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Genetic Selection in Dual-Purpose Cattle: Insights from the Girolando Breed and Its Implications for Sustainable Breeding

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Abstract | Genetic improvement in dual-purpose breeds should take into account the genetic relationships between traits associated with milk and beef production, as well as the inclusion of functional traits that are critical to animal welfare. This study focused on estimating the genetic correlations between milk and beef traits currently under selection in the native dual-purpose Girolando breed, together with their relationships to somatic cell number. The observed opposing correlations between milk and beef traits highlight the importance of assigning appropriate economic weights to all traits under selection, including functional traits. This approach is essential to preserve the unique dual-purpose characteristics of the breed while ensuring animal welfare and sustainable productivity.

Keywords | Dual-purpose, Cattle, Girolando, Breed, Sustainable breeding, Northern Iraq

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INTRODUTION

Dual-purpose cattle breeds have traditionally been selected to enhance both milk and beef production, with a stronger emphasis on milk due to its higher economic value (Aass, 1996). Compared to highly specialized dairy or beef breeds, dual-purpose breeds exhibit valuable functional traits such as health, fertility, and longevity. These characteristics enable them to thrive in challenging environments and marginal areas with minimal maintenance requirements (Krupová *et al.*, 2016).

Despite their practical advantages, limited research has focused on the genetic relationships among traits relevant to the dual-purpose profile. This is likely due to the greater economic significance of specialized breeds and the relatively localized distribution of dual-purpose cattle. However, interest in local dual-purpose breeds has grown in recent years, driven by their role in landscape conservation, their contribution to the production of traditional goods such as Protected Designation of Origin (POD) cheeses, and their indirect support of local economies (Gandini and Villa, 2003).

Recent studies on dual-purpose cattle breeds have identified negative genetic associations between milk and beef traits. For example, research on the Grey Alpine breed highlighted the challenges of simultaneously improving milk and beef production due to antagonistic genetic relationships between these traits (Mansin *et al.*, 2021). This study emphasized the need to integrate productive and functional traits into selection indices to ensure animal welfare and maintain dual-purpose breed characteristics. Similarly, a genome-wide association study on domestic cattle breeds investigated beef traits and found genetic associations that suggest the importance of considering

both productive and functional traits in breeding programs (Mansin *et al*., 2022). The study emphasized the need for balanced selection strategies to maintain the dual-purpose nature of these breeds.

Despite these findings, some selection indices for dual-purpose cattle still focus primarily on productive traits, underscoring the need for a more balanced approach that includes functional traits to maintain the health and longevity of the animals. Considering the Girolando breed as a case study, this research aimed to investigate the genetic associations between key productive traits associated with the dual-purpose profile. These traits included milk, fat and protein production, factor scores for udder and muscle composition derived from linear traits, as well as beef traits recorded in young bulls through performance testing.

Additionally, the study explored the genetic correlations between productive traits and a functional udder health trait somatic cell count as a potential selection criterion aimed at enhancing animal well-being. Lastly, the genetic response to selection was quantified using the selection index theory approach, providing insights into optimizing breeding strategies for sustainable genetic improvement.

MATERIALS AND METHODS

Subject in the study

The Girolando breed represents a success in selective breeding programs, combining high productivity with environmental resilience, making it one of the best choices for dairy farmers in hot climates (Agro Export, 2023).

A study conducted by Cardoso *et al*. (2011) revealed that the Girolando breed, resulting from the crossbreeding of the Gir and Holstein breeds, possesses unique characteristics that combine the robustness inherited from Gir with the high milk productivity of Holstein. This breed is responsible for producing 80% of the milk in Brazil, reflecting its success in selective breeding programs. Additionally, Girolando cattle exhibit strong adaptability to hot environments, making them an ideal choice for dairy farmers in tropical regions.

In addition, genomic studies have demonstrated that incorporating genomic information can enhance the accuracy of genetic predictions for beef traits in the Girolando breed. This suggests that combining genomic and pedigree data can be a useful approach, even for small landraces with limited population sizes (Oliveira *et al*., 2023).

This study focused on the productive traits currently included in the Girolando genetic improvement program, as well as somatic cell count (SCC) as a potential indicator of udder health for inclusion in the Total Selection Index (TSI). Incorporating SCC into selection indices has been shown to improve genetic evaluations for udder health in dairy cattle (Panetto *et al*., 2021).

Milk production traits

Data, including milk yield, fat, and protein content, were collected from individual cow records between 2013 and 2023, following the Iranian official milk recording system (Ghavi Hossein-Zadeh and Ardalan, 2011). After data editing, the dataset comprised 281,497 records from 16,974 cows up to the third lactation, associated with a lineage of 22,542 animals. This comprehensive dataset provides valuable insights into the genetic parameters influencing milk production traits in Iranian dairy cattle (Nazari *et al*., 2021).

Linear qualitative traits

Factorial traits for udder conformation and muscle were extracted from linear type assessments of first-born cows, performed annually by trained raters. A one- to five-point scale of biological significance was used for assessment (Silva *et al*., 2022). Of the 20 routinely scored qualitative traits, this study focused on 10 traits associated with udder and muscle characteristics. Higher phenotypic scores were desirable for all traits except teat length (Machado *et al*., 2021). After data editing, 11,992 individual cow records, corresponding to the pedigrees of 18,652 animals, were retained for analysis. Factor analysis was performed on the phenotypic data for these 10 qualitative traits (Ferreira *et al*., 2020).

Beef performance traits

Beef traits include average daily gain (ADG) and visual assessments of SEUROP flesh percentage (FL) and florescence percentage (DP) *in vivo* (Mantovani *et al*., 1997). Approximately 60 male candidate calves were tested annually from 1 to 11 months of age at the performance testing station, grouped by month of birth (Senczuk *et al*., 2024). Average daily gain (kg/day) was calculated as a linear regression of weight on age. At the end of the testing period, three trained raters provided separate scores for FL and DP, which were then averaged for each trait (Mancin *et al*., 2021). FL assessment applied the same scoring system used for postmortem carcass assessment in SEUROP, with the median "R" class equal to 100 points and differences of 10 points assigned to higher or lower classes (Bobbo *et al*., 2021). The study looked at all recorded data from 2013 to 2023, totaling 1,428 records of individual young bulls, linked to the pedigrees of 4,954 animals (Senczuk *et al*., 2024).

Somatic cell count (SCC)

The number of somatic cells per milliliter of milk, routinely

recorded under national functional controls, was converted to the somatic cell score (SCS) using the formula:

$SCS = 3 + \log_2(SCC/100{,}000)$ (Ali and Shook, 1980). Data lacking information on somatic cells or with negative values were discarded. The same thresholds applied to milk yield data were used, resulting in a final dataset of 239,698 records from 14,586 cows, linked to a pedigree of 20,592 animals (Bobbo *et al*., 2021). All datasets and pedigree information were provided by the Animal Science Research Institute of Iran (ASRI, 2023).

Estmation of genetic parameters

Variance components were estimated using single-trait animal models, which are routinely applied in genetic evaluations. The (co)variance between each pair of target traits was obtained through bi-trait analyses. The Average Information Restricted Maximum Likelihood (AIREML) algorithm was employed using the AIREMLF90 software, with 30 iterations under the Expectation-Maximization (EM) REML method to determine initial variance estimates (Misztal *et al*., 2002).

A repeat day test model was applied to estimate the variance components of milk production (MY, kg/day). This model was preferred over a random regression model to prevent inaccurate assessments at extreme values, which are more likely in small populations such as the Girolando breed, which follows a seasonal grazing system (Daltro *et al*., 2020).

In matrix notation, the model can be represented as:

$$y=X\beta+Wp+Zu+ey$$

Where: y is the vector of records for milk, fat, or protein yield (kg/day) of a given cow; X, W, and Z are incidence matrices corresponding to fixed effects, permanent environmental effects, and genetic effects, respectively; β\betaβ includes the fixed effects of herd-test-day within lactation number (LN), gestation stage, age at parity within LN (AP), and month of parity (MP), both of which were fitted as covariates using 4th order Legendre polynomials; p, u, ep, u, ep, u, e represent the permanent environmental effect, additive genetic component, and residuals, respectively.

The factor scores obtained for muscularity and udder conformation traits were analyzed using the following animal model:

$$y=X\beta+Zu+e$$

Where y is the vector of factor scores, X and Z are incidence matrices for fixed and genetic effects, β\betaβ is the vector of fixed effects, u represents the additive genetic effects, and e accounts for residuals (Meyer, 2020).

Where: y is the vector of type factor scores for each cow; β\betaβ includes fixed effects such as herd-year-classifier evaluation, age at first calving, and days in milk; u represents the additive genetic effects; e denotes the residual effects; X and Z are incidence matrices corresponding to the fixed and genetic effects, respectively.

For the analysis of performance traits (PT) in young bulls, a single-trait animal model with similar matrix notation is applied:

$$y=X\beta+Zu+e$$

In this context: y comprises phenotypic records for traits such as average daily gain (ADG), fleshiness (FL), or dressing percentage (DP); β\betaβ includes fixed effects like contemporary group, parity order of the dam, and individual age at the end of the test (used as a covariate, except for ADG); u and e represent the additive genetic and residual effects, respectively.

For somatic cell score (SCS) data, the same model structure as used for milk yield (MY) is employed.

To estimate (co)variance components, bi-trait animal model analyses are conducted for each pair of traits, resulting in a total of 45 analyses. Bivariate datasets are constructed by combining the relevant single-trait datasets. The (co) variance matrices for these bi-trait analyses are structured accordingly.

This modeling approach allows for the estimation of genetic parameters across multiple traits, facilitating a comprehensive understanding of the genetic architecture influencing both productive and functional characteristics in the population.

$$\text{Matrix G: } G = \begin{bmatrix} \sigma^2\alpha 1 & \sigma\alpha 1\alpha 2 \\ \sigma\alpha 1\alpha 2 & \sigma^2\alpha 1 \end{bmatrix}$$

$$\text{Matrix Pe: } Pe = \begin{bmatrix} \sigma^2 pe1 & \sigma pe1 pe2 \\ \sigma pe1 pe2 & \sigma^2 pe1 \end{bmatrix}$$

$$Matrix\ R: G = \begin{bmatrix} \sigma^2 e1 & 0 \\ 0 & \sigma^2 e1 \end{bmatrix}$$

Each matrix represents specific statistical components: G: Genetic variance-covariance matrix. Pe: Permanent environmental variance-covariance matrix. R: Residual variance-covariance matrix.

Matrix definitions

G (Additive Genetic (Co)variances):
Represents the genetic variance and covariance for traits 1 and 2:

$\sigma^2\alpha1$: Genetic variance for trait 1.
$\sigma^2\alpha2$: Genetic variance for trait 2.
σ $\alpha1$, $\alpha2$: Genetic variance for trait 1 and 2.
Pe (Permanent Environmental (Co)variances):
Represents the permanent environmental variance and covariance:
• σ^2pe1: Permanent environmental variance for trait 1.
• σpe1pe2: Permanent environmental covariance between traits 1 and 2.
• σ^2pe2: Permanent environmental variance for trait 2.
R (Residual (Co)variances):
Represents the residual variance and covariance:

Special case: σe1e2 is set to 0 in bivariate analyses when traits come from different datasets or are measured at different time points.

Specific insights

- In bivariate analyses involving traits from different datasets, σe1e2\sigma {e1e2} σe1e2 (residual covariance) is set to 0 because there is no overlapping measurement time or condition.
- Even if some traits (e.g., MY and SCS vs. factor type traits, or PT) are measured only once, a permanent environmental (co)variance is included to capture biologically meaningful relationships due to the shared environment (e.g., the individual's influence).
- For factorial traits and PT, the component σ^2_{pe2} (permanent environmental variance) is part of the residual variance, meaning it needs to be added to σ^2_{e2} to get the total residual variance.

The genetic correlation (r_a) was estimated using the formula:

$$r_a = \sigma_{a1a2} / \sqrt{(\sigma^2_{a1} \cdot \sigma^2_{a2})}$$

Similarly, the phenotypic correlation (r_p) was calculated as:

$$r_p = \sigma_{p1p2} / \sqrt{(\sigma^2_{p1} \cdot \sigma^2_{p2})}$$

Where σ_{p1p2} represents the total of all relevant covariances.

The standard errors of these estimates were computed using the delta method, as detailed by Lynch and Walsh (1998), leveraging the standard errors of the variance components. To assess the significance of the heritability and correlation estimates, a z-score was derived as the ratio of the parameter estimate to its standard error:

$$z = \text{Estimate}/ \text{SE}$$

These z-scores were analyzed using a two-tailed significance test under the assumption of a standardized normal distribution, following the methodology described by Maricopa Open Digital Press (2020).

Genetic trends and response to selection

Individual estimated breeding values (EBV) were obtained as solutions for additive genetic influence in individual trait analyses (Mrode and Thompson, 2020) and then standardized using the mean and standard deviation of the newborns (EBV std). Individual estimated breeding values were plotted in a histogram to track annual genetic differences for traits across birth years.

The genetic response to selection (R) in the target traits, representing the predicted change in trait mean after a generation, was calculated by applying the multivariate breeder's equation:

$$R=G\beta R = G \backslash beta$$

Where: R: Vector of predicted responses to selection for each trait. G: Additive genetic variance-covariance matrix among the traits. β: Vector of selection gradients, indicating the direction and strength of selection on each trait.

This formulation accounts for the genetic correlations between traits, providing a comprehensive prediction of evolutionary responses under selection (Walsh and Blows, 2009).

$$R = (i / \sigma_i) \cdot b' \cdot P^{-1}$$

Where: i is the selection intensity (set to 1.755), σ_i is the SD of the selection index, calculated as, σ_i = (b'Pb)^(1/2), b is the vector of the weights for selection index, and b'is its transpose.

The vector b is calculated as:

$$b = P^{-1}Ga$$

Where: P and G are the phenotypic and genetic (co) variance matrices, respectively, - a is the vector including the economic weights of traits, which are currently used in the genetic improvement of the GIROLANDO breed and detailed in the Materials and Methods.

Following Hazel *et al.* (2020), the relative emphasis of the traits in the selection index was expressed as:

$$a_s = a \times \sigma_a$$

Compared with the sum of all standardized values of the traits in the index, moving from the current economic weights of traits, a relative emphasis ranging from 0 to 1, with intermediate values, was alternatively attributed to milk and beef traits.

Milk, fat, protein, and the two factor scores referring to the udder were considered as milk traits, whereas the factor score for muscularity, ADG (average daily gain), FL (fleshiness score), and DP (dressing percentage) were considered as beef traits. Somatic cell score (SCS) was included in the selection index by restricting its genetic gain to zero, as proposed by Smith *et al.* (2022).

A standardized response to selection (R_sd_i) was calculated as:

$$R_s d_i = \frac{R}{\sigma Pi}$$

R_s where σP_i is the phenotypic standard deviation (SD) of the trait. The annual selection rate (R_sd_i/ t_i) was then determined by dividing R_sd_i by the population generation length (t = 4.48), as previously quantified from pedigree data.

RESULTS

Descriptive statistics

Descriptive statistics for the traits are presented in Table 1. The girolando cows produced an average of 16.5 kg/day of milk, containing an average of 3.5% and 3.3% of fat and protein, respectively. Many of the qualitative traits showed a mean value around 3, the most preferred value being teat length, while high values were preferred for the others. Muscle traits, with the exception of the thigh and buttocks (lateral view), were below average (around 2.8 points).

An ADG (average daily gain) of 1.051 kg/day was observed in young bulls, and a SCS (somatic cell score) of 2.89 in cows, roughly corresponding to 93,000 somatic cells/ml of milk. Factor analysis allowed the identification of three factor scores with eigenvalue ⩾1 and a specific biological meaning (Table 2 and Figure 1):

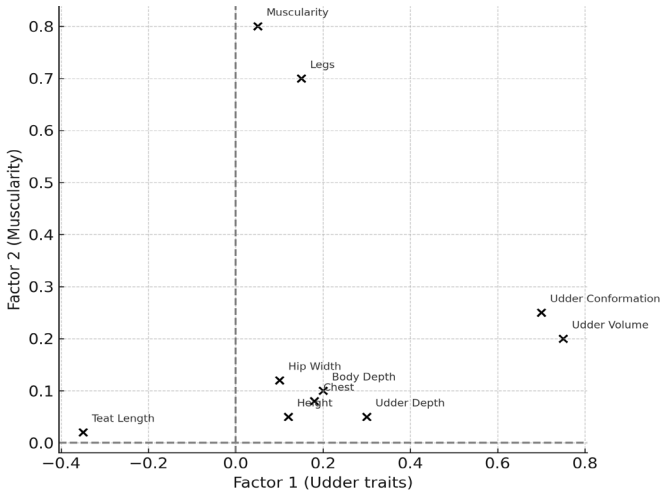

Figure 1: Factor loadings of linear type traits (Varimax rotation).

Muscularity (F1, MU) - Udder Volume (F2, UV), and - Udder Conformation (F3, UC).

All traits included in a single factor had a loading coefficient greater than 0.25. Teat length entered the UC factor with a sign opposite to its phenotypic variation. Therefore, a high value of UV is appropriate for a cow with a broad udder and a tight fore attachment.

On the other hand, high values for UC indicate a cow with a shallow udder, a strong suspensory ligament, and short teats, making it more adapted to milking machinery. Finally, developed front muscularity, back, loins, and rump, as well as rounded thighs and buttocks, are appropriate for a cow with a great MU.

Table 1: Descriptive statistics of the target phenotypic data in the Girolando breed.

Traits	Mean	SD	Minimum	Maximum
Milk yield traits (MY; kg/day)				
Milk	16.5	5.6	0.6	47.1
Fat	0.58	0.21	0.01	2.13
Protein	0.54	0.18	0.01	1.95
Morphological traits (Points)				
Fore udder attach	3.26	0.96	Loose	Tight
Rear udder attach	2.99	0.90	Short	Tall
Udder width	3.01	0.94	Narrow	Broad
Udder depth	3.34	0.70	Deep	Shallow
Suspensory ligament	3.01	0.92	Weak	Strong
Teat length	3.05	0.82	Short	Long
Front muscularity	2.77	0.82	Score	Developed
Back, loins, and rump	2.93	0.80		
Thigh, buttocks side view	3.00	0.77	Hollow	Rounded
Thigh, buttocks rear view	2.83	0.80	Hollow	Rounded
Performance test traits (PT)				
Average daily gain (ADG; kg/day)	1.051	0.116	0.481	1.407
In vivo SEUROP fleshiness (FL)	98.9	3.8	80.0	111.1
In vivo dressing percentage (DP)	54.2	0.97	50.0	57.7
Somatic Cell Score (SCS)	2.89	1.91	-3.64	10.78

Muscularity explained 49.54% of the whole phenotypic variation, UV 31.28%, and UC 19.18%. Communality, the proportion of traits variation explained by factors, was ⩾0.75 for muscularity traits and udder width, and <0.50 only for suspensory ligament and teat length.

Genetic parameters

Heritabilities (Table 3) were moderate for all traits

Table 2: Phenotypic factors, loading of individual type traits for coefficients ≥ 0.25, communality, and eigenvalues obtained after Varimax rotation of linear type traits.

Type Traits	F1 – Muscularity (MU)	F2 – Udder Volume (UV)	F3 – Udder Conformation (UC)	Communality
Fore udder attach	0.753			0.589
Rear udder attach		0.805		0.686
Udder width		0.866		0.755
Udder depth		0.710		0.560
Suspensory ligament		0.609		0.412
Teat length			-0.604	
Shoulder fore view	0.868			0.756
Back, loins, and rump	0.912			0.835
Thigh, buttocks side view	0.915			0.840
Thigh, buttocks rear view	0.899			0.810
Variance Explained (%)	49.54	31.28	19.18	
Eigenvalues	3.333	2.049	1.238	

Table 3: Variance components, heritability (h^2) with relative standard error (SEh^2), and additive genetic variance coefficients estimated by single-trait analyses for the target traits in the Girolando breed.

Traits	σ^2_pe	σ^2_a	σ^2_r	h^2	SE_h^2
Milk yield traits (MY; kg)					
Milk	5.237	2.167	4.137	0.188	0.011
Fat[1]	6.307	3.008	9.868	0.157	0.009
Protein[1]	4.877	1.910	4.787	0.165	0.010
Morphological factors (Standardized Points)					
Udder Volume (UV)	-	0.359	0.544	0.398	0.023
Udder Conformation (UC)	-	0.260	0.639	0.289	0.023
Muscularity (MU)	-	0.268	0.501	0.348	0.023
Performance test traits (PT)					
Average Daily Gain (ADG; kg/day)	-	0.004	0.008	0.323	0.069
In vivo SEUROP fleshiness (FL; points)	-	4.494	9.470	0.322	0.072
In vivo dressing percentage (DP; points)	-	0.159	0.200	0.442	0.074
Somatic Cell Score (SCS)	0.945	0.244	1.577	0.088	0.007

σ^2_pe: Phenotypic variance, σ^2_a: Additive genetic variance, σ^2_r: Residual variance. All h^2: Heritability values were significant with $P < 0.001$, [1] Variances multiplied by 10^3.

excluding SCS (0.088). Milk yield traits showed similar heritability (from 0.157 to 0.188), whereas UV had greater values (0.398) than MU (0.348) and UC (0.289). Heritability for ADG and FL were intermediate between MU and UC, whereas DP showed the greatest value (0.442). All heritabilities were significantly different from zero (Table 3). High genetic correlations (ra > 0.79) were found among MY traits (Table 4), and between FL and DP. Close values were also found for the corresponding phenotypic correlations (rp). High ra were achieved between MU and both FL (0.594) and DP (0.546), and the rp were slightly greater than 0.20. The UV showed ra with MY between 0.397 and 0.460 and rp between 0.223 and 0.277.

Moderate ra (around 0.36) were found for ADG with FL and DP, whereas the rp were rather higher (>0.50). Negative ra were obtained between MU and both MY (about −0.33) and UV (0.421), and the related rp were low but also negative (about −0.10). Udder volume showed a moderate negative ra (−0.218) also with FL. Low but negative relationships were found between MY and UC (ra from −0.164 to −0.100; rp close to zero).

Somatic cell score showed a moderate genetic correlation only with ADG (0.386), and low but positive ra (around 0.10) with UV, protein, and milk, even if in this latter case ra was not significantly different from zero. The rp between SCS and MY were negative (−0.14 on average).

Table 4: Genetic (above the diagonal) and phenotypic (below the diagonal) correlations between 10 target traits in girolando.

Traits	Milk	Fat	Protein	UV	UC	MU	ADG	FL	DP	SCS
Milk	-	0.798 (0.02)***	0.794 (0.014)***	0.873 (0.009)***	0.460 (0.02)**	-0.164 (0.05)*	-0.342 (0.022)***	0.022 (0.102)	-0.035 (0.102)	0.096 (0.052)
Fat	0.794 (0.014)***	-	0.819 (0.013)***	0.425 (0.02)**	-0.100 (0.05)*	-0.323 (0.045)**	-0.348 (0.009)***	0.048 (0.099)	-0.152 (0.089)	0.099 (0.062)
Protein	0.870 (0.01)***	0.928 (0.001)***	-	0.460 (0.02)**	-0.160 (0.05)*	-0.344 (0.01)***	-0.407 (0.01)***	0.028 (0.1)	-0.172 (0.09)	0.111 (0.05)**
UV	0.228 (0.01)**	0.277 (0.01)***	0.223 (0.006)**	-	-0.074 (0.05)*	-0.041 (0.047)*	-0.210 (0.01)***	-0.101 (0.02)**	-0.107 (0.05)**	-0.095 (0.03)*
UC	-0.28 (0.008)**	-0.22 (0.01)*	-0.30 (0.06)**	-0.04 (0.011)**	-	0.067 (0.056)	-0.042 (0.011)	0.120 (0.110)	0.103 (0.100)	-0.193 (0.09)**
MU	-0.12 (0.007)**	-0.14 (0.008)***	-0.13 (0.007)*	0.01 (0.025)	0.07 (0.056)	-	0.038 (0.107)	0.594 (0.093)**	0.546 (0.087)**	-0.385 (0.067)**
ADG	0.11 (0.028)	0.087 (0.07)**	0.09 (0.025)	0.05 (0.042)*	0.09 (0.045)	0.019 (0.038)	-	0.378 (0.125)*	0.857 (0.110)	0.386 (0.099)**
FL	-0.09 (0.029)	-0.11 (0.025)	-0.07 (0.041)	-0.03 (0.039)	0.03 (0.035)	0.29 (0.034)***	0.55 (0.022)**	-	0.984 (0.011)**	0.818 (0.110)
DP	0.01 (0.007)	0.05 (0.005)**	0.02 (0.005)**	0.04 (0.007)*	0.06 (0.011)*	0.25 (0.002)**	0.50 (0.007)	0.84 (0.009)	-	0.860 (0.098)*
SCS	-0.184 (0.005)**	-0.117 (0.004)**	-0.131 (0.005)**	-0.011 (0.004)**	-0.092 (0.007)**	-0.072 (0.007)	0.22 (0.004)*	0.31 (0.002)	0.24 (0.014)*	-

This text explains the notation and statistical significance levels used in the table: std. = standardized; pts = points. Standard errors of estimates are shown in brackets. Correlations significantly different from zero are indicated as: *P < 0.05, **P < 0.01, ***P < 0.001.

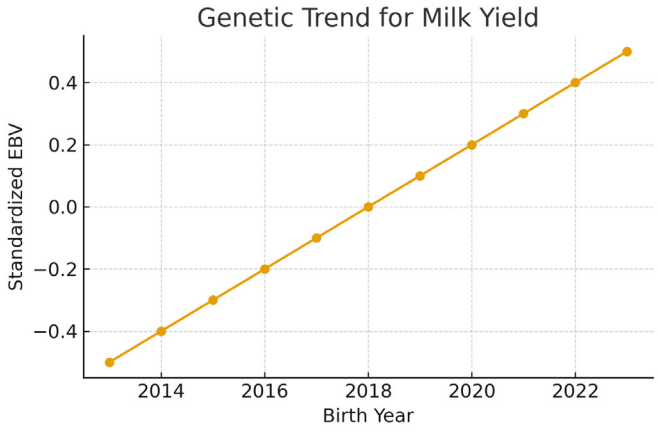

Figure 2A: Genetic trend for Milk Yield (standardized EBV means per birth year).

Somatic cell score showed a negative significant ra (–0.193) only with UC, suggesting that a well-conformed but not necessarily big udder is genetically linked to a lower production of somatic cells. The corresponding rp was also negative (–0.070). None of the other correlations differed from zero (Table 4).Genetic trends and response to different selection scenarios Positive genetic variation was observed from 2013 to 2023 for most traits (Figure 2), with the largest variations in MY (average linear regression coefficient b 1.4 standardized points per year), followed by ADG (b = 1.036), UV (b = 0.957), FL and DP (average b = 0.643). A trend close to 0 was observed in UC (b = 0.090), and a negative variation was found in MU (b = –0.522). Moving from a selection for a single milk position (unified economic weight of milk traits, asmilk=1; as for beef traits, asbeef=0; selection index R2, Table 5) to one for a single beef (asmilk=0; asbeef=1; selection index R6), the multi-trait response, expressed as the annual unified selection rate for traits (Rds/t), moved from positive values for milk traits and negative for beef, to slightly negative values for milk and strongly positive for beef traits (Table 5). Milk and beef traits, respectively, assumed total Rds/t of 0.290 and -0.148 in R2, and -0.073 and 0.510 in R6.

In R1, the current selection index, the ratio as milk: as beef is 0.75:0.25, the overall response for milk (Rds/t=0.269) is threefold the response for beef (Rds/t=0.099), and a positive selection rate is expected for all traits excluding UC and MU. The same selection rate for milk and beef attitudes (Rds/t=0.229) is realized when as milk: as beef is 0.66:0.34 (R3). All the traits apart from UC had a positive response under R3. The as ratio of 0.61:0.39 (R4) avoided the negative response for UC. A greater selection response for beef than for milk traits was also observed under R4, and it increased when the same standardized economic weight was assigned to milk and beef traits (R5). The ADG was the only productive trait assuming positive Rds/t for the whole range of as combinations. The indirect selection for SCS produced a slightly positive variation of the trait under all combinations of the global

Table 5: Genetic gain in 10 traits in response to selection for alternative global indexes in GIROLANDO, including the current selection index (R1) and five alternatives (R2 to R6).

Traits	σp[1]	a²s	R1	R2	R3	R3SCS	R4	R4SCS	R5
Milk	3.397	0.000	0.069	0.075	0.058	0.050	0.051	0.042	0.032
Fat	0.139	1.63	0.057	0.056	0.045	0.041	0.037	0.033	0.018
Protein	0.108	0.488	0.066	0.065	0.054	0.048	0.044	0.040	0.030
Udder volume	0.950	0.000	0.085	0.088	0.074	0.066	0.067	0.059	0.046
Udder conformation	0.948	0.100	-0.007	-0.015	-0.002	-0.007	-0.012	-0.017	-0.019
Muscularity	0.877	0.100	-0.003	-0.067	0.034	0.034	0.051	0.062	0.087
Average daily gain	0.107	0.045	0.031	0.010	0.011	0.021	0.036	0.037	0.043
In vivo SEUROP fleshiness	3.737	0.053	0.030	-0.048	0.071	0.093	0.126	0.077	0.103
In vivo dressing percentage	0.599	0.040	0.042	-0.043	0.085	0.109	0.133	0.126	0.124
Somatic cell score	1.663	0.000	0.016	0.013	0.016	0.016	0.014	0.014	0.010
Overall a²s									
Milk traits[3]	0.75	0.75	1	0.663	0.663	0.61	0.61	0.5	0.5
Beef traits[4]	0.25	0	0.337	0.337	0.39	0.39	0.5	1	1
Overall Rsd/t									
Milk traits	0.269	0.290	0.229	0.217	0.202	0.189	0.129	0.073	-0.073
Beef traits	0.099	-0.148	0.229	0.209	0.288	0.272	0.403	0.510	0.510

selection index, meaning an increase in somatic cells and a detriment in udder health.

A restriction for the genetic gain of SCS was applied to R3 and R4, and this solution produced a slight reduction of the overall Rds/t for both milk and beef attitudes in both global indexes (R3SCS and R4SCS). All the traits considered had a trivial reduction of their Rds/t as well, excluding UC (positive under both R3SCS and R4SCS) and FL.

The charts illustrate the genetic variation of traits over an 10-year period, from 2013 to 2023. Below is an interpretation of each chart:

Milk yield traits

This chart shows the genetic trends for milk yield traits, including Milk, Fat, and Protein, across the years.
A clear positive trend is observed for all traits, indicating continuous genetic improvement. The annual rate of increase is as follows:

- Milk: 1.48 standardized units per year.
- Fat: 1.29 standardized units per year.
- Protein: 1.41 standardized units per year.

Factors

- This chart represents three factors: Udder Volume, Udder Conformation, and Muscularity.
- Udder Volume shows a strong upward trend, reflecting consistent genetic improvement in udder size.
- Udder Conformation remains relatively stable over the years, with no significant genetic changes.
- Muscularity displays a slight downward trend, indicating a minor decline in this trait.

Performance Test Traits

- This chart highlights the genetic trends for performance-related traits, including ADG (Average Daily Gain), Fleshiness, and Dressing Percentage.
- All traits exhibit a positive trend, demonstrating steady genetic gains:
  - ADG: Annual increase of 1.036 standardized units.
  - Fleshiness: Annual increase of 0.603 standardized units.
  - Dressing Percentage: Annual increase of 0.650 standardized units.

Somatic Cell Score (SCS)

- This chart shows the trend for Somatic Cell Score (SCS), an indicator of udder health.
- A slight upward trend is observed, with an annual increase of 0.438 standardized units. This may suggest a minor deterioration in udder health over time.
- The charts reflect positive genetic progress for most traits, particularly in milk yield and performance-related traits.
- However, Muscularity and SCS exhibit unfavorable trends, emphasizing the need for balanced selection to prevent adverse effects on functional traits such as udder health.

Two selection scenarios: These scenarios aim to achieve either:

- Equal genetic gain for both milk and beef traits (R3).

- A balanced genetic gain with no negative response for any traits (R4). These approaches include a restriction to null genetic gain for somatic cell score (SCS) in R3SCS and R4SCS.

1. Phenotypic standard deviation: The standard deviation of the observed trait values in the population.
2. Standardized economic weight: A normalized value reflecting the relative economic importance of traits in the selection index.
3. Milk-related traits: Includes milk, fat, protein, udder volume, and udder conformation.
4. Beef-related traits: Includes muscularity, average daily gain, fleshiness, and dressing percentage.
5. Standardized selection rate Where RR is the selection response, σp\sigma_p is the phenotypic standard deviation, and tt is the generation interval (4.48 years).

DISCUSSION

Positive correlations among milk traits indicate consistent genetic progress, while antagonistic correlations with muscularity underscore the importance of including functional and health traits in breeding goals. Implementing comprehensive selection strategies can help sustain productivity and animal welfare.

The muscularity factor has a negative genetic correlation with MY (Table 4), and the current selection index (R1, Table 5), assigning to milk a three-times greater weight than to beef traits, causes a negative selection response to muscularity, as seen in the genetic trend (Figure 2). The antagonism between milk yield traits and muscularity has been observed, reporting moderate-high negative genetic correlations (e.g., in Turkish Holstein cattle; Ermetin and Dağ (2021), and in Brazilian Girolando; Machado *et al.* (2021). This may be due to a different allocation of available metabolic energy in cows, either directed to increased milk production or to muscle mass growth. However, no studies have focused extensively on this issue in these populations yet.

Lower genetic correlations have been recently highlighted in dual-purpose breeds. For example, in Montbéliarde and Normande cattle, SEUROP conformation scores exhibited null to slightly negative genetic correlations with milk, fat, and protein yields (Mancin *et al.*, 2020).

Traits recorded at performance test stations generally show medium to high heritability. In studies conducted on Turkish and Brazilian dual-purpose cattle, heritability estimates for various performance traits aligned with these findings (Machado *et al.*, 2021).

A wide range of heritability estimates has been observed for in vivo fleshiness, ranging from 0.19 in Romagnola to 0.55 in Chianina breeds. Similarly, zero to negative genetic correlations have been reported between average daily gain (ADG) and milk traits, as well as between net daily gain and fat and protein yields (Ermetin and Dağ, 2021).

Moderately low to negative genetic relationships (-0.15 to -0.20) between in vivo EUROP scoring and dressing percentage (DP) with milk and protein yields were found in dual-purpose breeds such as Austrian Fleckvieh and Brown Swiss (Ghavi Hossein-Zadeh, 2016).

In the present study, the genetic correlation between performance test traits (PT) and milk yield (MY), estimated to be close to zero (Table 4), showed that it is feasible to improve both milk production in cows and beef traits in young bulls, as suggested by the selection index R1.

An enhanced selection for only one attitude may cause a detriment in the other due to the whole framework of genetic relationships among productive traits. Simulations suggest (Table 5) that when as of 0.61 to milk traits and 0.39 to beef traits are assigned (R4), both attitudes improve without detriments.

A slight but positive selection response is expected for SCS under all combinations of economic weights due to the positive ra with ADG and MY (Table 4). This is undesirable, as it corresponds to an increase in milk somatic cells. A low SCS heritability, similar to the estimate of the present study, was found for Finnish Ayrshire (from 0.07 to 0.12; Martínez *et al.*, 2022), Italian Brown Swiss (0.14; Rossi *et al.*, 2020), and Canadian Holstein (0.17; Patel and Wong, 2021). Low but positive genetic correlations between SCS and milk have been reported in literature, for example in Canadian Holstein (0.14; Patel and Wong, 2021), and Italian Brown Swiss (0.18; Rossi *et al.*, 2020). In the latter study, SCS showed no significant ra with protein and fat yield, similar to the findings of this study.

These results highlight the potential usefulness of including somatic cells within breeding goals in dairy and dual-purpose breeds, as already implemented in some selection indexes. For example, in the Total Merit Indexes approved in 2016 for Austrian Fleckvieh and Brown Swiss, udder health had an economic value of 0.10, with 70% assigned to somatic cells (Martinez *et al.*, 2023). The approach of restricting the genetic gain for SCS to zero, as a means to counteract its increase, was previously adopted by Rossi *et al.* (2020) to stabilize the genetic value of carcass fat in beef breeds. Restricting a trait in a global index necessitates recalibrating the standardized economic weights of all included traits.

When the genetic value of SCS is kept constant via

restriction (R3SCS, Table 5), a positive selection response is expected for all traits. Moreover, R3SCS allows for similar responses for both aptitudes (standardized selection rates of 0.217 and 0.209 for milk and beef traits, respectively; Table 4). R4SCS also permits a positive response with null genetic gain for SCS, but since this index has a greater standardized selection rate for beef, R3SCS is preferred. The latter appears to be the most effective selection index proposed and could be considered for genetic improvement.

The choice of a proper selection index is important in cattle breeding and depends on the genetic SD of traits, the economic weights assigned, and the complex framework of genetic correlations. The inclusion of functional traits in a selection index is effective for a responsible, forward-oriented, and socially accepted genetic improvement plan (Martinez *et al.*, 2023: Al-Jryan *et al.*, 2022). Current genetic trends suggest a slight but progressive change towards a milk conformation. Therefore, a long-term maintenance of the dual-purpose attitude, including a control of somatic cells, could be attained using proper economic weights for selected traits, as in the R3SCS index. This study has not considered other functional traits such as mothering ability or productive life as GIROLANDO is a rustic breed with good levels of longevity, fertility, and calving ease, but in some selection indexes (Rossi *et al.*, 2020: Al-Jebory *et al.*, 2024) they have been included due to their importance for dual-purpose breeds.

To summarize, this study has considered GIROLANDO as an example of a local cattle breed with a dual-purpose attitude. The antagonism between milk and beef attitudes has been highlighted by the negative genetic correlations of milk, fat, protein, and udder volume with muscularity. The beef traits recorded at the performance test stations have mostly shown genetic correlations not different from zero with milk traits, but also high-positive genetic correlations with muscularity. The composite framework of genetic relationships among traits leads to assigning proper economic weights to traits to avoid detrimental effects on one attitude due to the improvement of the other. Moreover, somatic cells may undesirably increase via indirect selection, reducing animal well-being. A good knowledge of traits' genetic correlations and the proper weights to be included in a global index for dual-purpose attitude may be effective for genetic improvement in GIROLANDO and other dual-purpose breeds (Martinez *et al.*, 2023; Rossi *et al.*, 2020: Salman *et al.*, 2024).

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NOVELTY STATEMENT

This study represents the first comprehensive genetic evaluation of the Girolando dual-purpose breed in Iraq, combining large-scale phenotypic and pedigree datasets over a ten-year period. The research provides unique insights into the genetic correlations among milk production traits, beef performance indicators, and functional traits such as somatic cell score (SCS). Unlike previous studies that focused on specialized breeds or single traits, this work highlights the antagonistic genetic relationships that can arise in dual-purpose breeding programs and demonstrates the importance of balanced selection indices. These findings will guide future breeding strategies to preserve the dual-purpose nature of the Girolando breed while enhancing animal welfare, productivity, and long-term sustainability.

AUTHOR'S CONTRIBUTION

EKAA-Z: Conceived the research concept, designed the study framework, supervised all stages of the project, and critically revised the manuscript for important intellectual content.
HMS: Collected and curated the phenotypic and pedigree data, performed statistical and genetic analyses, and contributed substantially to writing and editing the manuscript.
AJA: Assisted with data interpretation, conducted the literature review, prepared figures and tables, and participated in the drafting and revision of the manuscript.
All authors have read and approved the final version of the manuscript and agree to be accountable for all aspects of the work.

Generative AI and AI-assisted technology statement

We confirm that artificial intelligence was not used in the manuscript's creation.

Conflict of interest

The authors declare that there is no financial, personal, or professional conflict of interest that could be perceived as influencing the research reported in this manuscript. The study was conducted with full academic independence,

and all analyses and interpretations are solely those of the authors.

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