genomic information (Genomic BLUP - GBLUP) can increase the reliability of estimation of breeding values (EBV) of young animals (VanRaden, 2008). More recently, in order to exploit the simultaneous use of the pedigree and genomic information, the single-step GBLUP (ssGBLUP) method was developed (Aguilar et al., 2010; Legarra et al., 2009) and successfully applied (Teissier et al., 2019). GS has deeply changed dairy cattle breeding, doubling the rate of genetic progress as a consequence of the reduced generation interval and increased reliability of genetic merit estimates (Weller et al., 2017; Wiggans et al., 2017). Apart from milk yield, fat and protein contents that remain the most important breeding goals, other traits are getting an increasing relevance and they can further benefit from the application of GS programs (Wiggans et al., 2017). The fatty acid (FA) profile affects milk technological properties, sensory quality and shelf life of dairy products (Campbell et al., 2003), and it has also potential effects on human health (Gibson, 2011). This has led the dairy industry to develop strategies for modifying the milk fat composition aiming to improve its nutritional quality. Deep knowledge of factors affecting milk FA composition is a prerequisite to achieving this goal (Arnould & Soyeurt, 2009; Glantz et al., 2009; Lock & Bauman, 2004; Pegolo, Cecchinato, Casellas, et al., 2016; Shingfield et al., 2013). Although the diet is considered the most important source of milk FA variability, a heritable variation in milk FA profile has been reported for dairy cattle, with heritability values ranging from ~5% to ~39% (Garnsworthy et al., 2010; Hein et al., 2018; Krag et al., 2013; Soyeurt et al., 2007), suggesting that selection on FA profile could contribute to obtain permanent modifications on nutritional and healthy milk properties.

Genomic studies carried out in dairy cattle on milk FA have been mainly focused on its genetic determinism (Bouwman et al., 2011, 2012; Buitenhuis et al., 2014; Cruz et al., 2019; Li et al., 2014; Palombo et al., 2018; Stoop, Schennink, et al., 2009), but quite recently some GS reports have been published (Freitas et al., 2020; Gebreyesus et al., 2019; Petrini et al., 2019). GS can accurately predict the genetic ability of an animal, without the need for recording phenotypic performance of its own or from close relatives, such as sibs or offspring (Meuwissen et al., 2001). Its use for the genetic improvement of the milk FA profile is particularly interesting. Indeed, although more rapid and cost-effective alternatives are possible (Marchi et al., 2011; Rutten et al., 2009; Soyeurt et al., 2007), the standard method for measuring the milk FA profile is the gas chromatography (GC) analysis which is expensive and time-consuming. This has precluded the inclusion of this trait in breeding schemes in the past. A further issue is represented by the FA covariance structure. FA profile consists of multiple genetically correlated variables generally with low heritabilities (Bastin et al., 2011). This can lead to the EBV with low accuracies, as already demonstrated for other complex traits (Aguilar et al., 2011; Guo et al., 2014). One possible strategy to deal with such constraint might be the use of multi-trait genomic prediction methods, which have proven to be effective (Aguilar et al., 2011; Calus & Veerkamp, 2011; Guo et al., 2014). Another option could be the use of dimension reduction methods. Multivariate statistics offer several techniques able to investigate complex covariance patterns by using a lower number of new explanatory variables. In this regard, multivariate factor analysis (MFA) was reported to be able to derive latent variables (factors) that represent groups of FAs with a common origin and function (Mele et al., 2016). Furthermore, the use of latent variables extracted by multivariate analysis has been already successfully applied to perform genetic and genomic analyses, providing evidence for their potential use in the study of milk major components in cattle breeding (Cecchinato et al., 2019; Dadousis et al., 2018; Palombo, Conte, et al., 2020) as well as in other species (Palombo, Gaspa, et al., 2020) or for other traits (Fatumo et al., 2019).

The present work aims to explore the feasibility of improving milk FA composition in three Italian cattle breeds by combining GS technology with novel phenotypes derived by the MFA method. For this purpose, considering the same populations of previous studies (Cecchinato et al., 2019; Palombo, Conte, et al., 2020), the breeding value prediction

for the new concise MFA phenotypes was carried out with the pedigree-based (ABLUP) and the single-step genomic evaluation (ssGBLUP) approaches.

2 | MATERIAL AND METHODS

2.1 | Data

The data used in our study included 965 Italian Brown Swiss (IBS), 408 Italian Holstein (IH) and 407 Italian Simmental (IS) cows with both genotypes and phenotypes available. A complete pedigree with 6,729, 3,929 and 10,203 animals was also available for IBS, IH and IS respectively. Milk and blood samples were collected for IBS in 83 farms located in Trento Province (north-eastern Italy), whereas for IH and IS the samples were collected from 10 farms located in the Friuli Venezia Giulia (FVG) region (north-eastern Italy). Milk samples collection was carried out within each breed in the same period. Information about cows and herds was obtained from the Superbrown Consortium of Trento and FVG Farm Breeders Association. Pedigree information was supplied by Italian Brown Swiss Cattle Breeders Association (www.anarb.it), Italian Friesian National Breeders Association (www.anafi.it) and Italian Simmental National Breeders Association (www.anapri.it). The inclusion criteria for the enrolment were clinically healthy cows. The average days in milk (DIM) were 171 (±102) for IBS, 167 (±63) for IH and 153 (±70) for IS (Table S1). Individual milk samples were collected, immediately refrigerated at 4°C without preservative, frozen within 2 hr and stored at −20°C for FA analysis. Peripheral blood samples were collected and stored at −20°C before DNA isolation. FA composition was determined by GC analysis using a GC2010 Shimadzu gas chromatographer (Shimadzu) equipped with a flame ionization detector and a highly polar fused-silica capillary column (Chrompack CP-Sil88 Varian, Middelburg, the Netherlands; 100 m, 0.25 mm i.d.; film thickness 0.20 μm). A total of 40 individual FAs were analysed in our study. Genomic DNA was isolated from whole blood using a GenElute Mammalian Genomic DNA Miniprep Kit (Sigma-Aldrich). After extraction, the quality and quantity of nucleic acid were assessed by electrophoresis and spectrophotometry. The DNA was stored at −20°C. Fifty nanograms of genomic DNA were sent to the genotyping facility for marker analysis. All IBS cows were genotyped with the Illumina BovineSNP50 v.2 BeadChip (Illumina Inc.), whereas for IH and IS breeds, 152 cows were genotyped with the BovineHD Genotyping BeadChip (Illumina), the others with the GeneSeek GGP Bovine 150K array from Neogene. The initial number of markers before the filtering steps was 37,419 in IBS, 121,645 SNPs in IH and 118,135 SNPs in IS. Quality control (QC) of SNP genotypes was carried out with PLINK software (Chang et al., 2015). QC was performed within each breed separately, excluding samples and/or markers that did not satisfy the following criteria: (a) call rate >90%, (b) minor allele frequency >0.05 and (c) no extreme deviation from Hardy–Weinberg proportions ($p > .00001$). Cows genotyped with the BovineHD chip were de-imputed to the lower density using BEAGLE software v4.0 (Browning & Browning, 2007) to generate uniform SNPchip densities, as already described (Palombo et al., 2018). The final data set consisted of 32,207 SNPs in 965 IBS animals, 121,330 SNPs in 408 IH animals and 117,770 SNPs in 407 IS animals, respectively. More details about data sampling, FA analyses and genotyping were reported by Pegolo, Cecchinato, Mele, et al. (2016), Palombo et al. (2018) and Cecchinato et al. (2019).

2.2 | Multivariate factor analysis (MFA)

An MFA was carried out on the correlation matrix of 40 variables consisting of individual FA measured in all 1,780 cows enrolled in the study, as detailed in Mele et al. (2016). The principal aim of MFA is to explain the (co)variance of a system defined by n traits (y_1, …, y_n) measured on observation units by deriving a smaller number p ($p < n$) of latent unobservable variables (X_1, …, X_p), named latent factors. Assuming that the variance of original variables can be decomposed into two components, one common to variables (communality) and one unique to each variable (uniqueness), the factor model decomposes the covariance matrix of the measured traits (S) as follows:

$$S = \mathrm{BB}' + \Psi$$

where BB′ and Ψ are the communality and the uniqueness (co) variance matrices, respectively (Morrison, 1976). According to the (co)variance model, the measured traits can be represented as a combination of p unobservable common factors (X) plus a unique variable (e):

$$y_1 = b_{11}X_1 + \ldots + b_{1p}X_p + e_1$$

$$y_n = b_{n1}X_1 + \ldots + b_{np}X_p + e_n$$

where X_j is the jth common factor, b_{ij} are factor coefficients (or loadings, i.e., correlations between the jth common factor) and e_i is the ith residual specific variable (Morrison, 1976). Loadings are the elements of the B matrix used in the factor model. Common factors generate covariances between original variables, whereas the residual specifically contributes only to the individual variation. To assess the sampling adequacy of the data and quantify the difference between the Pearson and partial correlations of the 40 variables, the Kaiser measure of sampling adequacy (MSA) was applied. A high MSA value

indicates a latent structure existing in the data (Dziuban & Shirkey, 1974; Kaiser & Rice, 1974). The empirical threshold of 0.80 flags a data set as particularly suitable for MFA (Macciotta et al., 2012). The number of extracted factors was selected based on eigenvalues, the relationships with the original variables, and the amount of explained variance. More in details, we retained factors with eigenvalues greater than 1, with a reasonable proportion of variance explained by the latent variables, identified in ~70% of the total variance and allowing an optimal readability/interpretation of the original variables. To identify a simple structure, a *varimax* factor rotation was used. Only variables exhibiting correlations ≥ |0.55| were included in each factor, in other words the interpretation of the extracted factors was assessed considering only the variables that exhibited a moderate/high correlation with the factors. The MFA analysis was performed using the *factanal* function in R *stats* package (R Core Team, 2018).

2.3 | Variance component estimation

Variance components of factor scores were carried out separately for each breed with a Bayesian approach implemented in the GIBBS2F90 module from the BLUPF90 family of programs (Misztal et al., 2014). Settings of the Gibbs sampling were assessed by inspection of trace-plots and the Geweke's convergence diagnostic of the chain (Geweke, 1992). The following settings were used: 50,000 iterations, a burn-in period of 5,000 iterations, sample values saved every 10 cycles. Variance components and heritability value were retrieved from the posterior means using a single-trait model. Data were analysed with the following mixed linear model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Qf} + \mathbf{Za} + \mathbf{e}$$

where **y** is the vector of investigated factor scores; **X** is the incidence matrix linking records to fixed effects and **b** is the related vector. **X** has dimension $n \times b$, where n is the number of observations in the data set and b is the number of fixed effect parameters in the model. The fixed effects considered in the model were DIM (five classes, considering intervals of 60 days) and parity (three classes, considering ordinal values of 1 for first calving, two for second calving, three for third or greater calving). **Q** is the incidence matrix for herd as random effect, and **f** is the related vector (83 classes in IBS, five and six in IH and IS respectively) distributed as $\sim N(0, \mathbf{I}\sigma^2_{\text{herd}})$, where **I** is an identity matrix and σ^2_{herd} is the associated variance component. **Q** has dimension $n \times f$, where f is the number of random effect coefficients in the model. **Z** is the incidence matrix for random genetic effects, relating records to animals, and **a** is the vector of breeding values (**a** distributed according to the relationship matrix used); and **e** is the vector of random residuals distributed as $\sim N(0, \mathbf{I}\sigma^2_{\text{e}})$, where σ^2_{e} is the residual variance. **Z** has dimension $n \times m$, where m is the total number of animals in relationship matrix. Statistics and distribution of records for the effects considered in the analysis are reported in Table S1. The additive genetic effect was modelled using two genetic (co)variance structures. In the first model (ABLUP), the pedigree relationship matrix (**A**) was used and the animal effect was distributed as $\sim N(0, \mathbf{A}\sigma^2_{\text{a}})$, where σ^2_{a} is the additive genetic variance. In the second model, a blend of genomic and pedigree relationship matrix (**H**, ssGBLUP) was used with **a** distributed as $\sim N(0, \mathbf{H}\sigma^2_{\text{a}})$. From whole pedigree, three generations were traced back (3,574, 2,012 and 1,703 animals for IBS, IH and IS respectively). The **H** matrix was computed according to VanRaden (2008) and Aguilar et al. (2010). The inverse of **H** has the following structure:

$$\boldsymbol{H}^{-1} = \boldsymbol{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \boldsymbol{G}^{-1} - \boldsymbol{A}_{22}^{-1} \end{bmatrix}$$

where $\mathbf{A}_{22}$ is the sub-matrix of **A** for the genotyped animals. To avoid singularity, **G** was blended with 5% of $\mathbf{A}_{22}$ using the default options in the BLUPF90 family of programs (VanRaden, 2008; Vitezica et al., 2011). The heritability (h^2) and the intra-herd heritability (h^2_{ih}) for each breed were computed respectively as:

$$h^2 = \frac{\sigma^2_{\text{a}}}{(\sigma^2_{\text{a}} + \sigma^2_{\text{herd}} + \sigma^2_{\text{e}})}$$

$$h^2_{\text{ih}} = \frac{\sigma^2_{\text{a}}}{(\sigma^2_{\text{a}} + \sigma^2_{\text{e}})}$$

Moreover, variance explained by herd (h_{herd}) was computed as:

$$h_{\text{herd}} = \frac{\sigma^2_{\text{herd}}}{(\sigma^2_{\text{a}} + \sigma^2_{\text{herd}} + \sigma^2_{\text{e}})}$$

2.4 | Breeding value predictions

Breeding values were predicted by using the ABLUP and the ssGBLUP approaches. Accuracy of breeding values animals was estimated as Henderson (1975) and Hayes, Bowman, Chamberlain, Verbyla, et al. (2009):

$$\text{accuracy} = \sqrt{1 - \text{SEP}^2 / \sigma^2_{\text{a}}}$$

where SEP is the standard error of prediction, derived from the diagonal element of the left-hand side inverse of the mixed model equations (Henderson, 1975). A fair comparison among

accuracies obtained in the two different methods was ensured by the use of the same variance components (the ones estimated with ABLUP) in breeding value predictions and accuracy computation. A resampling strategy was applied to create a fivefold cross-validation scheme. Briefly, only young animals (i.e., at first lactation) were used to create five validation sets (~20% of the total population). Thus, the genomic predictions analysis was performed five times for each trait (i.e., factor), the phenotypic records of the validation animals were set to missing and all remaining individuals with phenotypes and genotypes (80% of the total population) were used as the training data set. The relationship of individuals in the cross-validation groups was checked (data not shown) in order to verify a homogeneous structure among the training and validation sets. The prediction accuracies were reported as the average values of the five replicates (folds). The size of training and validation groups was 772 and 193 animals for IBS, 327 and 81 animals for both IH and IS breed.

3 | RESULTS

3.1 | Milk FA factors

The overall pattern of milk FA composition consisted of 40 individual FA (constituted by 19 saturated FA, 12 monounsaturated FA and nine polyunsaturated FA). The MFA was able to extract nine latent factors, accounting for about 71% of the total variance (Table S2). The suitability of the data set for MFA was checked by calculating the MSA. In the present study, the MSA value was 0.82, higher than the empirical threshold of 0.80 that flags a data set as particularly suitable for MFA (Macciotta et al., 2012). The proposed factor classification is reported in Table 1.

3.2 | Genetic parameters

Relevant variations among different factors were detected in terms of heritability (h^2) values (Table 2). The same pattern

TABLE 1 Proposed classification for the nine factors extracted

Factor	Fatty acids[a]	Name assigned
Factor1	C18:1t6−8, C18:1t9, C18:1t10, C18:1c12, C18:1t16	Biohydrogenation
Factor2	C8:0, C10:0, C12:0, C14:0, C18:1c9	Neosynthesis/ desaturation_1
Factor3	C15:0iso, C16:0iso, C16:1t9, C18:1t11, C18:2c9t11	VA/CLA
Factor4	C17:0iso, C17:0anteiso, C17:0, C17:1c9	C17 Metabolism
Factor5	C4:0, C6:0, C8:0	Short-chain FA
Factor6	C14:1c9, C16:1c9, C18:0	Minor SCD products
Factor7	C20:3n6, C20:4n6	Arachidonic acid synthesis
Factor8	C11:0, C13:0, C15:0	OCFA metabolism
Factor9	C16:0, C18:1c9	Neosynthesis/ desaturation_2

[a]Fatty acids showing a correlation greater than |0.55| for that factor

TABLE 2 Mean (standard deviation in parentheses) values of heritability for factors obtained from milk fatty acid composition in Italian Brown Swiss (IBS), Italian Holstein (IH) and Italian Simmental (IS) breeds

		IBS		IH		IS	
		Matrix[a]		Matrix[a]		Matrix[a]	
Factor	Trait	A	H	A	H	A	H
F1	Biohydrogenation	0.06 (±0.02)	0.07 (±0.01)	0.11 (±0.06)	0.05 (±0.03)	0.03 (±0.01)	0.03 (±0.02)
F2	Neosynthesis/ desaturation_1	0.12 (±0.02)	0.10 (±0.02)	0.19 (±0.03)	0.08 (±0.02)	0.11 (±0.02)	0.17 (±0.03)
F3	VA/CLA	0.09 (±0.02)	0.06 (±0.01)	0.05 (±0.03)	0.05 (±0.01)	0.07 (±0.01)	0.06 (±0.01)
F4	C17 Metabolism	0.09 (±0.02)	0.09 (±0.01)	0.05 (±0.01)	0.05 (±0.01)	0.05 (±0.01)	0.07 (±0.03)
F5	Short-chain FA	0.03 (±0.00)	0.04 (±0.01)	0.15 (±0.02)	0.09 (±0.01)	0.21 (±0.04)	0.24 (±0.07)
F6	Minor SCD products	0.32 (±0.04)	0.27 (±0.01)	0.38 (±0.10)	0.24 (±0.05)	0.21 (±0.02)	0.24 (±0.04)
F7	Arachidonic acid synthesis	0.10 (±0.04)	0.09 (±0.01)	0.10 (±0.02)	0.08 (±0.03)	0.05 (±0.01)	0.06 (±0.01)
F8	OCFA metabolism	0.08 (±0.02)	0.04 (±0.02)	0.08 (±0.03)	0.09 (±0.03)	0.20 (±0.09)	0.29 (±0.09)
F9	Neosynthesis/ desaturation_2	0.31 (±0.03)	0.19 (±0.01)	0.27 (±0.04)	0.21 (±0.02)	0.13 (±0.04)	0.17 (±0.05)

[a]A, pedigree relationship matrix; H, pedigree and genomic relationship matrices are blended into a single matrix.

was detected considering the intra-herd heritability (h^2_{ih}; Table S3). Overall, genomic heritability showed lower values compared with ABLUP estimates for IBS and IH breed, whereas an opposite trend was detected in IS breed. More in details, ABLUP heritabilities ranged from 0.03 to 0.32 in IBS, from 0.05 to 0.38 in IH and from 0.03 to 0.29 in IS, respectively. The ssGBLUP estimates ranged from 0.04 to 0.28 in IBS, from 0.05 to 0.24 in IH and from 0.05 to 0.29 in IS, respectively. The highest heritability value ($0.24 \leq h^2 \leq 0.38$) was obtained for factor 6 ("Minor SCD products") using the two tested matrices both in IBS and IH, whereas in IS the highest values ($0.21 \leq h^2 \leq 0.29$) were observed for factors 5 ("Short-chain FA") and 6 ("Minor SCD products") using **A** matrix and in factor 8 ("OCFA metabolism") using the **H** matrix. The lowest ($0.03 \leq h^2 \leq 0.04$) estimates were obtained for factor 5 ("Short-chain FA") and 8 ("OCFA metabolism") in IBS, for factor 4 ("C17 Metabolism") in IH, and factor 1 ("Biohydrogenation") in IS, respectively. Differences among h^2 estimates were mainly due to changes in the additive genetic components (σ^2_a) as shown in Table S4. The herd contribution (h_{herd}) to the total phenotypic variance (Table S5) ranged from low (0.20) to high (0.65) across all different models and factors. The exceptions are the factor 6 ("Minor SCD products") in IBS and factor 5 ("short-chain FA") in IH where a very low herd contribution was observed ($0.06 < h_{herd} < 0.09$), as well as the factor 4 ("C17 Metabolism") in IH and IS, and factor 1 ("Biohydrogenation") in IS where very high herd contribution ($h_{herd} > 0.65$) were detected.

3.3 | Genomic predictions

Accuracies of breeding values (EBV) ranged from 0.30 to 0.74 and from 0.15 to 0.48 in training and validation datasets, respectively. Detailed results of EBV accuracies obtained with the ABLUP and ssGBLUP approaches for each factor and breed were reported in Table 3. Considering all factors and groups, higher EBV accuracies (+ ~20%) were obtained with the combined relationship matrix (**H**) compared to the pedigree matrix (**A**). In particular, the use of the ssGBLUP approach increases the accuracy values more in the validation sets (+ ~35%) than in the training ones (+ ~5%), that corresponding to the younger cohorts in our populations. Focusing on a single factor and considering each breed separately, the largest accuracy values were observed for factor 6 ("Minor SCD products") and factor 9 ("Neosynthesis/desaturation_2") in IBS and IH breeds whereas in IS breed the largest values were detected in factor 6 ("Minor SCD products") and factor 8 ("OCFA metabolism"). The lowest accuracy values were observed in factor 5 ("Short-chain FA") and factor 8 ("OCFA metabolism") in IBS, in factor 3 ("VA/CLA") and factor 8 ("OCFA metabolism") in IH, in factor 1 ("Biohydrogenation") and factor 7 ("Arachidonic acid synthesis") in IS breed, respectively.

4 | DISCUSSION

4.1 | Factor interpretation

The latent factor pattern (i.e., the correlations between each factor and FA) was quite easy to read. In particular, few FA exhibited correlations $\geq |0.55|$ in each factor, while the remainder showed a very low correlation (in many cases close to zero). If we examine the pattern across factors, we can see that each variable was highly correlated with only one factor and poorly with the others. This type of simple structure is an indicator of the suitability of factor model assumptions for the kind of data analysed (Morrison, 1976).

The first latent factor was named "Biohydrogenation" because it was positively related to some products of rumen biohydrogenation (C18:1t6–8, C18:1t9, C18:1t10, C18:1c12 and C18:1t16; Table S2). Vaccenic acid (C18:1t11), which represents the principal product of biohydrogenation, did not show a large loading on this factor, and it was included in factor 3. During biohydrogenation, linoleic acid (C18:2c9,c12) and α-linolenic (C18:3c9,c12,c15) present in dietary lipids are hydrogenated by rumen bacteria to stearic acid (C18:0), with the production of a large spectrum of cis and trans isomers of C18:1, including C18:1t6–8, C18:1t9, C18:1t10, C18:1t16 and C18:1c12 (Shingfield et al., 2010). The same factor was obtained by Mele et al. (2016) and Conte et al. (2016) in previous works on Italian Brown and Italian Holstein respectively.

The second latent factor was positively associated with medium-chain SFA (C8:0 to C14:0) and negatively C18:1c9 (Tables 1 and S2). All FA showing positive correlations with this factor share a common metabolic origin, being de novo synthesized in the mammary gland from acetate by the FA synthase enzyme (Chilliard et al., 2000). On the contrary, C18:1c9, which showed negative loadings for factor 2, is related to the activity of the stearoyl Co-A desaturase enzyme (SCD) that catalyses the desaturation of the carbon chain at the Δ9 position (Ntambi, 1999). Therefore, factor 2 was named "Neosynthesis/desaturation_1." All FA related to this factor are involved in the regulation of milk fat fluidity. In fact, according to Chilliard et al. (2000), selective esterification of de novo short-chain FA (from 4 to 14 carbons) and C18:1c9 to the glycerol backbone at sn-3 position plays a pivotal role in the regulation of milk fat fluidity.

The third latent factor was positively related to vaccenic acid (VA - C18:1t11) and its mammary desaturation product, C18:2c9,t11, which represent the most abundant CLA in milk (Table S2). So, the factor was named "VA/CLA." Several studies have demonstrated that more than 80% of milk C18:2c9,t11 is due to mammary desaturation of C18:1t11, synthesized during rumen biohydrogenation of dietary PUFA (Shingfield et al., 2010). The same factor was extracted by Mele et al. (2016), confirming a different association of SCD

TABLE 3 Mean (standard deviation in parentheses) values of estimated breeding and genomic breeding value accuracy of factors obtained from milk fatty acid composition using the two relationship matrices in Italian Brown Swiss (IBS), Italian Holstein (IH) and Italian Simmental (IS) breeds

		Training groups			Validation groups	
		Matrix[a]			Matrix[a]	
Factor	Trait	A	H		A	H
F1	Biohydrogenation	0.37 (±0.06)	0.42 (±0.06)	IBS	0.22 (±0.04)	0.31 (±0.04)
F2	Neosynthesis/ desaturation_1	0.43 (±0.04	0.47 (±0.04)		0.25 (±0.02)	0.34 (±0.02)
F3	VA/CLA	0.49 (±0.04)	0.54 (±0.04)		0.29 (±0.02)	0.39 (±0.02)
F4	C17 Metabolism	0.51 (±0.05)	0.55 (±0.04)		0.30 (±0.02)	0.39 (±0.02)
F5	Short-chain FA	0.31 (±0.01)	0.35 (±0.01)		0.18 (±0.01)	0.26 (±0.01)
F6	Minor SCD products	0.61 (±0.03)	0.65 (±0.03)		0.34 (±0.02)	0.46 (±0.02)
F7	Arachidonic acid synthesis	0.50 (±0.08)	0.55 (±0.08)		0.29 (±0.03)	0.39 (±0.03)
F8	OCFA metabolism	0.37 (±0.05)	0.42 (±0.05)		0.22 (±0.03)	0.31 (±0.03)
F9	Neosynthesis/ desaturation_2	0.67 (±0.03)	0.71 (±0.03)		0.36 (±0.02)	0.49 (±0.02)
F1	Biohydrogenation	0.55 (±0.04)	0.59 (±0.03)	IH	0.21 (±0.01)	0.30 (±0.01)
F2	Neosynthesis/ desaturation_1	0.64 (±0.03)	0.67 (±0.02)		0.23 (±0.01)	0.34 (±0.02)
F3	VA/CLA	0.36 (±0.03)	0.39 (±0.07)		0.13 (±0.03)	0.20 (±0.03)
F4	C17 Metabolism	0.49 (±0.03)	0.53 (±0.05)		0.18 (±0.02)	0.27 (±0.03)
F5	Short-chain FA	0.42 (±0.01)	0.45 (±0.03)		0.16 (±0.01)	0.23 (±0.02)
F6	Minor SCD products	0.72 (±0.02)	0.74 (±0.06)		0.26 (±0.02)	0.37 (±0.03)
F7	Arachidonic acid synthesis	0.47 (±0.05)	0.50 (±0.04)		0.18 (±0.01)	0.26 (±0.02)
F8	OCFA metabolism	0.39 (±0.04)	0.43 (±0.08)		0.14 (±0.03)	0.22 (±0.04)
F9	Neosynthesis/ desaturation_2	0.65 (±0.02)	0.67 (±0.05)		0.24 (±0.02)	0.34 (±0.03
F1	Biohydrogenation	0.35 (±0.05)	0.34 (±0.10)	IS	0.15 (±0.03)	0.18 (±0.05)
F2	Neosynthesis/ desaturation_1	0.55 (±0.15)	0.58 (±0.14)		0.25 (±0.07)	0.30 (±0.07)
F3	VA/CLA	0.44 (±0.03)	0.45 (±0.02)		0.20 (±0.01)	0.24 (±0.01)
F4	C17 Metabolism	0.46 (±0.05)	0.48 (±0.05)		0.21 (±0.03)	0.26 (±0.02)
F5	Short-chain FA	0.54 (±0.05)	0.54 (±0.02)		0.25 (±0.02)	0.29 (±0.01)
F6	Minor SCD products	0.62 (±0.02)	0.62 (±0.04)		0.29 (±0.01)	0.33 (±0.02)
F7	Arachidonic acid synthesis	0.37 (±0.03)	0.40 (±0.06)		0.17 (±0.02)	0.21 (±0.03)
F8	OCFA metabolism	0.56 (±0.11)	0.58 (±0.11)		0.26 (±0.04)	0.30 (±0.05)
F9	Neosynthesis/ desaturation_2	0.53 (±0.07)	0.57 (±0.03)		0.25 (±0.04)	0.30 (±0.02)

[a]A, pedigree relationship matrix; H, pedigree and genomic relationship matrices are blended into a single matrix.

activity and the unsaturation degree of the substrate, as proposed by the same authors.

The fourth factor was positively correlated with all FA with 17 C (C17:0iso, C17:0anteiso, C17:0, C17:1c9) and was named "C17:0 metabolism" (Tables 1 and S2). Interestingly, all these FAs were not associated with the other OCFA, as previously observed by Fievez et al. (2003). This suggests that the metabolic role of C17:0 in milk fat secretion differs from the other OCFA, probably due to its affinity with the mammary enzymes (Palmquist et al., 2004; Vlaeminck et al., 2006).

The fifth latent factor was named "Short-chain FA" because it was positively correlated with the contents of C4:0,

C6:0, and C8:0 (Tables 1 and S2). All FAs from C4 to C14 are endogenously synthesized in the mammary gland by acetyl-CoA carboxylase and FA synthase enzymes (Chilliard et al., 2000). As just revealed by Mele et al. (2016) and Conte et al. (2016), FAs from C10:0 to C14:0 were associated with a different factor than FA from C4:0 to C8:0, confirming the hypothesis that differences may be present in the endogenous synthesis of even-chain FA according to the carbon chain length. Unlike medium-chain FA (from C10:0 to C14:0), short-chain FA may be partly synthesized in the mammary gland by metabolic pathways not dependent on acetyl-CoA carboxylase (Chilliard et al., 2007; Mele et al., 2016). Thanks to factor analysis, we highlight this metabolic difference by extracting two different latent variables, one representing short-chain and one representing medium-chain FA metabolism.

Latent factor 6 was positively correlated with C14:1c9 and C16:1c9 and negatively with stearic acid (C18:0; Tables 1 and S2). The first two FA derive from SCD activity on the respective SFA (C14:0 and C16:0). On the contrary, the SCD enzyme acts on C18:0 as a preferred substrate (Ntambi, 1999). Therefore, high scores in factor 6 suggest high activity of the SCD enzyme, which results in high contents of C14:1c9 and C16:1c9, and a low content of 18:0 in milk fat. Since oleic acid (C18:1c9), which represents the principal product of SCD activity, is associated with factor 2, this factor was named "Minor SCD products."

The seventh factor was positively correlated with C20:3n6 and C20:4n6 (arachidonic acid), which represents the substrate and product of Δ5-desaturase (encoded by *FADS1* gene), respectively (Nakamura & Nara, 2004; Tables 1 and S2). For this reason, the factor was named "Arachidonic acid synthesis." Δ-5 desaturase is crucial in the endogenous synthesis of long-chain polyunsaturated FA from the precursor essential FAs, linoleic and α-linolenic acid, obtained from the diet. Ibeagha-Awemu et al. (2014) revealed the presence of a SNP within *FADS1*, associated with the level of C20:3n6 and C20:4n6. To our knowledge, this is the first time that a factor describing the synthesis of long-chain polyunsaturated FA was extracted.

Latent factor 8 was positively associated with odd-chain FA C11:0, C13:0 and C15:0 and was therefore named "OCFA metabolism" (Tables 1 and S2). These FAs are mainly synthesized by rumen microbes, with a repeated condensation of malonyl-coenzyme A using propionate as primer (Vlaeminck et al., 2006). They are abundant in the rumen when diets are rich in non-structural carbohydrates.

Finally, the ninth factor was positively and negatively associated with C18:1c9 and C16:0 (Tables 1 and S2), respectively. Palmitic acid is the last step of FA biosynthesis, so it represents a good parameter to estimate the mammary synthesis related to acetate by the FA synthase enzyme (Chilliard et al., 2000). On the contrary, C18:1c9, with C18:0, is the most representative FA of extra-mammary origin (blood and adipose tissue; Conte et al., 2017; Loften et al., 2014). Douglas et al. (2007) found a different level of C16:0 and C18:1c9 with the progression of the lactation. However, C16:0 and C18:1c9 showed an opposite trend in response to the energetic balance of dairy cow as demonstrated by several works (Dann et al., 2005; Kay et al., 2005; Loften et al., 2014; Stoop, Bovenhuis, et al., 2009). Immediately after calving, the cow is usually in a negative energy balance, so mammary de novo synthesis of FAs is reduced, and milk FAs derived principally from extra-mammary sources. In this situation, the relative abundance of circulating C18:1c9 is higher. On the contrary, C16:0 increases in milk fat with the progress of lactation, when the energy balance becomes positive (Conte et al., 2010).

4.2 | Heritability estimates

In general, our heritability estimates were mostly low ($h^2 < 0.20$), but moderate values were detected for some factors, notably for factor 6 ("Minor SCD products") and 9 ("Neosynthesis/desaturation_2"; Table 2). Our results are comparable with those reported in a previous study where heritabilities were estimated from latent variables related to the milk FA profile (Cecchinato et al., 2019). Overall, the heritability estimates of our FA factors agreed with those of the individual traits comprising each factor. For instance, the heritability of factor 2 ("Neosynthesis/desaturation_1"; ~0.11 in IBS, ~0.12 in IH, ~0.13 in IS) was in line not only with the estimates obtained for "De novo FA" factor (~0.14) reported by Cecchinato et al. (2019) but also for C8:0, C10:0, C12:0 and C14:0 single FA (0.10–0.24) and for the "De Novo FA" group (~0.15) described by Pegolo, Cecchinato, Mele, et al. (2016) and Garnsworthy et al. (2010), respectively. The moderate heritability of factor 6 ("Minor SCD products"; ~0.29 in IBS and IH, ~0.24 in IS) was also comparable to that reported in the previously cited works (Cecchinato et al., 2019; Pegolo, Cecchinato, Casellas, et al., 2016) and more precisely for the "Desaturation" factor (~0.31), for C14:1c9, C16:1c9 and C18:0 (0.22–0.36) single FA, and for "Desaturase index" group (0.05–0.38). The low heritability of factor 1 ("Biohydrogenation"; ~0.07 in IBS and IH, ~0.03 in IS) was in line with that obtained by Pegolo, Cecchinato, Mele, et al. (2016) for C18:1t6-8, C18:1t9, C18:1t10, C18:1c12 and C18:1t16 traits (0.056–0.089). The low heritability of factor 3 ("VA/CLA"; ~0.07 in IBS and IS, ~0.05 in IH) was consistent with the estimates for C15:0iso, C16:0iso, C16:1t9, C18:1t11 and C18:2c9t11 single FA (0.03–0.09) obtained in previous work (Pegolo, Cecchinato, Casellas, et al., 2016). The low heritability of factor 4 ("C17 Metabolism"; ~0.09 in IBS, ~0.05 IH and ~0.06 in IS) was consistent with the estimates for C17:0iso, C17:0anteiso, C17:0, and C17:1c9 single FA (0.050–0.102) obtained by Pegolo, Cecchinato, Mele, et al. (2016). The low heritability of factor 7 ("Arachidonic

acid synthesis"; ~0.10 in IBS, ~0.09 IH and ~0.06 in IS) was also consistent with the estimates for C20:3n6 and C20:4n6 single FA (0.08–0.11) described by Pegolo, Cecchinato, Mele, et al. (2016). A common pattern among heritability estimates, additive variance (Table S4) and herd contribution to phenotypic variance (Table S5) are easy to recognize. In general, low additive genetic variance in combination with a moderate/high herd contribution on phenotypic variance ($h_{herd} > 0.20$) determinates small heritability. This pattern generally agrees with the underlying metabolic pathway represented by each factor (mainly de novo synthetized or influenced by feeding and environmental effects). Nevertheless, some peculiar differences among the breeds can be observed. For instance, it is worth to note the markedly lower heritability (~0.04) estimated for factor 5 ("Short-chain FA") in IBS in comparison with the other breeds, particularly IS (~0.25). This finding is likely influenced by the notable herd contribution (~0.58) and by the low additive genetic variance (~0.06) found for this factor. This scenario seems to reflect the known monomorphic nature of gene encoding diacylglycerol acyl-transferase in IBS cattle (Conte et al., 2010; Pegolo, Cecchinato, Casellas, et al., 2016). Simultaneously, it is noteworthy that the factor 5 ("Short-chain FA") showed a higher heritability in IH (~0.12) and IS (~0.24) despite a quite similar additive genetic variance (~0.08) to IBS. In particular, the very low (~0.05) herd contribution detected for this factor in IH seems to suggest the role played by a higher standardized feeding and management practices and their effects on a single-purpose breed such as IH with a pronounced selection favouring fat content (Conte et al., 2010). Indeed, short FAs are formed de novo in the mammary gland by FA synthase but its activity is markedly influenced by dietary factors (Chilliard et al., 2007; Shingfield et al., 2013). A peculiar aspect of IS breed is the higher heritability of factor 8 ("OCFA metabolism"; ~0.26) compared with the other two breeds (~0.07). This value is a function mainly of the high additive genetic variance (~0.39) detected. This result was surprising since OCFAs are principally synthesized by rumen microbes (Vlaeminck et al., 2006). In this regard, it is worth noting that researches on host-microbiome interplay in ruminants have reported that breed has a significant effect on rumen microbiome and consequently on end products of fermentation and methane emission (Difford et al., 2018; Li et al., 2019; Roehe et al., 2016; Sandri et al., 2018). In the study of Roehe et al. (2016), not only differences of rumen microbiome were found between Aberdeen Angus and Limousine, but also a significant sire effect was reported.

4.3 | Genomic prediction accuracy

Overall, the accuracies of breeding values predicted for all factors obtained from milk FA composition were low to high, ranging from 0.13 to 0.72 and from 0.18 to 0.74 considering the ABLUP and ssGBLUP models, respectively (Table 3). In our case, the differences between the accuracies estimated from the two models were likely due to the reduction of the prediction error as a consequence of the inclusion in the genetic evaluation of "realized" relationships among animals inferred from genotypes, instead of the "expected" additive relationships estimated from the pedigree. For this reason, the accuracies obtained with the ssGBLUP model were higher than those obtained using ABLUP, confirming the contribution of genomic information in yielding more accurate predictions compared with the traditional ABLUP methodology and, more in general, that genomic relationships are superior to pedigree-based values (Wang, 2016). More in detail, the gain in accuracy in genetic prediction due to the addition of genomic information was ~5% in training, corresponding to the older cohorts in our populations, whereas a remarkable increase (~35%) was observed in validation sets. These results were expected since, although the inclusion of genomic information is important to correct pedigree errors (Misztal et al., 2013; Patry & Ducrocq, 2011), the mean differences in the accuracies obtained between the genomic relationship and the relationship based on the pedigree are generally low for animals with phenotypes available (Misztal et al., 2013) and were consistent with the fact that lower prediction errors are expected when the amount of information available is high, as it is the case of animals with own phenotypes and genotypes and with measured progeny (i.e., training data sets). Overall, our accuracy results are in line with previous reports on single FA or categories of FA (Cesarani et al., 2019; Gebreyesus et al., 2019), whereas some differences were observed with reliability values reported in other studies (Freitas et al., 2020; Petrini et al., 2019) where different strategies were used for the evaluation of the predictive ability of breeding values. In general, prediction accuracies for validation animals were low (ranging from 0.18 to 0.49), but always higher for GEBV in comparison with EBV. Focusing on validation sets, higher GEBV accuracy values were observed in the IBS breed (an average of 0.37) compared with the other two breeds. This difference is likely attributable to the larger number of animals available for the IBS since it is known that increasing the number of phenotypic records in the training set leads to increased measures of accuracy in the validations sets and particularly for the traits with low heritability (Hayes, Bowman, Chamberlain, & Goddard, 2009; Hayes et al., 2010), such as milk FA. In this regard, it is important to note that, despite the growing interest in the inclusion of milk FA composition traits in the breeding goals of dairy cattle (Boichard & Brochard, 2012), FA traits still represent an expensive and time-consuming phenotype, traditionally measured by GC method. This affects the size of the reference population, usually numerically small, and thus the genomic prediction accuracies (Gebreyesus et al., 2019).

Nevertheless, the sample size in our populations allowed us to obtain prediction accuracy values in agreement with those reported in other studies (Cesarani et al., 2019; Gebreyesus et al., 2019) and reasonable standard deviations also in IH and IS breeds (an average of ~0.03) indicating the consistency of our estimates also with the numerically smaller sample size. Higher accuracies were obtained for factors with higher heritability, such as factors 2 ("Neosynthesis/desaturation_1"), 6 ("Minor SCD products") and 9 ("Neosynthesis/desaturation_2"). We expected these results since the accuracy is a function of additive variance (Table S4) and heritability (Table 2), but also it depends on the genetic architecture of the trait (e.g., number of loci affecting the trait and distribution of their effects; Daetwyler et al., 2008; Goddard, 2009; Meuwissen, 2009). In this regard, the pattern of accuracy values across the factors agrees with the underlying metabolic meaning represented by each FA latent variables, since factors 2 ("Neosynthesis/desaturation_1"), 6 ("Minor SCD products") and 9 ("Neosynthesis/desaturation_2") encompass short- and medium-chain length FA (C4:0 to C14:0) that are synthesized de novo in the bovine mammary gland (Bauman & Griinari, 2003) or FA that are products (C14:1c9, C16:1c9, C18:1c9) of Δ9-desaturase activity (Soyeurt et al., 2008). Various research reported the effects of main lipogenic genes, along with novel promising genes on such single FA (Houaga et al., 2018; Li et al., 2014; Marchitelli et al., 2013; Nafikov et al., 2014; Palombo et al., 2018; Pegolo, Cecchinato, Mele, et al., 2016). More recently, such results were confirmed by genome-wide association studies on FA latent factors obtained by MFA (Cecchinato et al., 2019; Palombo, Conte, et al., 2020). Although further studies are required to confirm our findings, possibly using a larger sample size, the accuracies results obtained in the present work support the idea to exploit the information acquired through the MFA in selection programs and when designing further studies on milk FA composition.

5 | CONCLUSIONS

Using MFA, nine latent factors replaced 40 individual milk FA traits. The factors distinguished the underlined metabolic origin or function that each group of FA was representing. Overall, genetic analysis results were in agreement with the given name of the factor and the heritability estimates presented in the current investigation showed that FA latent factors are heritable traits in dairy cattle, exhibiting low to moderate heritability. Breeding value accuracies obtained with the ssGBLUP method were higher than those estimated with the ABLUP approach. Although further studies with a larger sample size are required to confirm our findings, overall our results are in favour of the potential use of MFA in combination with GS for breeding purposes and the genetic improvement of milk FA composition in dairy cows.

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CONFLICT OF INTEREST

The authors declare that they have no competing interests.

AUTHOR CONTRIBUTIONS

MD, ACec, PAM, MM and NPPM conceived and designed the experiment. MD, ACec, MM and BS performed the experiment. VP, SP, GC and ACes analysed the data. MD, NPPM, PAM and ACec interpreted the results. VP, SP and GC wrote the paper. MD, BS, NPPM, MM and ACec edited and reviewed the manuscript. All authors read and approved the final manuscript.

ETHICAL APPROVAL

The cows included in this study belonged to commercial private herds and were not subjected to any invasive procedures. Milk and blood samples were previously collected during the routine milk recording coordinated by technicians working at the Breeder Associations and therefore authorized by a local authority.

CONSENT FOR PUBLICATION

Not applicable.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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REFERENCES

Aguilar, I., Misztal, I., Johnson, D. L., Legarra, A., Tsuruta, S., & Lawlor, T. J. (2010). Hot topic: A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. *Journal of Dairy Science*, *93*, 743–752. https://doi.org/10.3168/jds.2009-2730

Aguilar, I., Misztal, I., Tsuruta, S., Wiggans, G. R., & Lawlor, T. J. (2011). Multiple trait genomic evaluation of conception rate in Holsteins. *Journal of Dairy Science*, *94*, 2621–2624. https://doi.org/10.3168/jds.2010-3893

Arnould, V.-M.-R., & Soyeurt, H. (2009). Genetic variability of milk fatty acids. *Journal of Applied Genetics*, *50*, 29–39. https://doi.org/10.1007/BF03195649

Bastin, C., Gengler, N., & Soyeurt, H. (2011). Phenotypic and genetic variability of production traits and milk fatty acid contents across days in milk for Walloon Holstein first-parity cows. *Journal of Dairy Science*, *94*, 4152–4163. https://doi.org/10.3168/jds.2010-4108

Bauman, D. E., & Griinari, J. M. (2003). Nutritional regulation of milk fat synthesis. *Annual Review of Nutrition*, *23*, 203–227. https://doi.org/10.1146/annurev.nutr.23.011702.073408

Boichard, D., & Brochard, M. (2012) New phenotypes for new breeding goals in dairy cattle. *Animal*, *6*, 544–550. https://doi.org/10.1017/S1751731112000018

Bouwman, A. C., Bovenhuis, H., Visker, M. H. P. W., & van Arendonk, J. A. M. (2011). Genome-wide association of milk fatty acids in Dutch dairy cattle. *BMC Genetics*, *12*, 43. https://doi.org/10.1186/1471-2156-12-43

Bouwman, A. C., Visker, M. H. P. W., van Arendonk, J. A. M., & Bovenhuis, H. (2012). Genomic regions associated with bovine milk fatty acids in both summer and winter milk samples. *BMC Genetics*, *13*, 93. https://doi.org/10.1186/1471-2156-13-93

Browning, S. R., & Browning, B. L. (2007). Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies by use of localized haplotype clustering. *American Journal of Human Genetics*, *81*, 1084–1097. https://doi.org/10.1086/521987

Buitenhuis, B., Janss, L. L. G., Poulsen, N. A., Larsen, L. B., Larsen, M. K., & Sørensen, P. (2014). Genome-wide association and biological pathway analysis for milk-fat composition in Danish Holstein and Danish Jersey cattle. *BMC Genomics*, *15*, 1112. https://doi.org/10.1186/1471-2164-15-1112

Calus, M. P., & Veerkamp, R. F. (2011). Accuracy of multi-trait genomic selection using different methods. *Genetics Selection Evolution*, *43*, 26. https://doi.org/10.1186/1297-9686-43-26

Campbell, W., Drake, M. A., & Larick, D. K. (2003). The Impact of fortification with conjugated linoleic acid (CLA) on the quality of fluid Milk. *Journal of Dairy Science*, *86*, 43–51. https://doi.org/10.3168/jds.S0022-0302(03)73582-6

Cecchinato, A., Macciotta, N., Mele, M., Tagliapietra, F., Schiavon, S., Bittante, G., & Pegolo, S. (2019). Genetic and genomic analyses of latent variables related to the milk fatty acid profile, milk composition, and udder health in dairy cattle. *Journal of Dairy Science*, *102*, 5254–5265. https://doi.org/10.3168/jds.2018-15867

Cesarani, A., Gaspa, G., Correddu, F., Cellesi, M., Dimauro, C., & Macciotta, N. (2019). Genomic selection of milk fatty acid composition in Sarda dairy sheep: Effect of different phenotypes and relationship matrices on heritability and breeding value accuracy. *Journal of Dairy Science*, *102*, 3189–3203. https://doi.org/10.3168/jds.2018-15333

Chang, C. C., Chow, C. C., Tellier, L. C. A. M., Vattikuti, S., Purcell, S. M., & Lee, J. J. (2015). Second-generation PLINK: Rising to the challenge of larger and richer datasets. *Gigascience*, *4*, 7. https://doi.org/10.1186/s13742-015-0047-8

Chilliard, Y., Ferlay, A., Mansbridge, R. M., & Doreau, M. (2000). Ruminant milk fat plasticity: Nutritional control of saturated, polyunsaturated, trans and conjugated fatty acids. *Annales De Zootechnie*, *49*, 181–205. https://doi.org/10.1051/animres:2000117

Chilliard, Y., Glasser, F., Ferlay, A., Bernard, L., Rouel, J., & Doreau, M. (2007). Diet, rumen biohydrogenation and nutritional quality of cow and goat milk fat. *European Journal of Lipid Science and Technology*, *109*, 828–855. https://doi.org/10.1002/ejlt.200700080

Conte, G., Mele, M., Chessa, S., Castiglioni, B., Serra, A., Pagnacco, G., & Secchiari, P. (2010). Diacylglycerol acyltransferase 1, stearoyl-CoA desaturase 1, and sterol regulatory element binding protein 1 gene polymorphisms and milk fatty acid composition in Italian Brown cattle. *Journal of Dairy Science*, *93*, 753–763. https://doi.org/10.3168/jds.2009-2581

Conte, G., Serra, A., Cremonesi, P., Chessa, S., Castiglioni, B., Cappucci, A., Bulleri, E., & Mele, M. (2016). Investigating mutual relationship among milk fatty acids by multivariate factor analysis in dairy cows. *Livestock Science*, *188*, 124–132. https://doi.org/10.1016/j.livsci.2016.04.018

Conte, G., Serra, A., & Mele, M. (2017). Dairy cow breeding and feeding on the milk datty acid pattern. In R. R. Watson, R. J. Collier, & V. R. Preedy (Eds.), *Nutrients in dairy and their implications on health and disease* (pp. 19–41). Academic Press.

Cruz, V. A. R., Oliveira, H. R., Brito, L. F., Fleming, A., Larmer, S., Miglior, F., & Schenkel, F. S. (2019). Genome-wide association study for milk fatty acids in Holstein cattle accounting for the DGAT1 gene effect. *Animals*, *9*(11), 997. https://doi.org/10.3390/ani9110997

Dadousis, C., Cipolat-Gotet, C., Bittante, G., & Cecchinato, A. (2018). Inferring genetic parameters on latent variables underlying milk yield and quality, protein composition, curd firmness and cheese-making traits in dairy cattle. *Animal*, *12*, 224–231. https://doi.org/10.1017/S1751731117001616

Daetwyler, H. D., Villanueva, B., & Woolliams, J. A. (2008). Accuracy of predicting the genetic risk of disease using a genome-wide approach. *PLoS One*, *3*, e3395. https://doi.org/10.1371/journal.pone.0003395

Dann, H. M., Morin, D. E., Bollero, G. A., Murphy, M. R., & Drackley, J. K. (2005). Prepartum intake, postpartum induction of ketosis, and periparturient disorders affect the metabolic status of dairy cows. *Journal of Dairy Science*, *88*, 3249–3264. https://doi.org/10.3168/jds.S0022-0302(05)73008-3

Difford, G. F., Plichta, D. R., Løvendahl, P., Lassen, J., Noel, S. J., Højberg, O., Wright, A.-D., Zhu, Z., Kristensen, L., Nielsen, H. B., Guldbrandtsen, B., & Sahana, G. (2018). Host genetics and the rumen microbiome jointly associate with methane emissions in dairy cows. *PLOS Genetics*, *14*, e1007580. https://doi.org/10.1371/journal.pgen.1007580

Douglas, G. N., Rehage, J., Beaulieu, A. D., Bahaa, A. O., & Drackley, J. K. (2007). Prepartum nutrition alters fatty acid composition in plasma, adipose tissue, and liver lipids of periparturient dairy cows. *Journal of Dairy Science*, *90*, 2941–2959. https://doi.org/10.3168/jds.2006-225

Dziuban, C. D., & Shirkey, E. C. (1974). When is a correlation matrix appropriate for factor analysis? Some decision rules. *Psychological Bulletin*, *81*, 358–361. https://doi.org/10.1037/h0036316

Fatumo, S., Carstensen, T., Nashiru, O., Gurdasani, D., Sandhu, M., & Kaleebu, P. (2019). Complimentary methods for multivariate genome-wide association study identify new susceptibility genes for blood cell traits. *Frontiers in Genetics*, *10*, 334. https://doi.org/10.3389/fgene.2019.00334

Fernando, R. L., & Grossman, M. (1989). Marker assisted selection using best linear unbiased prediction. *Genetics Selection Evolution*, *21*, 467. https://doi.org/10.1186/1297-9686-21-4-467

Fievez, V., Vlaeminck, B., Dhanoa, M. S., & Dewhurst, R. J. (2003). Use of principal component analysis to investigate the origin of

heptadecenoic and conjugated linoleic acids in milk. *Journal of Dairy Science*, *86*, 4047–4053. https://doi.org/10.3168/jds.S0022-0302(03)74016-8

Freitas, P., Oliveira, H. R., Silva, F. F., Fleming, A., Miglior, F., Schenkel, F. S., & Brito, L. F. (2020). Genomic analyses for predicted milk fatty acid composition throughout lactation in North American Holstein cattle. *Journal of Dairy Science*, *103*, 6318–6331. https://doi.org/10.3168/jds.2019-17628

Garnsworthy, P. C., Feng, S., Lock, A. L., & Royal, M. D. (2010). Short communication: Heritability of milk fatty acid composition and stearoyl-CoA desaturase indices in dairy cows. *Journal of Dairy Science*, *93*, 1743–1748. https://doi.org/10.3168/jds.2009-2695

Gebreyesus, G., Bovenhuis, H., Lund, M. S., Poulsen, N. A., Sun, D., & Buitenhuis, B. (2019). Reliability of genomic prediction for milk fatty acid composition by using a multi-population reference and incorporating GWAS results. *Genetics Selection Evolution*, *51*, 16. https://doi.org/10.1186/s12711-019-0460-z

Geweke, J. (1992). Evaluating the accuracy of sampling-based approaches to the calculation of posterior moments. In J. M. Bernardo, J. O. Berger, A. P. Dawid, & F. M. Smith (Eds.), *Bayesian statistics* (pp. 169–193). Clarendon Press.

Gibson, R. A. (2011). Milk fat and health consequences. *Nestlé Nutrition Institute Workshop Series: Pediatric Program*, *67*, 197–207. https://doi.org/10.1159/000325585

Glantz, M., Lindmark Månsson, H., Stålhammar, H., Bårström, L.-O., Fröjelin, M., Knutsson, A., Teluk, C., & Paulsson, M. (2009). Effects of animal selection on milk composition and processability. *Journal of Dairy Science*, *92*, 4589–4603. https://doi.org/10.3168/jds.2008-1506

Goddard, M. (2009). Genomic selection: Prediction of accuracy and maximisation of long term response. *Genetica*, *136*, 245–257. https://doi.org/10.1007/s10709-008-9308-0

Guo, G., Zhao, F., Wang, Y., Zhang, Y., Du, L., & Su, G. (2014). Comparison of single-trait and multiple-trait genomic prediction models. *BMC Genetics*, *15*, 30. https://doi.org/10.1186/1471-2156-15-30

Hayes, B. J., Bowman, P. J., Chamberlain, A. J., & Goddard, M. E. (2009). Invited review: Genomic selection in dairy cattle: Progress and challenges. *Journal of Dairy Science*, *92*, 433–443. https://doi.org/10.3168/jds.2008-1646

Hayes, B. J., Bowman, P. J., Chamberlain, A. C., Verbyla, K., & Goddard, M. E. (2009). Accuracy of genomic breeding values in multi-breed dairy cattle populations. *Genetics Selection Evolution*, *41*, 51. https://doi.org/10.1186/1297-9686-41-51

Hayes, B. J., Pryce, J., Chamberlain, A. J., Bowman, P. J., & Goddard, M. E. (2010). Genetic architecture of complex traits and accuracy of genomic prediction: Coat colour, milk-fat percentage, and type in Holstein cattle as contrasting model traits. *PLOS Genetics*, *6*, e1001139. https://doi.org/10.1371/journal.pgen.1001139

Hein, L., Sørensen, L. P., Kargo, M., & Buitenhuis, A. J. (2018). Genetic analysis of predicted fatty acid profiles of milk from Danish Holstein and Danish Jersey cattle populations. *Journal of Dairy Science*, *101*, 2148–2157. https://doi.org/10.3168/jds.2017-13225

Henderson, C. R. (1975). Best linear unbiased estimation and prediction under a selection model. *Biometrics*, *31*, 423–447. https://doi.org/10.2307/2529430

Houaga, I., Muigai, A. W. T., Ng'ang'a, F. M., Ibeagha-Awemu, E. M., Kyallo, M., Youssao, I. A. K., & Stomeo, F. (2018). Milk fatty acid variability and association with polymorphisms in SCD1 and DGAT1 genes in White Fulani and Borgou cattle breeds. *Molecular Biology Reports*, *45*, 1849–1862. https://doi.org/10.1007/s11033-018-4331-4

Ibeagha-Awemu, E. M., Akwanji, K. A., Beaudoin, F., & Zhao, X. (2014). Associations between variants of FADS genes and omega-3 and omega-6 milk fatty acids of Canadian Holstein cows. *BMC Genetics*, *15*, 25. https://doi.org/10.1186/1471-2156-15-25

Kaiser, H. F., & Rice, J. (1974). Little Jiffy, Mark Iv. *Educational and Psychological Measurement*, *34*, 111–117. https://doi.org/10.1177/001316447403400115

Kay, J. K., Weber, W. J., Moore, C. E., Bauman, D. E., Hansen, L. B., Chester-Jones, H., Crooker, B. A., & Baumgard, L. H. (2005). Effects of week of lactation and genetic selection for milk yield on milk fatty acid composition in holstein cows. *Journal of Dairy Science*, *88*, 3886–3893. https://doi.org/10.3168/jds.S0022-0302(05)73074-5

Krag, K., Poulsen, N. A., Larsen, M. K., Larsen, L. B., Janss, L. L., & Buitenhuis, B. (2013). Genetic parameters for milk fatty acids in Danish Holstein cattle based on SNP markers using a Bayesian approach. *BMC Genetics*, *14*, 79. https://doi.org/10.1186/1471-2156-14-79

Legarra, A., Aguilar, I., & Misztal, I. (2009). A relationship matrix including full pedigree and genomic information. *Journal of Dairy Science*, *92*, 4656–4663. https://doi.org/10.3168/jds.2009-2061

Li, C., Sun, D., Zhang, S., Wang, S., Wu, X., Zhang, Q., Liu, L., Li, Y., & Qiao, L. V. (2014). Genome wide association study identifies 20 novel promising genes associated with milk fatty acid traits in Chinese Holstein. *PLoS One*, *9*, e96186. https://doi.org/10.1371/journal.pone.0096186

Li, F., Li, C., Chen, Y., Liu, J., Zhang, C., Irving, B., Fitzsimmons, C., Plastow, G., & Guan, L. L. (2019). Host genetics influence the rumen microbiota and heritable rumen microbial features associate with feed efficiency in cattle. *Microbiome*, *7*, 92. https://doi.org/10.1186/s40168-019-0699-1

Lock, A. L., & Bauman, D. E. (2004). Modifying milk fat composition of dairy cows to enhance fatty acids beneficial to human health. *Lipids*, *39*, 1197–1206. https://doi.org/10.1007/s11745-004-1348-6

Loften, J. R., Linn, J. G., Drackley, J. K., Jenkins, T. C., Soderholm, C. G., & Kertz, A. F. (2014). Invited review: Palmitic and stearic acid metabolism in lactating dairy cows. *Journal of Dairy Science*, *97*, 4661–4674. https://doi.org/10.3168/jds.2014-7919

Macciotta, N. P. P., Cecchinato, A., Mele, M., & Bittante, G. (2012). Use of multivariate factor analysis to define new indicator variables for milk composition and coagulation properties in Brown Swiss cows. *Journal of Dairy Science*, *95*, 7346–7354. https://doi.org/10.3168/jds.2012-5546

Marchi, M. D., Penasa, M., Cecchinato, A., Mele, M., Secchiari, P., & Bittante, G. (2011). Effectiveness of mid-infrared spectroscopy to predict fatty acid composition of Brown Swiss bovine milk. *Animal*, *5*, 1653–1658. https://doi.org/10.1017/S1751731111000747

Marchitelli, C., Contarini, G., De Matteis, G., Crisà, A., Pariset, L., Scatà, M. C., Catillo, G., Napolitano, F., & Moioli, B. (2013). Milk fatty acid variability: Effect of some candidate genes involved in lipid synthesis. *Journal of Dairy Research*, *80*, 165–173. https://doi.org/10.1017/S002202991300006X

Mele, M., Macciotta, N., Cecchinato, A., Conte, G., Schiavon, S., & Bittante, G. (2016). Multivariate factor analysis of detailed milk fatty acid profile: Effects of dairy system, feeding, herd, parity, and stage of lactation. *Journal of Dairy Science*, *99*, 9820–9833. https://doi.org/10.3168/jds.2016-11451

Meuwissen, T. H. (2009). Accuracy of breeding values of "unrelated" individuals predicted by dense SNP genotyping. *Genetics Selection Evolution*, *41*, 35. https://doi.org/10.1186/1297-9686-41-35

Meuwissen, T. H., Hayes, B. J., & Goddard, M. E. (2001). Prediction of total genetic value using genome-wide dense marker maps. *Genetics*, *157*, 1819–1829.

Misztal, I., Aggrey, S. E., & Muir, W. M. (2013). Experiences with a single-step genome evaluation. *Poultry Science*, *92*, 2530–2534. https://doi.org/10.3382/ps.2012-02739

Misztal, I., Tsuruta, S., Lourenco, D., Masuda, Y., Aguilar, I., Legarra, A., & Vitezica, Z. (2014). *Manual for BLUPF90 family of programs*. Retrieved from http://nce.ads.uga.edu/wiki/lib/exe/fetch.php?media=blupf90_all2.pdf

Morrison, D. F. (1976). *Multivariate statistical methods*. McGraw-Hill Ryerson.

Nafikov, R. A., Schoonmaker, J. P., Korn, K. T., Noack, K., Garrick, D. J., Koehler, K. J., Minick-Bormann, J., Reecy, J. M., Spurlock, D. E., & Beitz, D. C. (2014). Polymorphisms in lipogenic genes and milk fatty acid composition in Holstein dairy cattle. *Genomics*, *104*, 572–581. https://doi.org/10.1016/j.ygeno.2014.10.001

Nakamura, M. T., & Nara, T. Y. (2004). Structure, function, and dietary regulation of Δ6, Δ5, and Δ9 desaturases. *Annual Review of Nutrition*, *24*, 345–376. https://doi.org/10.1146/annurev.nutr.24.121803.063211

Ntambi, J. M. (1999). Regulation of stearoyl-CoA desaturase by polyunsaturated fatty acids and cholesterol. *Journal of Lipid Research*, *40*, 1549–1558.

Palmquist, D. L., St-Pierre, N., & McClure, K. E. (2004). Tissue fatty acid profiles can be used to quantify endogenous rumenic acid synthesis in lambs. *Journal of Nutrition*, *134*, 2407–2414. https://doi.org/10.1093/jn/134.9.2407

Palombo, V., Conte, G., Mele, M., Macciotta, N. P. P., Stefanon, B., Marsan, P. A., & D'Andrea, M. (2020). Use of multivariate factor analysis of detailed milk fatty acid profile to perform a genome-wide association study in Italian Simmental and Italian Holstein. *Journal of Applied Genetics*, *61*(3), 451–463. https://doi.org/10.1007/s13353-020-00568-2

Palombo, V., Gaspa, G., Conte, G., Pilla, F., Macciotta, N., Mele, M., & D'Andrea, M. (2020). Combined multivariate factor analysis and GWAS for milk fatty acids trait in Comisana sheep breed. *Animal Genetics*, *51*, 630–631. https://doi.org/10.1111/age.12948

Palombo, V., Milanesi, M., Sgorlon, S., Capomaccio, S., Mele, M., Nicolazzi, E., Ajmone-Marsan, P., Pilla, F., Stefanon, B., & D'Andrea, M. (2018). Genome-wide association study of milk fatty acid composition in Italian Simmental and Italian Holstein cows using single nucleotide polymorphism arrays. *Journal of Dairy Science*, , *101*(12), 11004–11019. https://doi.org/10.3168/jds.2018-14413

Patry, C., & Ducrocq, V. (2011). Evidence of biases in genetic evaluations due to genomic preselection in dairy cattle. *Journal of Dairy Science*, *94*, 1011–1020. https://doi.org/10.3168/jds.2010-3804

Pegolo, S., Cecchinato, A., Casellas, J., Conte, G., Mele, M., Schiavon, S., & Bittante, G. (2016). Genetic and environmental relationships of detailed milk fatty acids profile determined by gas chromatography in Brown Swiss cows. *Journal of Dairy Science*, *99*, 1315–1330. https://doi.org/10.3168/jds.2015-9596

Pegolo, S., Cecchinato, A., Mele, M., Conte, G., Schiavon, S., & Bittante, G. (2016). Effects of candidate gene polymorphisms on the detailed fatty acids profile determined by gas chromatography in bovine milk. *Journal of Dairy Science*, *99*, 4558–4573. https://doi.org/10.3168/jds.2015-10420

Petrini, J., Souza Iung, L. H., Petersen Rodriguez, M. A., Salvian, M., Alberto Rovadoscki, G., Colonia, S. R. R., Cassoli, L. D., Lehmann Coutinho, L., Fernando Machado, P., Wiggans, G., & Mourão, G. B. (2019). Assessing the accuracy of prediction for milk fatty acids by using a small reference population of tropical Holstein cows. *Journal of Animal Breeding and Genetics*, *136*, 453–463. https://doi.org/10.1111/jbg.12434

R Core Team (2018). *R: A language and environment for statistical computing*. R Foundation for Statistical Computing Vienna. Retrieved from: https://www.R-project.org/

Roehe, R., Dewhurst, R. J., Duthie, C.-A., Rooke, J. A., McKain, N., Ross, D. W., Hyslop, J. J., Waterhouse, A., Freeman, T. C., Watson, M., & Wallace, R. J. (2016). Bovine host genetic variation influences rumen microbial methane production with best selection criterion for low methane emitting and efficiently feed converting hosts based on metagenomic gene abundance. *PLoS Genetics*, *12*, e1005846. https://doi.org/10.1371/journal.pgen.1005846

Rutten, M., Bovenhuis, H., Hettinga, K. A., van Valenberg, H., & van Arendonk, J. (2009). Predicting bovine milk fat composition using infrared spectroscopy based on milk samples collected in winter and summer. *Journal of Dairy Science*, *92*, 6202–6209. https://doi.org/10.3168/jds.2009-2456

Sandri, M., Licastro, D., Dal Monego, S., Sgorlon, S., & Stefanon, B. (2018). Investigation of rumen metagenome in Italian Simmental and Italian Holstein cows using a whole-genome shotgun sequencing technique. *Italian Journal of Animal Science*, *17*, 890–898. https://doi.org/10.1080/1828051X.2018.1462110

Shingfield, K. J., Bernard, L., Leroux, C., & Chilliard, Y. (2010). Role of trans fatty acids in the nutritional regulation of mammary lipogenesis in ruminants. *Animal*, *4*, 1140–1166. https://doi.org/10.1017/S1751731110000510

Shingfield, K. J., Bonnet, M., & Scollan, N. D. (2013). Recent developments in altering the fatty acid composition of ruminant-derived foods. *Animal*, *7*(Suppl 1), 132–162. https://doi.org/10.1017/S1751731112001681

Smith, C. (1967). Improvement of metric traits through specific genetic loci. *Animal Science*, *9*, 349–358. https://doi.org/10.1017/S0003356100038642

Soller, M., & Beckmann, J. S. (1983). Genetic polymorphism in varietal identification and genetic improvement. *Theoretical and Applied Genetics*, *67*, 25–33. https://doi.org/10.1007/BF00303917

Soyeurt, H., Dehareng, F., Mayeres, P., Bertozzi, C., & Gengler, N. (2008). Variation of Δ9-desaturase activity in dairy cattle. *Journal of Dairy Science*, *91*, 3211–3224. https://doi.org/10.3168/jds.2007-0518

Soyeurt, H., Gillon, A., Vanderick, S., Mayeres, P., Bertozzi, C., & Gengler, N. (2007). Estimation of heritability and genetic correlations for the major fatty acids in bovine milk. *Journal of Dairy Science*, *90*, 4435–4442. https://doi.org/10.3168/jds.2007-0054

Stoop, W. M., Bovenhuis, H., Heck, J. M. L., van Arendonk, J. (2009). Effect of lactation stage and energy status on milk fat composition of Holstein-Friesian cows. *Journal of Dairy Science*, *92*, 1469–1478. https://doi.org/10.3168/jds.2008-1468

Stoop, W. M., Schennink, A., Visker, M., Mullaart, E., van Arendonk, J., & Bovenhuis, H. (2009). Genome-wide scan for bovine milk-fat composition. I. Quantitative trait loci for short- and medium-chain

fatty acids. *Journal of Dairy Science*, *92*, 4664–4675. https://doi.org/10.3168/jds.2008-1966

Teissier, M., Larroque, H., & Robert-Granie, C. (2019). Accuracy of genomic evaluation with weighted single-step genomic best linear unbiased prediction for milk production traits, udder type traits, and somatic cell scores in French dairy goats. *Journal of Dairy Science*, *102*, 3142–3154. https://doi.org/10.3168/jds.2018-15650

VanRaden, P. M. (2008). Efficient methods to compute genomic predictions. *Journal of Dairy Science*, *91*, 4414–4423. https://doi.org/10.3168/jds.2007-0980

Vitezica, Z. G., Aguilar, I., Misztal, I., & Legarra, A. (2011). Bias in genomic predictions for populations under selection. *Genetics Research*, *93*, 357–366. https://doi.org/10.1017/S001667231100022X

Vlaeminck, B., Fievez, V., Tamminga, S., Dewhurst, R. J., van Vuuren, A., De Brabander, D., & Demeyer, D. (2006). Milk odd- and branched-chain fatty acids in relation to the rumen fermentation pattern. *Journal of Dairy Science*, *89*, 3954–3964. https://doi.org/10.3168/jds.S0022-0302(06)72437-7

Wang, J. (2016). Pedigrees or markers: Which are better in estimating relatedness and inbreeding coefficient? *Theoretical Population Biology*, *107*, 4–13. https://doi.org/10.1016/j.tpb.2015.08.006

Weller, J. I., Ezra, E., & Ron, M. (2017). Invited review: A perspective on the future of genomic selection in dairy cattle. *Journal of Dairy Science*, *100*, 8633–8644. https://doi.org/10.3168/jds.2017-12879

Wiggans, G. R., Cole, J. B., Hubbard, S. M., & Sonstegard, T. S. (2017). Genomic selection in dairy cattle: The USDA experience. *Annual Review of Animal Biosciences*, *5*, 309–327. https://doi.org/10.1146/annurev-animal-021815-111422

SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section.

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