Genetic parameters for growth traits in the Slovenian beef cattle population

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Abstract: This study compared genetic parameter estimates and correlations between estimated breeding values (EBVs) obtained using four single-trait animal models differing in the definition of the common herd-time environmental effect. Analyses were based on field performance records for birth weight (BW), weight at 90 days (W90), and weight at 210 days (W210) in Charolais and Limousin calves born in Slovenian suckler herds between 1990 and 2017. Model variants defined contemporary groups by herd only (H), or by herd combined with one-year (HY), two-year (HY2), or five-year (HY5) time periods. Heritability estimates varied across models: for BW, direct h² ranged from 0.25 to 0.39, for W90 from 0.11 to 0.37, and for W210 from 0.34 to 0.57. Corresponding maternal h² ranged from 0.10 to 0.13 (BW), 0.12 to 0.18 (W90), and 0.20 to 0.29 (W210). The proportion of variance due to common herd-time effects ranged from 0.25 to 0.44, and EBV correlations between models ranged from 0.61 to 0.95. The HY2 model provided the most balanced partitioning of phenotypic variance across traits and herds, providing the most practical solution for national genetic evaluations under the current data structure.

Key words: beef cattle, Charolais, Limousin, suckler cows, growth traits, genetic evaluation, heritability, models, model comparison, Slovenia

Ocena genetskih parametrov za lastnosti rasti v populaciji slovenskega mesnega goveda

Izvleček: V raziskavi smo primerjali ocene genetskih parametrov in korelacije med plemenskimi vrednostmi (PV), ocenjenimi s štirimi različnimi eno-lastnostnimi modeli živali, ki so se razlikovali v definiciji skupnega okoljskega vpliva črede skozi čas. Analize so temeljile na podatkih terenskih meritev za telesno maso ob rojstvu (BW), pri 90 dneh (W90) in pri 210 dneh starosti (W210) telet pasem šarole in limuzin, rojenih v slovenskih čredah krav dojilj med letoma 1990 in 2017. Primerjalne skupine so bile definirane kot: samo čreda (H), ali čreda v kombinaciji z enoletnim (HY), dvoletnim (HY2) oziroma petletnim (HY5) časovnim obdobjem. Ocenjeni dednostni deleži so bili: za BW 0,25–0,39 (direktni) in 0,10–0,13 (maternalni); za W90 0,11–0,37 in 0,12–0,18; za W210 0,34–0,57 in 0,20–0,29. Delež variance zaradi skupnega okoljskega vpliva črede je znašal 0,25–0,44, korelacije med PV različnih modelov pa 0,61–0,95. Model HY2 je zagotovil najbolj uravnoteženo razdelitev fenotipske variance med vplive in se je izkazal kot najustreznejša izbira za uporabo v nacionalnem genetskem vrednotenju pri obstoječi strukturi podatkov.

Ključne besede: mesno govedo, šarole, limuzin, dojilje, lastnosti rasti, genetsko vrednotenje, heritabiliteta, modeli, primerjava modelov, Slovenija

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1   INTRODUCTION

Charolais (CHA) and Limousin (LIM) are the most important specialised beef breeds in Slovenia, where suckler herds are managed extensively, primarily relying on grazing during the vegetation season (e.g., Krupová et al. (2025)). The main commercial products of these herds are weaned calves, with birth weight (BW), weight at 90 days (W90; corresponding to the onset of grazing), and weaning weight at 210 days (W210; end of grazing) routinely recorded for national genetic evaluations. Among these, W90 and W210 are particularly relevant for assessing both the calf's genetic potential for growth and the dam's maternal ability, while W210 directly affects breeder income (Simčič and Čepon, 2007; Madsen et al., 2025). Phenotypic expression of calf growth is influenced by both genetic and environmental sources of variation. The genetic contribution is typically partitioned into direct additive genetic effects and maternal additive genetic effects, the latter acting through the dam's genotype as well as the maternal environment she provides (Willham, 1972; Koch, 1971; Assan, 2025; Daneshi et al., 2025). These maternal effects are particularly pronounced in suckler systems, where calves rely entirely on their dams for milk (e.g., Davies & Denholm, 2025; Gellatly et al., 2025).

Environmental influences on calf growth traits include both permanent and temporary effects, such as climatic and nutritional variation, as well as measurement error, which reduces precision in genetic studies (Falconer, 1989). In the context of Slovenian extensive herds, important sources of shared environmental variation also arise from common herd environment and year of birth. The year effect typically captures annual fluctuations in climate and vegetation, affecting milk production and thus early growth. The common herd environment includes management practices such as feeding, health care, calving protocols, culling strategies, and grazing routines, which are shared by all animals within a herd (Troxel & Simon, 2007; Hasan et al., 2024; Edwards et al., 2025). To account for both spatial and temporal variation in management and environmental conditions, many genetic evaluation models use a herd-year interaction effect as an environmental grouping factor (Robinson, 1991; Phocas & Laloë, 2004; Schenkel et al., 2024). Such grouping enables more accurate separation of environmental and genetic effects, thereby improving the estimation of breeding values (EBVs).

The objective of this study was to assess how different specifications of the common environmental effect – defined as herd, herd-year, herd-2 years, or herd-5 years (collectively referred to as herd(-time)) – influence the estimation of genetic parameters and breeding values for early growth traits in Slovenian beef cattle. Specifically, we evaluated how these alternative temporal definitions of the common herd effect affect variance partitioning and EBV rankings.

2   MATERIALS AND METHODS

Genetic parameters and EBVs were estimated for BW, W90, and W210 using field test records from the Slovenian national routine genetic evaluation scheme for beef cattle. The analysed dataset included Charolais (CHA) and Limousin (LIM) calves of both sexes, born between 1990 and 2017 and reared in suckler herds under extensive conditions. All three traits were recorded in accordance with ICAR guidelines (International agreement of recording practices, 2018). The data structure was comparable across breeds and sexes.

Calvings predominantly occurred in late winter and spring, with animals typically kept on pasture from May to October. The parity effect was categorised into four groups based on parity number and calving performance, reflecting current national evaluation practice: first- and second-parity cows were assigned to separate classes, cows in their third to ninth parity were assigned to class 3, and those in their tenth or higher parity to class 4. The number of records per parity class was as follows: for BW, 993 (class 1), 859 (class 2), 2529 (class 3), and 159 (class 4); for W90, 737, 609, 1880, and 112; and for W210, 949, 792, 2447, and 157, respectively.

The data originated from 57 herds of varying sizes. While three herds had more than 500 animals, most contained fewer than 100 animals. The breeding programme initially involved the largest herd, with others joining progressively over time, resulting in an increase in average herd size during the study period. Due to the predominance of small herds, a single sire was used in 60.4–62.0% of herds per year, and two sires in up to 19.0% of herds (Figure 1). Larger herds typically used artificial insemination and multiple sires, thereby contributing most to genetic connectedness across herds. Genetic ties between herds were assessed based on pedigree links and sire usage, confirming sufficient relatedness to support across-herd evaluation.

Although phenotypic data were available for animals born between 1990 and 2017, analyses of sire distribution (Figure 1) were limited to 1995–2017 to reflect stable recording practices. Pedigree information used for the genetic evaluation of all three traits spanned five generations of ancestors (Table 1), including some animals originating from other breeds.

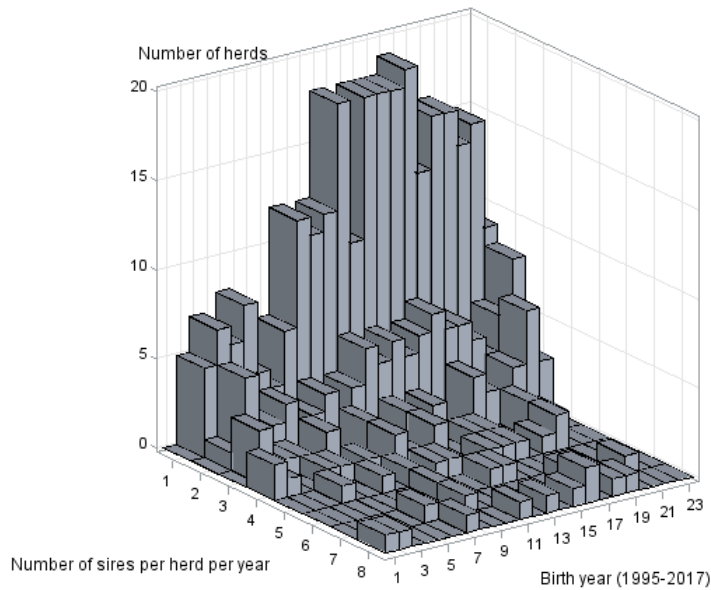Adjusted weights for W90 and W210 were calcu-

Figure 1: Distribution of sires across herds (birth years are denoted by sequential numbers: 1 = 1995, …, 23 = 2017)

Table 1: Pedigree structure

| N | Breed | | | |
	LIM	CHA	Other	Total
Animals	3060	3126	151	6337
Sires	265	273	10	548
Dams	781	847	141	1769

N: number; LIM: Limousin; CHA: Charolais; Other: other breeds

lated by interpolation to the exact ages of 90 and 210 days, in accordance with ICAR standards. Throughout this paper, W90 and W210 refer to these pre-adjusted weights. The number of records available for analysis

was similar for BW (4540) and W210 (4345), as both traits are mandatory in routine recording, while fewer observations were available for the optional W90 (3338) (Table 2). Birth weight was assumed to correspond to age 0 days, as calves are weighed within 24 hours of birth. The average trait values were 43.8 kg for BW, 142.3 kg for W90, and 257.9 kg for W210.

2.1 MODEL STRUCTURE

Four alternative single-trait animal models were tested to analyse sources of variation in each trait. These included the model currently used in the nation-

Table 2: Data structure and descriptive statistic

| Trait | Number of records | | Breed | | Weight (kg) | | Age (days) | |
			LIM	CHA	$\bar{x}$	SD	$\bar{x}$	SD
	T	4540	2333	2207	43.8	6.6	0	0
BW	M	2208	1126	1082	45.2	6.7		
	F	2332	1207	1125	42.5	6.5		
	T	3338	1846	1492	142.3	11.9	87.8	9.4
W90	M	1653	875	778	145.7	12.1	88.2	9.4
	F	1685	971	714	139.1	11.8	87.5	9.4
	T	4345	2181	2164	257.9	16.0	204.0	14.3
W210	M	2165	1082	1083	266.5	16.3	205.6	14.3
	F	2180	1099	1081	249.4	15.8	202.5	14.2

BW: birth weight; W90: weight at 90 days; W210: weight at 210 days; T: total; M: male; F: female; $\bar{x}$: mean; SD: standard deviation

al evaluation. The overall model structure was identical across variants, differing only in the definition of the common herd(-time) environmental effect. All models included the same fixed effects: breed, sex, year of birth, and parity class. Random effects included the direct additive genetic effect, the maternal additive genetic effect, and the residual. In addition, a random common herd(-time) effect was included to account for shared environmental influences.

The statistical model included both fixed and random effects, with the main distinction among model variants being the definition of the common environmental grouping (Table 3). Fixed effects were breed (B_i; i = 1, 2), sex (S_j; j = 1, 2), year of birth (L_k; k = 1995, …, 2017), and parity class (P_l; l = 1–4). Random effects included the common herd(-time) environmental ef-

Table 3: Model description

Model	Model equation		
HY		hy_m	
HY2	$y_{ijklmn} = \mu_{ijklmn} + B_i + S_j + L_k + P_l +$	hy_{2m}	$+ a_{ijklmn} + m_{ijklmn} + e_{ijklmn}$
HY5		hy_{5m}	
H		h_m	

HY: herd-year; HY2: herd-2 years; HY5: herd-5 years; H: herd

fect, direct additive genetic effect (a), maternal additive genetic effect (m), and residual error (e). Depending on the model variant, the random common environmental effect was defined either as a single herd effect (h_m) or a herd-time interaction effect defined for each calendar year (hy_m), two-year period (hy_{2m}), or five-year period (hy_{5m}). In the H model, a single group was defined per herd over the entire period, without any time division. The HY5 and HY2 models defined the herd–year interaction using five-year and two-year periods, respectively. The most detailed structure was applied in the HY model, where a separate group was defined for each calendar year. The HY model corresponds to the model used for BW in the national genetic evaluation, while the H model is used for W90 and W210 (Ocena plemenskih vrednosti, 2018). The response variable (y_{ijklmn}) represented the observed trait value (BW, W90, or W210, in kg) for each animal. The distributions of BW, W90, and W210 were approximately normal.

The (co)variance structure included direct and maternal additive genetic effects, their covariance, common herd-time effects (depending on the model), and residual error. Genetic effects were assumed to follow a multivariate normal distribution with variances proportional to the additive relationship matrix, while environmental and residual effects were assumed uncorrelated and homoscedastic.

2.2 CONTEMPORARY GROUP STRUCTURE

As expected, increasing the fragmentation of the time component resulted in smaller contemporary groups. The median group size clearly reflected this pattern, ranging from 5 to 27 animals per herd for BW, 4 to 16.5 for W90, and 5 to 22 for W210 (Table 4). This pattern indicates that most herds were small, with only a few large herds forming the upper range of group sizes. The number of contemporary groups increased, while their median size decreased, as the temporal definition of the herd effect became more detailed. The impact was most pronounced in smaller herds, whereas larger herds contributed disproportionately to the overall data structure in all model variants. This high variability in group size reflects the heterogeneous and unbalanced structure of the Slovenian beef population, particularly in terms of herd size distribution.

Table 4: Number and size of contemporary groups

Trait	Model	N Groups	Number of animals within group		
			Median	Min	Max
BW	HY	427	5	1	77
	HY2	254	9	1	142
	HY5	142	13	1	291
	H	54	27	4	965
W90	HY	345	4	1	64
	HY2	220	6	1	127
	HY5	122	10	1	267
	H	50	16.5	4	850
W210	HY	422	5	1	76
	HY2	264	7	1	125
	HY5	149	12	1	276
	H	57	22	4	985

BW: birth weight; W90: weight at 90 days; W210: weight at 210 days; N: number; Min: minimum; Max: maximum

2.3 ESTIMATION PROCEDURES

(Co)variance components were estimated for each trait using the restricted maximum likelihood (REML) method implemented in the VCE-6 software package (Kovač & Groeneveld, 2008). Based on these estimates, EBVs were obtained using best linear unbiased prediction (BLUP) under a single-trait model. The same pedigree file was used for all models to ensure comparability.

To assess the impact of different definitions of the common herd(-time) effect on sire ranking, Pearson correlation coefficients between sire EBVs were calculated. Only sires with EBV accuracy ≥ 0.30 were included in the comparison. Descriptive statistics and correlation analyses were performed using SAS/STAT software (SAS 9.4 Institute Inc., Cary, NC, USA).

3 RESULTS AND DISCUSSION

This study aimed to evaluate the impact of modelling the common herd(-time) environment on the estimation of genetic parameters and breeding values for early growth traits in Slovenian Charolais and Limousin calves. Using national field data, we analysed three economically relevant traits; birth weight (BW), weight at 90 days (W90), and weight at 210 days (W210), under four model variants differing in the temporal definition of the common herd environment (herd only, herd-year, herd-2 years, and herd-5 years). The analysis re-

vealed that the choice of herd(-time) grouping notably affected the partitioning of phenotypic variance and EBV ranking. Among the tested models, the two-year herd-time interaction (HY2) provided the best balance between precision and interpretability of genetic parameters.

To explore how different model structures influence genetic evaluation, we compared estimates of additive and maternal variances, common environmental effects, and residual components across traits. Additionally, correlations between estimated breeding values (EBVs) from different models were analysed to assess their robustness under alternative grouping schemes.

Variance component estimates for each trait and model combination are presented in Table 5. The estimates are reported in the original measurement units (kg²) and include direct additive genetic variance (σ^2_a), maternal additive genetic variance (σ^2_m), common herd(-time) environmental variance (σ^2_c), and residual variance (σ^2_e). Where available, standard errors (SEs) are shown in parentheses. Heritabilities and genetic correlations are summarised in Table 6, including direct heritability (h^2_a), maternal heritability (h^2_m), the proportion of variance explained by the common herd(-time) effect (c^2), residual proportion (e^2), and direct–maternal additive genetic correlation (r_{am}).

3.1 BIRTH WEIGHT (BW)

Phenotypic variance (σ^2_p) for BW was similar across all models, ranging from 27.5 to 32.3 kg², with

Table 5: Estimates of variances for body weight at birth (BW), weight at age 90 (W90) and 210 (W210) days (in kg²). Standard errors are shown in parentheses.

Trait	Model	σ^2_p	σ^2_c	σ^2_a	σ^2_m	σ^2_e
BW	HY	27.5	6.8 (1.0)	10.8 (1.6)	3.5 (0.8)	11.5 (0.9)
	HY2	30.5	10.4 (1.5)	8.5 (1.4)	3.0 (0.7)	13.0 (0.8)
	HY5	32.2	12.4 (1.9)	7.9 (1.3)	3.1 (0.7)	13.5 (0.8)
	H	32.3	12.3 (2.6)	9.2 (1.3)	3.9 (0.7)	13.4 (0.8)
W90	HY	604.8	264.9 (31.0)	66.7 (27.1)	70.1 (17.4)	266.1 (17.3)
	HY2	567.7	224.8 (30.4)	127.5 (33.2)	78.9 (18.0)	259.0 (19.3)
	HY5	561.1	220.8 (37.0)	155.5 (37.1)	90.8 (18.6)	261.3 (21.0)
	H	558.9	205.1 (47.9)	205.9 (38.0)	99.2 (18.2)	250.5 (21.3)
W210	HY	1752.0	734.6 (86.2)	600.7 (109.7)	409.5 (58.1)	574.1 (55.4)
	HY2	1861.9	809.6 (100.7)	636.0 (112.5)	376.6 (56.7)	616.9 (60.4)
	HY5	1750.1	709.7 (113.3)	806.7 (112.0)	410.7 (54.7)	590.5 (55.0)
	H	1611.9	527.4 (114.8)	919.0 (106.6)	466.7 (58.0)	601.8 (57.1)

σ^2_p: phenotypic variance; σ^2_a: direct additive genetic variance; σ^2_m: maternal additive genetic variance; σ^2_c: variance for the common herd environment; σ^2_e: residual variance; HY: herd-year; HY2: herd-2 years; HY5: herd-5 years; H: herd

Table 6: Estimates of genetic parameters and variance component proportions. Standard errors are shown in parentheses.

Trait	Model	c^2	h^2_a	h^2_m	e^2	r_{am}
BW	HY	0.25 (0.03)	0.39 (0.05)	0.13 (0.03)	0.42 (0.04)	−0.42 (0.11)
	HY2	0.34 (0.04)	0.28 (0.05)	0.10 (0.02)	0.43 (0.04)	−0.43 (0.12)
	HY5	0.38 (0.04)	0.25 (0.04)	0.10 (0.02)	0.42 (0.04)	−0.48 (0.11)
	H	0.38 (0.05)	0.28 (0.04)	0.12 (0.02)	0.41 (0.04)	−0.54 (0.08)
W90	HY	0.44 (0.03)	0.11 (0.04)	0.12 (0.03)	0.44 (0.04)	−0.46 (0.17)
	HY2	0.40 (0.04)	0.22 (0.05)	0.14 (0.03)	0.46 (0.05)	−0.61 (0.10)
	HY5	0.39 (0.04)	0.28 (0.06)	0.16 (0.03)	0.47 (0.06)	−0.70 (0.08)
	H	0.37 (0.06)	0.37 (0.07)	0.18 (0.03)	0.45 (0.06)	−0.71 (0.07)
W210	HY	0.42 (0.04)	0.34 (0.06)	0.23 (0.03)	0.33 (0.04)	−0.57 (0.08)
	HY2	0.43 (0.04)	0.34 (0.06)	0.20 (0.02)	0.33 (0.04)	−0.59 (0.07)
	HY5	0.41 (0.04)	0.46 (0.06)	0.23 (0.02)	0.34 (0.05)	−0.67 (0.06)
	H	0.33 (0.05)	0.57 (0.06)	0.29 (0.03)	0.37 (0.05)	−0.69 (0.05)

c^2: proportion of common herd in environmental variance; h^2_a: direct heritability; h^2_m: maternal heritability; e^2: proportion of residual variance; r_{am}: direct-maternal (additive) genetic correlation; HY: herd-year; HY2: herd-2 years; HY5: herd-5 years; H: herd

the lowest value in the HY model (Table 5). Slight variation in the estimated variance components, and thus in phenotypic variance, reflects differences in model structure, particularly in the specification of the common herd(-time) environmental effect. Direct additive genetic variance (σ^2_a) declined when the herd-only model (H) was replaced with longer herd-time interaction groupings (HY5), but increased again with finer fragmentation (HY2 and HY). Maternal additive genetic variance (σ^2_m) was lowest in HY2 and HY5, and slightly higher in HY and H models. The proportion of phenotypic variance attributed to the common herd(-time) effect (c^2) decreased substantially in the HY model (25%) compared to 38% in the HY5 and H models. Residual variance (σ^2_e) was relatively stable, contributing 41%–43% across models (Table 6).

Estimates of direct heritability (h^2_a) ranged from 0.25 (HY5) to 0.39 (HY), and maternal heritability (h^2_m) from 0.10 to 0.13 (Table 6). The highest h^2_a in HY may be inflated due to small group sizes and low sire overlap, leading to confounding of environmental effects with genetic variance. Broader groupings (H, HY5) likely produced more accurate separation of genetic and environmental components. Genetic correlations between direct and maternal additive effects (r_{am}) were moderately negative, ranging from –0.42 (HY) to –0.54 (H) (Table 6). Stronger antagonism in H and HY5 suggests clearer distinction of direct and maternal contributions when contemporary groups are broader.

There is limited literature on the genetic evaluation of traits in suckler populations, particularly under extensive systems. However, several studies provide estimates for BW in similar breeds. For LIM, Meyer (1992) reported h^2_a = 0.22, h^2_m = 0.05, and r_{am} = –0.16, while for CHA, reported values were h^2_a = 0.42, h^2_m = 0.17, and r_{am} = –0.39. These results are broadly comparable to our estimates, especially those from the HY5 and HY models, suggesting that the different degrees of herd-time fragmentation can yield estimates similar to published benchmarks when appropriately structured. In our data, the HY5 model for LIM yielded heritability close to Meyer's estimates, while the HY model for CHA showed strong agreement with values for that breed. These consistencies suggest that the definition of contemporary group plays a pivotal role in aligning genetic parameter estimates with known breed characteristics.

In comparison, Crews et al. (2004) reported h^2_a = 0.53, h^2_m = 0.16, and σ^2_e = 9.6 kg^2 for BW in Canadian Charolais cattle, which are generally higher than our estimates. Genetic correlations in H and HY5 models were closest to their results. Differences may reflect larger dataset, more consistent management, and single-herd structure. Čepon et al. (2008, 2009) reported higher h^2_a (0.62–0.74) and lower h^2_m and r_{am}, but these were based on test station data without common herd(-time) effects, which likely reduced environmental variance.

In summary, the results for birth weight reveal that direct heritability was moderate (0.25–0.39), and maternal heritability was low (0.10–0.13). The choice of herd(-time) grouping substantially affected variance partitioning, with HY inflating genetic variance and H/HY5 better balancing environmental sources.

3.2 WEIGHT AT 90 DAYS (W90)

For W90, phenotypic variance (σ^2_p) ranged between 558.9–604.8 kg² across models (Table 5). Genetic variances (σ^2_a, σ^2_m) decreased as herd-time groups became more fragmented. In the HY model, σ^2_a dropped markedly (66.7 kg²), likely due to inadequate sire overlap across small herds, confounding genetic with environmental effects. The maternal component (σ^2_m) was less variable but still showed the highest value in the H model (99.2 kg²). Common herd(-time) variance (σ^2_c) increased with fragmentation: from 205.1 kg² (H) to 264.9 kg² (HY), contributing 37% to 44% of σ^2_p. Residual variance remained high across all models (44%–47%) (Table 6). Direct heritability (h^2_a) ranged from 0.11 (HY) to 0.37 (H). Maternal heritability (h^2_m) was highest in H (0.18) and lowest in HY (0.12). The genetic correlation r_{am} became more negative with fragmentation (Table 6), from –0.46 (HY) to –0.71 (H), indicating stronger antagonism where genetic effects were better separated.

Only a few studies include W90 specifically. Čepon et al. (2008, 2009) reported h^2_a = 0.23–0.33, h^2_m = 0.12, and r_{am} = –0.61 for W90 in Slovenian CHA herds under test-station conditions, which differ from our more field-based population structure. Our estimates in HY2 and HY5 are relatively consistent with these findings, supporting their applicability in structured genetic evaluations.

Ulutaş et al. (2001) reported r_{am} = –0.46 for 100-day weights in Welsh Black suckler cattle, which aligns closely with our HY model estimate (r_{am} = –0.46). These values are consistent with Lee (2002), who summarised genetic antagonism between direct and maternal additive effects in beef breeds, with r_{am} ranging from –0.21 in Gelbvieh to –0.32 in Simmental. The more extreme values observed in our study may reflect higher variability in management conditions, maternal dependence of early calf growth, and the explicit modelling of both direct and maternal additive effects in fragmented herd structures.

The results for W90 indicate that direct heritability was the lowest among traits (0.11–0.37), while maternal heritability was moderate. Increased fragmentation inflated c² and reduced h^2_a. The H and HY2 models provided the most balanced partitioning. Negative r_{am} values indicate strong antagonism.

3.3 WEIGHT AT 210 DAYS (W210)

Phenotypic variance for W210 ranged from 1611.9 kg² (H) to 1861.9 kg² (HY2) (Table 5). Di-

rect additive genetic variance (σ^2_a) was highest in H (919.0 kg²) and decreased with fragmentation, especially in HY2 (636.0 kg²) and HY (600.7 kg²). Maternal additive variance (σ^2_m) followed a similar pattern, with H having the highest value (466.7 kg²). Common herd(-time) variance (σ^2_c) ranged from 527.4 kg² (H) to 809.6 kg² (HY2), accounting for 33% to 43% of phenotypic variance (Table 6). Residual variance was lowest for this trait (33%–37%). Direct heritability (h^2_a) was highest for this trait, ranging from 0.34–0.57, with the highest in H. Maternal heritability also reached 0.29 in H, compared to 0.20–0.23 in other models (Table 6). The genetic correlation r_{am} was again most negative in H (–0.69) and least negative in HY (–0.57).

Compared to the literature, Crews et al. (2004) reported h^2_a = 0.22, h^2_m = 0.10, and σ^2_e = 500.2 kg² in Canadian CHA cattle, all lower than our W210 estimates, particularly for residual variances. Similarly, Meyer (1992) summarised literature values for weaning weight in LIM cattle, reporting h^2_a = 0.16 and h^2_m = 0.15, both lower than our findings. Čepon et al. (2008, 2009) reported h^2_a = 0.29, h^2_m = 0.12, and r_{am} = –0.30, all lower than our findings except for the genetic correlation, suggesting that our broader dataset and inclusion of herd effects enabled better variance separation. Meyer (1997) reported r_{am} ranging from –0.65 to –0.30 for LIM weaning weight, matching our range of r_{am} from –0.69 to –0.57. These results reinforce the importance of modelling both direct and maternal components, particularly in extensive systems where the dam's influence on calf growth is substantial.

In Czech CHA populations, Vostrý et al. (2007) found σ^2_a = 71.3–167.2 kg², σ^2_m = 27.2–76.8 kg², and r_{am} = –0.15–0.42 for weaning weight, generally lower than our values. Their higher residual variance (σ^2_e = 658–690 kg²) may reflect differences in data completeness or environmental noise. In contrast, our higher additive and maternal variance, and lower residuals, suggest successful partitioning in our chosen models (HY2/HY5). Kennedy and Henderson (1975) reported σ^2_c = 222–238 kg² (25–28%) for Hereford and 178–331 kg² (25–41%) for Aberdeen Angus at weaning, while other estimates ranged from 0–8%. Our estimates of σ^2_c = 527–810 kg² (33–43%) for W210 are higher and may reflect greater heterogeneity in Slovenian herds, smaller group sizes, or stronger maternal dependence. These results highlight the substantial influence of common herd(-time) effects, particularly in fragmented, extensive systems.

W210 stood out as the trait with the highest total genetic contribution. The h^2_a and h^2_m were highest among all traits, and c² was also substantial. Models H

and HY5 provided the best balance of variance components.

Phenotypic correlations (r) between body weights at different ages vary among beef-type breeds and production systems. In Bali and Nguni cattle, both reared primarily for beef, low to moderate correlations were reported between birth and weaning weights (r = 0.10–0.34), while correlations between weaning and later weights were substantially higher (r = 0.90) (Assan, 2006; Gunawan and Sari, 2012). Similar patterns were described in European beef breeds (Krupa et al., 2005) and are supported by a meta-analysis demonstrating that prenatal and early postnatal nutrition influence both calf birth and weaning weights (Barcelos et al., 2022). Collectively, these findings indicate that birth weight has only a limited association with weaning weight, whereas weights measured at later developmental stages are more strongly interrelated and better reflect cumulative growth potential.

3.4 ESTIMATED BREEDING VALUE (EBV) CORRELATIONS BETWEEN MODELS

Table 7 presents Pearson correlations between sire EBVs across models. Only sires with EBV accuracy ≥ 0.3 were included. Correlation coefficients were highest for BW and W210 (up to 0.95) and lowest for W90 (as low as 0.61). The highest agreement was between HY and HY2 (0.89–0.95), indicating that adding an extra year did not substantially change the genetic evaluation. The lowest correlations were between H and HY (0.61–0.80), where environmental grouping structure

Table 7: Correlations among estimated breeding values for BW, W90 and W210 between models (sires with EBV accuracy ≥ 0.3)

Trait	N	Model	HY5	HY2	HY
BW	113	H	0.85	0.81	0.80
		HY	0.87	0.95	
		HY2	0.92		
W90	87	H	0.72	0.65	0.61
		HY	0.80	0.89	
		HY2	0.87		
W210	109	H	0.87	0.77	0.75
		HY	0.80	0.89	
		HY2	0.89		

BW: birth weight; W90: weight at 90 days; W210: weight at 210 days; HY: herd-year; HY2: herd-2 years; HY5: herd-5 years; H: herd; N: number of estimated breeding values

differed most. These patterns indicate that EBV rankings were sensitive to the definition of the common herd(-time) effect. Greater fragmentation (HY) led to lower EBV correlations with broader groupings (H).

3.5 LIMITATIONS AND FUTURE PERSPECTIVES

Across all traits, genetic correlations between direct and maternal additive effects became progressively less negative with increasing fragmentation of the herd(-time) grouping. The largest shift occurred for W90 in the HY model, consistent with patterns observed in other suckler systems. While such correlations reflect genetic associations, they do not imply causality. Calf growth is influenced by both its own genetic potential and the genetic merit of the dam, particularly in early development. These effects are known to be negatively correlated due to physiological and evolutionary trade-offs (Willham, 1972).

As shown by the literature, negative r_{am} values are common and relevant for breeding decisions, particularly in suckler herds where the maternal contribution is substantial and cannot be ignored. The inclusion of both direct and maternal additive genetic effects in models is therefore essential for unbiased genetic evaluations. Although the distinction between maternal additive genetic and environmental effects was acknowledged, they were not separated in this study due to small herd sizes and convergence challenges. Combining them resulted in more stable model fitting. Interpretation of comparative genetic parameters should consider that, with the exception of Simčič and Čepon (2007) and Čepon et al. (2008, 2009), most referenced studies were conducted on populations considerably larger than the Slovenian cattle population, potentially limiting direct comparability due to differences in population size effects on parameter estimation precision. Future research using larger, more balanced datasets from similarly-sized populations would help address both the limiaions in parameter estimation precision and enable better separation of maternal genetic and environmental effects. Direct heritability was highest for W210 and lowest for W90, while maternal heritability was similar across traits, with a slight peak at W210. W90 had the highest environmental (c^2 and e^2) proportions, making it most sensitive to herd(-time) grouping.

Although season of calving could theoretically account for additional environmental variation, its inclusion in the model was not expected to substantially improve model fit, as more than 95% of calvings occurred within the same season. In addition, introducing season into the model would further fragment the contempo-

rary groups, which in the context of our dataset was not considered an optimal approach. Therefore, season was not included as a model effect, since its potential impact on the results was expected to be negligible.

This study underscores the importance of contemporary group definition in genetic evaluation, particularly in small, extensively managed herds. Although limited by the absence of SNP data, the use of single-trait models, and potentially inconsistent measurement timing, the findings highlight the influence of herd(-time) fragmentation on variance estimates and EBV rankings. Incorporating SNP genotypes and genomic prediction models (e.g., GBLUP or ssGBLUP) in future research would enable more accurate partitioning of genetic and environmental effects, improve prediction accuracy, and support early genomic selection, especially when opportunities for extensive progeny testing across herds are limited.

4   CONCLUSIONS

The common herd environment significantly affected genetic parameter estimates for early growth traits. Among the models tested, the two-year herd-time interaction (HY2) provided the most balanced variance partitioning and stable EBV correlations. Excessive fragmentation (e.g., by year) distorted results, while broader intervals (HY5) performed similarly to HY2. Future evaluations should adapt contemporary group definitions to herd structure and data size. Including genomic information is recommended to further improve the accuracy of genetic evaluations in small, extensively managed beef cattle populations.

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