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The effect of sire and birth year on breeding values and milk production data of Hungarian Simmental cows

Az apa és a születési év hatása a magyar tarka tehenek tenyészértékére és tejtermelési adataira

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SUMMARY

Genomic selection represents the most advanced form of breeding value estimation currently available. In the case of the Hungarian Simmental cattle breed, the genomic selection program launched in 2020 as part of an international collaborative effort. In the process the SNP markers, identified within single-step procedure, and the phenotypic production data of individuals in the population are integrated with pedigree information. Breeders receive genomic estimated breeding values as results three times per year. Owing to the dual-purpose nature of the breed, the following breeding values are estimated: dual breeding value, milk breeding value, meat breeding value, and fitness breeding value. In this study, the authors analyzed data from a large-scale dairy herd. The evaluation included both the genomic breeding values (GBV) of cows and the first-lactation milk yield corrected to 305 days. For animals born between 2010 and 2020, breeding value (89,4 < 101point) and milk production data were compared between birth-year groups. The potential influence of sire origin was also assessed, as the herd included cows sired by Hungarian, German, and Austrian bulls. The average GBV and Milk BV of cows sired by Hungarian bulls were substantially lower than those of cows sired by Austrian (-10 points) and German (-8 points) bulls. In contrast, for 305-day first-lactation milk yield, the ranking was reversed: Hungarian-sired cows produced 986 kg more milk than the Austrian-sired cows and 269 kg more than the German-sired cows on average. Significant differences were found both between the birth-year groups and among sire-origin groups for the evaluated parameters. The results indicate that the phenotypic expression of genomic estimated breeding values is considerably affected by the actual production environment, particularly in the case of first-lactation performance (average 7300 kg, minimum 6855 kg in 2012, maximum value 7863 kg in 2013).

Keywords: GBV, Hungarian Simmental, corrected milk production

ÖSSZEFOGLALÁS

Vizsgálat célja: a genom alapján végzett tenyészkiválasztás a tenyészértékbecslés ma ismert legmodernebb formáján alapuló eljárás. A magyar tarka szarvasmarha fajta esetében 2020-ban elindult program egy több ország által közösen végzett folyamat részeként valósult meg. A „single-step" eljárásban azonosított SNP-minták mellett az érintett populáció egyedeinek fenotípusos termelési adatait is a pedigréadatok mellé rendezik, így becsülnek tenyészértéket. *Anyag és módszer:* évente három alkalommal kap a tenyésztő egyesület eredményeket, azaz genom alapján becsült tenyészértéket. A fajta kettős haszonvétele miatt egyesített (dual breeding value), tej- (milk breeding value), hús- (meat breeding value) és fitnesz- (fitness breeding value) paraméterek becslésére is sor kerül. A szerzők a vizsgálat során egy nagy egyedszámú fejt tenyészet tehénállományának adatait dolgozták fel. A vizsgálatban a tehenek új eljárással, genetikai mintából becsült genomtenyészértéke (GBV) mellett az első laktációs egyedek 305 napra korrigált tejtermelésének értékelésére került sor. *Eredmények*: a 2010 és 2020 között született egyedek esetében a születési évjárat alapján képzett csoportok tenyészérték- és tejtermelési adatait vetették össze. Értékelték az apa származási országa szerint fellelhető hatást is, mivel az állományban magyar, valamint német és osztrák apaságú tehenek is termelnek. Mind a tehenek születési évjárata, mind az apa származási országa szerinti csoportosítás bizonyított különbségeket eredményezett az értékelt paraméterekben. A genom alapján becsült tenyészértékek és a fenotípusos termelés trendjei nem esnek egybe, a genomtenyészérték jelentős javulása mellett (89,4<101) a fenotípusos termelés nem nőtt érdemben. Az import bikáktól származó tehenek tejtenyészértéke magasabb (osztrák +10 pont, bajor +8 pont), míg a 305 napra korrigált első laktációs tejtermelés magasabb a magyar apaságú teheneknél (osztrák apaság –986kg, bajor apaság –269 kg). *Következtetések:* érzékelhető, hogy a genom alapján becsült tenyészérték fenotípusos termelésben történő megjelenésére az aktuális termelési környezet jelentős hatást gyakorol, ami az első laktációs termelések esetében (átlag 7300 kg, minimum 6855 kg 2012 évben, maximum érték 7863 kg 2013 évben) erőteljesen megjelenik.

Kulcsszavak: genomikai tenyészérték, magyar tarka, tejtermelés

1 Introduction and literature review

A specific feature of Hungarian Simmental cattle breeding is its dual-purpose utilization, encompassing both dairy and beef-type herds. The selection program of the breed has been conducted for decades with this dual-purpose character in mind *(Ertl et al., 2014; Gao et al., 2025)*. Selection within dairy herds is based on a composite/aggregate breeding value index, which combines weighted index components of milk, meat, and fitness traits *(Elzo et al., 1987)*. The genomic selection program launched in Hungary in 2020 operates within a joint database shared with several European partner countries such as Germany, Austria, and the Czech Republic to estimate breeding values *(Ostler et al., 2005; Pryce et al., 2011)*. The single-step estimation procedure converts SNP information identified from genetic samples into breeding value parameters for more than 60 traits *(Legarra et al., 2014)*. In addition to genomic data, phenotypic records provided by the Association of Hungarian Simmental Breeders *(Kovács-Mesterházy, 2023)* are also included in the database of the estimation model. Breeding values for the evaluated traits are calculated and transmitted three times per year by the Bavarian working group to the Association. The weighting of traditional breeding value indices (dual breeding value, DBV), based on phenotypic data, differs from that of genomic breeding value indices (GBV), estimated using genomic information *(Aguilar et al., 2011; Cesarini et al., 2020ab)*.

The weighting of milk production traits in the model increased by 1%, while the weighting of meat production traits decreased by 9%, and that of fitness traits increased by 8%. Breeders of dairy-type Hungarian Simmental herds have monitored and evaluated the progress of the genomic selection program within their own populations *(Ablondi et al., 2023)*. The data security and reliability of genomic evaluations have already reached the level of traditional estimation methods. However, a considerable number of animals are still in production within the herds that were selected under the previous evaluation system, which relied on conventional pedigree and phenotypic information *(Röhrmoser and Pichler, 2003; Otwinowska-Mindur et al., 2025).* At the launch of the genomic program, herd-level sampling was conducted, making it possible to obtain genomic-based breeding value data for animals born over a period exceeding ten years. The herd examined in this study functions as a nucleus herd, where inseminations were occasionally performed using imported semen from high-merit bulls. These sires typically originated from Germany and Austria, the countries hosting the largest and genetically most valuable populations participating in the joint breeding value estimation program.

Table 1 The modification of the calculation method of the composite/aggregate breeding value index in dual-purpose herds

Breeding value index (1)	Dual breeding value DBV (traditionally estimated) (2)	Genomic breeding value GBV (genomic estimated) (3)
Milk production (4)	37%	38%
Meat production (5)	27%	18%
Fitness parameters (6)	36%	44%
Total (7)	100%	100%

1. táblázat. A kettős hasznosítású állományok összetett tenyészérték-indexének számítási módszere

tenyészérték-index (1); kettőshasznosítású tenyészérték (hagyományos becsléssel) (2); genomikai tenyészérték (genomikai becsléssel) (3); tejtermelés (4); hústermelés (5); fitnesz paraméterek (6); összesen (7)

The nucleus herd analysed in the study consisted of approximately 800 milking cows. The objectives of the investigation were to evaluate the effects of cow age and sire origin on genomic breeding values and to compare these with the phenotypic milk production performance of cows

2 Materials and methods

Genomic breeding value data were obtained for 1,452 cows born between 2010 and 2020 in the examined nucleus herd. Given that the weighting of fitness traits increased in genomic breeding value estimation compared to traditional evaluations, additional sub-trait data related to milk production – udder health, number of somatic cells, milking speed, and mastitis indicators – were also included in the analysis. Furthermore, the breeding value for the composite udder conformation score, assessed during phenotypic udder evaluation, was incorporated, as one of the key objectives of the selection program is to enhance udder conformation suitable for machine and robotic milking. Complete 305-day corrected milk production data were available for analysis in the case of 1,012 cows. At the time of genetic sampling, the 1,452 cows belonged to 11 birth-year groups. For the evaluation based on sire origin, three groups of offspring were identified: Austrian-sired (n = 162), German-sired (n = 181), and Hungarian-sired (n = 1,109) cows.

Within the database, both in terms of number of individuals and overall data, German and Austrian animals represent the largest population.

The collected and organized data were entered into Microsoft Excel for parameterization and figure preparation. Regression trend lines fitted to the data series were calculated using Excel's built-in module. Descriptive statistical analyses, correlation matrices, and variance analyses for effect evaluation were conducted using SPSS version 29.0. In the effect analyses, significance levels were generated by the ANOVA model with Tukey's post-hoc test.

3 Results and discussion

The genomic breeding value (GBV) scores of the 1,452 cows in the shared international database were slightly below the 100-point average. The mean value of the population is calculated based on data from 4 to 5 year old cows, with individual values evaluated relative to this reference *(Himmelbauer et al., 2021)*.

The estimated composite/aggregate genomic breeding value score of 95.13% indicates a minor lag of the examined Hungarian population. Within the studied herd, the average scores were 97.91 for milk production, 98.11 for meat production, and 97.24 for fitness traits, respectively *(Table 2)*. Among the milk production-related parameters, milking speed reached the international average, whereas the other parameters showed a 2 to 4 point deficit (for other parameters, we experience a lag of 2-4 5). The composite udder conformation score, a key trait in phenotypic evaluation, also indicated a similar circa 5% lag. The 305-day corrected milk production average was 7,328 kg in first lactation, which means the examined population is among the best-performing Hungarian Simmental dairy herds. Herds in Austria and Germany, typically in the Bavarian region, are characterized by production levels around 8,000 kg, although the average herd size in these populations is substantially smaller.

Table 2 Genomic breeding values and phenotypic milk production traits of Hungarian Simmental cows

Parameters (1)	N	Min	Max	Mean (2)	s	cv%
Genomic BV (3)	1 452	66	130	95.13	10.33	10.86%
Milk production BV (4)	1 452	71	127	97.91	9.13	9.32%
Meat production BV (5)	1 452	75	121	98.11	6.73	6.86%
Fitness BV (6)	1 452	66	126	97.24	8.59	8.83%
Udder health BV (7)	1 452	69	127	96.24	7.92	8.23%
No of somatic cells BV (8)	1 452	75	125	96.67	7.79	8.05%
Milking speed BV (9)	1 452	74	128	100.51	8.30	8.26%
Mastitis indicator BV (10)	1 452	70	124	98.22	8.03	8.17%
Udder score BV (11)	1 452	65	130	95.34	9.01	9.45%
305-day milk yield (kg) (12)	1 012	2 353.00	11 107.00	7 328.31	1 509.76	20.60%
305-day milk fat (kg) (13)	1 012	77.40	496.30	283.54	64.46	22.73%
305-day milk protein (kg) (14)	1 012	77.50	390.70	261.70	51.47	19.67%

BV = breeding value (15)

2. táblázat. A magyar tarka tehenek genomikai tenyészértékei és fenotípusos tejtermelési tulajdonságai

paraméterek (1); átlag (2); genomikai TÉ (3); tejtermelés TÉ (4); hústermelés TÉ (5); fitnesz TÉ (6); tőgyegészség TÉ (7); szomatikus sejtszám TÉ (8); tejleadási sebesség TÉ (9); tőgygyulladás TÉ (10); tőgypontszám TÉ (11); 305 napra korrigált laktációs tejtermelés (12); 305 napra korrigált laktációs tejzsírtermelés (13); 305 napra korrigált laktációs tejfehérje-termelés (14); tenyészérték (TÉ) (15)

The correlation matrix of the evaluated traits showed relationships consistent in both direction and magnitude with those reported in the literature. The composite/aggregate breeding value index exhibited a significant, positive, and strong correlation with the milk production breeding value (r = 0.827), a moderate correlation with the fitness breeding value (r = 0.589), and a weak correlation with the meat production index *(Crews, 2013)* (r = 0.311), respectively *(Table 3)*.

The composite/aggregate breeding value showed weak, negative correlations with the phenotypic milk production traits (r = –0.090). Both the milk breeding value (r = –0.079) and the fitness breeding value (r = –0.041) showed similarly weak and slightly negative correlations with phenotypic milk production. In the case of the 305-day milk yield, the volumes of fat production and protein production each showed strong, positive correlations.

Table 3 Correlation matrix between breeding value scores and 305-day milk yield traits

Pearson correlation coefficient (1)	Milk BV (2)	Meat BV (3)	Fitness BV (4)	305-day milk yield (5)	305-day milk fat (6)	305-day milk protein (7)
Genomic BV (8)	0.827	0.311	0.589	–0.090	–0.103	–0.095
–p	<0.001	<0.001	<0.001	0.004	0.001	0.003
Milk BV		0.104	0.130	–0.079	–0.077	–0.075
–p		<0.001	<0.001	0.012	0.015	0.017
Meat BV			–0.023	–0.012	0.015	–0.040
–			0.390	0.708	0.644	0.203
Fitness BV				–0.041	–0.083	–0.040
–p				0.197	0.009	0.207
305-day milk yield					0.834	0.971
–p					<0.001	<0.001
305-day milk fat						0.850
–p						<0.001

BV = breeding value (9)

3. táblázat. Korrelációs mátrix a tenyészérték pontszámok és a 305 napos tejhozam tulajdonságok között

Korrelációs együttható (1); tejtermelés TÉ (2); hústermelés TÉ (3); fitnesz TÉ (4); 305 napra korrigált laktációs tejtermelés (6); 305 napra korrigált laktációs tejzsírtermelés (7); 305 napra korrigált laktációs tejfehérje-termelés (8); kompozit TÉ (8); tenyészérték (TÉ) (9)

At the start of the genomic selection program the heterogeneous age structure of the breeding population caused that genetic samples were collected from animals of various ages. As the program progressed, however, sampling could be performed already at calf age as soon as newborn animals were selected for breeding purposes. For the evaluation period, 305-day corrected lactation records were available for cows born between 2010 and 2023. The impact assessment clearly confirmed that significant differences exist between the average breeding values of the birth-year groups *(Table 4)*. The average milk breeding values of cows born in 2019 and 2020 already correspond to the average of the international population. Across the time series, a consistent upward trend is evident for both the combined breeding value and the milk breeding value. The meat breeding value shows a modest increase, whereas the fitness breeding value overall remains stagnant, with a slight decline observed in the most recent years.

Table 4 Breeding values and first lactation milk yield averages by cow birth groups

Year of birth (1)	GBV	Milk BV (2)	Meat BV (3)	FBV	305-day milk yield (kg) (4)	305-day milk fat (kg) (4)	305-day milk protein (kg) (5)
2010	89.00	89.40	97.60	97.60	7,244.50	258.25	256.28
2011	87.29	89.57	95.43	98.29	7,786.80	291.64	271.52
2012	89.27	90.27	97.50	99.77	7,863.56	307.26	280.28
2013	94.00	92.75	100.00	101.20	6,855.40	257.13	244.43
2014	93.59	94.79	97.41	99.86	7,361.63	269.96	260.85
2015	90.50	94.85	96.28	94.58	7,440.05	294.19	263.84
2016	94.56	97.20	99.06	96.88	7,790.14	300.36	274.52
2017	92.30	95.95	97.67	95.48	7,311.28	281.01	260.75
2018	94.15	97.67	97.36	96.71	7,310.39	282.34	261.25
2019	98.46	100.83	98.04	98.75	7,084.39	276.89	256.71
2020	98.60	101.00	99.14	97.70	7,200.55	283.39	258.37
Mean (7)	95.80	97.85	98.11	97.25	7,328.31	283.54	261.70
p	<0.001	<0.001	0.009	<0.001	<0.006	<0.008	<0.067

BV = breeding value (8); GBV = genomic breeding value (9); FBV = fitness breeding value (10)

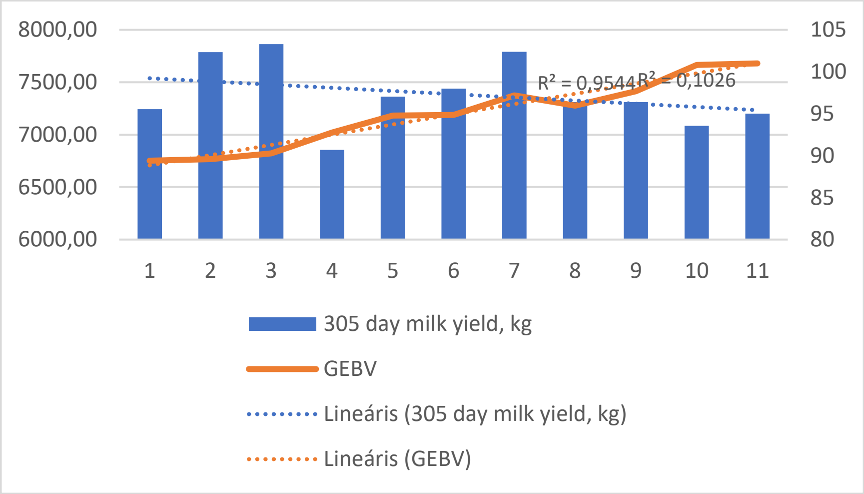
4. táblázat. A magyar tarka tehenek genomikai tenyészértékei és fenotípusos tejtermelési tulajdonságai

születési év (1); tejtermelés TÉ (2); hústermelés TÉ (3); 305 napra korrigált laktációs tejtermelés (4); 305 napra korrigált laktációs tejzsírtermelés (5); 305 napra korrigált laktációs tejfehérje-termelés (6); átlag (7); tenyészérték (TÉ) (8); genomikai TÉ (9) fitnesz TÉ (10)

The slight negative trend observed in the phenotypic production data was accompanied by no change in milk fat yield, while milk protein yield showed a minor decrease. The annual means and standard deviations of the evaluated traits displayed substantially greater variability than the breeding value data. The calculated milk fat and milk protein concentrations are characteristic of the Simmental breed group, averaging 3.87% and 3.57%, respectively.

The slope of the linear regression model for milk breeding value *(Figure 1)* clearly confirms the effectiveness of the selection program aimed at increasing milk production. Over a 20-year period, selection increased the average 305-day milk yield of the performance-tested Hungarian Simmental population by approximately 1,500 kg *(Polgár et al., 2023)*. In the context of dual-purpose breeding goals, the slight increase – or at least the maintenance – of beef production breeding values can also be regarded as a tangible achievement. For fitness traits, the trend is consistent with the general consensus in the literature, indicating that increasing milk yield may be associated with shrinking longevity and unfavourable changes in reproductive and physiological parameters.

The contrast between the improving trend of genomic estimated breeding values (GEBVs) for milk yield and the slightly negative trend observed in the phenotypic production of cows born in the same years is also striking. Notably, the 305-day milk yield records show outstanding results for the years 2011, 2012, and 2016, while data from the last four years are more homogeneous but remain below average (Figure 1). First-lactation milk yield does not follow the progression of the GEBV trend. The fit of the phenotypic milk yield trendline to the data (R^2 = 0.1026) is very weak, whereas the breeding value trendline (R^2 = 0.9544) indicates an exceptionally strong relationship.



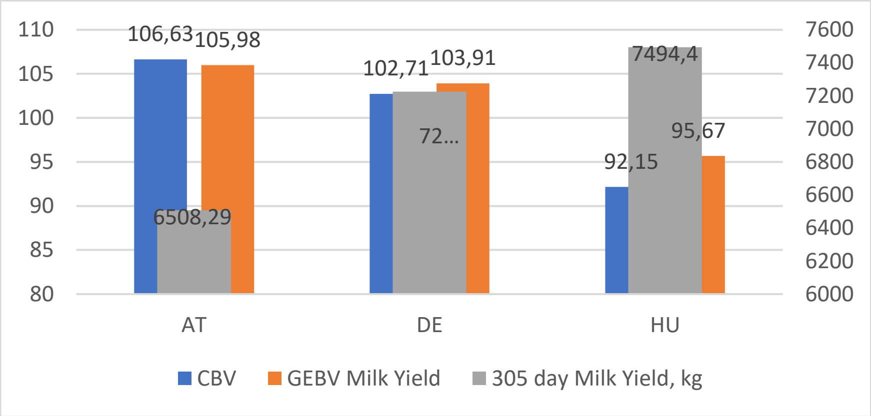
1. ábra. Fenotípusos 305 napos tejhozam és GEBV tejhozam trendek évjáratok alapján

Figure 1 Phenotypic 305 day milk yield and GEBV milk yield trends on the base of year groups

Collaborative breeding value estimation carried out jointly with other countries provides an excellent opportunity for those national breeders' association, which on its own would not be able to implement or finance such an activity *(Legarra and Ducrocq, 2012)*. At the same time, environmental factors affecting production, as well as genotype - environment interactions may amplify the genetic differences between the herds of the participating countries, thereby influencing the expression of breeding values under specific environmental conditions.

Because of the production of breeding bulls and the high number of bull-dam cows in the population, imported semen is used as well in the herd under investigation. The proportion of cows sired by Hungarian bulls (HU) was 77%, while those sired by Austrian (AT) and German (DE) bulls accounted for 11% and 12%, respectively. For both the average breeding values and the phenotypic milk production data, all evaluated traits showed statistically significant differences among the sire-origin groups.

The average GBV and Milk BV of cows sired by Hungarian bulls (HU) were substantially lower than those of cows sired by Austrian (AT)(–10 points) and German (DE) (–8 points) bulls. In contrast, for 305-day first-lactation milk yield, the ranking was reversed: Hungarian-sired cows produced 986 kg more milk than the Austrian-sired cows and 269 kg more than the German-sired cows on average. The smallest differences were observed for meat BV, while the fitness BV also showed a considerable lag for the Hungarian-sired population (–6 points compared with Austrian sires, –4 points compared with German sires) *(Figure 2* and *Table 5).*



2. ábra. GBV, GEBV tejhozam és 305 napos tejhozam apa származási csoportok alapján

Figure 2 GBV, GEBV milk yield and 305-day milk yield on the base of sire origin groups

Table 5 Effect of sire origin on breeding values and milk production traits

Parameters (1)	Country (2)	N	Mean (3)	SD	Minimum	Maximum
Genomic BV**	AT	162	106.63	7.80	89	130
	DE	181	102.71	8.02	86	120
	HU	1,109	92.15	9.14	66	123
	Total	1,452	95.08	10.36	66	130
Milk BV** (4)	AT	162	105.98	6.93	89	127
	DE	181	103.91	8.05	85	122
	HU	1,109	95.67	8.53	70	121
	Total	1,452	97.85	9.19	70	127

Parameters (1)	Country (2)	N	Mean (3)	SD	Minimum	Maximum
Meat BV** (5)	AT	162	100.32	7.55	83	121
	DE	181	99.51	7.72	77	119
	HU	1,109	97.56	6.31	75	120
	Total	1,452	98.11	6.72	75	121
FBV**	AT	162	102.80	8.16	84	122
	DE	181	100.03	8.34	77	126
	HU	1,109	95.99	8.26	66	121
	Total	1,452	97.25	8.59	66	126
305-day milk yield (kg) ** (6)	AT	125	6,508.29	1,319.66	3,203	10,011
	DE	155	7,225.42	1,575.71	3,089	11,031
	HU	732	7,494.40	1,481.03	2,353	11,107
	Total	1,012	7,331.40	1,510.79	2,353	11,107
305-day milk fat (kg) ** (7)	AT	125	256.40	51.19	129.2	402
	DE	155	268.74	66.26	87.2	491.3
	HU	732	291.58	64.48	77.4	496.3
	Total	1,012	283.73	64.56	77.4	496.3
305-day milk protein (kg) ** (8)	AT	125	233.33	46.01	115.1	347.3
	DE	155	258.46	54.68	98.1	360.5
	HU	732	267.38	50.10	77.5	390.7
	Total	1,012	261.81	51.52	77.5	390.7

** $p < 0.01$; BV = breeding value (9); GBV = genomic breeding value (10); FBV = fitness breeding value (11)

5. táblázat. Az apa származásának hatása a tenyészértékekre és a tejtermelési tulajdonságokra

paraméterek (1); az apa származási országa (2); átlag (3); tejtermelés TÉ (4); hústermelés TÉ (5); 305 napra korrigált laktációs tejtermelés (6); 305 napra korrigált laktációs tejzsírtermelés (7); 305 napra korrigált laktációs tejfehérje-termelés (8); tenyészérték (TÉ) (9); genomikai TÉ (10) fitnesz TÉ (11)

The average breeding value data and first-lactation milk yield for the German-sired group showed intermediate values in both cases, providing a consistent pattern. In the Austrian-sired group, the highest genomic estimated milk breeding values were observed, yet phenotypic milk production was the lowest. Conversely, Hungarian-sired cows exhibited the opposite trend, with the lowest estimated breeding values and the highest phenotypic milk yield.

4 Conclusions

The results of this study indicate that the genomic estimated breeding value of milk yield of the observed Hungarian population is approximately 5% below the average performance of the reference population. Nevertheless, the observed upward trend confirms the effectiveness of the conventional breeding strategies applied in previous years. When examining the actual milk production of progeny groups sired by bulls from different populations, substantial deviations from the expected performance based on genomic breeding values were observed. This discrepancy is likely due to the fact that genomic breeding value estimation has only been implemented for five years in Hungary, the Hungarian population contributes a relatively small number of cows to the estimation process, and there is a greater genetic distance from the reference population.

The declining trend in fitness traits can be attributed to selection efforts aimed at increasing milk production, which imposes greater physiological demands on the cows. In the genomic evaluation procedure, the fitness trait group receives the highest weighting, which indirectly promotes further improvement in milk and meat traits as well. The strong influence of the production environment on phenotypic performance highlights the critical role of technology and management in achieving optimal results.

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