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Genetic and genomic parameters of piglet birth-weight traits and litter size in Czech Large White and Landrace sows

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Abstract: This study aimed to estimate heritabilities of piglet birth-weight traits and to investigate the relationships between piglet birth-weight and litter-size traits using field data from Czech Large White and Landrace sows. Data including 86 241 piglets from 5 536 litters were analysed using repeatability, genetic, and genomic models. The investigated piglet-weight traits included arithmetic mean birth weight (MBW), within-litter standard deviation (SDBW), coefficient of variation in birth weight (CVBW), and the proportion of small piglets in the litter (SMALL). Heritability rates of piglet-weight traits were low, with the highest estimates for MBW (0.06–0.10) and SMALL (0.08–0.17), depending on the model used, while the other within-litter variability traits showed heritability rates from 0.03 to 0.05. The heritability rates of litter-size traits, including the number of piglets born alive (NBA) and the number of piglets weaned (NW), were low and ranged from 0.05 to 0.07. The realised accuracies of prediction were moderate to high, ranging from 0.50 to 0.72 for piglet-weight traits and from 0.54 to 0.77 for litter-size traits, with ssGBLUP improving realised accuracy by 4–15% in comparison to BLUP. Genetic correlations estimated using BLUP and ssGBLUP indicated that litter size at birth (NBA) tended to be negatively associated with MBW and positively or weakly associated with piglet-weight variability traits (SDBW, CVBW, and SMALL), whereas NW tended to show positive correlations with MBW and negative correlations with variability traits. However, none of the correlations were statistically significant.

Keywords: genetic correlation; heritability; litter size; pig; piglet variability

Selection for increased litter size in pigs has led to larger litters over recent decades (Knap et al. 2023). However, larger litters are associated with a higher proportion of piglets with low birth weight, increased within-litter variation in birth weight (Riddersholm et al. 2021), and a greater number of piglets affected by varying degrees of intrauterine growth delays (Matheson et al. 2018; Riddersholm et al. 2021). Piglets with low birth weight (weight ≤1.1 kg) showed a higher mortality rate than those with higher weights, particularly within the first week after birth. Such piglets also exhibited lower lean cut yield in carcasses, which can be positively affected by neonatal care (Romero et al. 2022). Small piglets consume significantly less colostrum (Schoos et al. 2023), and those that are small and weak are at an even greater disadvantage when they compete with their littermates for access to the sow's teats (Chou et al. 2022), which leads to a higher incidence of starvation (Romero

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et al. 2022). These facts lead to necessary management interventions, such as litter equalisation, cross-feeding, and the use of milk replacers in supplementary feeding devices, which are essential for improving the survival rates of piglets and those that are weak (Vande Pol et al. 2021a,b). While these interventions can improve piglet survival, they also increase labour inputs and production costs. The need for robust piglets is further emphasised by the anticipated shift towards loose farrowing systems, which can make stockperson interventions aimed at improving piglet survival more difficult despite improving sow welfare (Glencorse et al. 2019).

Studies show that balanced selection strategies reduce the antagonistic effects between litter size and birth weight, within-litter variability, and mortality. For example, Knap et al. (2023) concluded that balanced selection strategies mitigate the antagonistic effects between litter size and birth weight and that including additional traits in breeding goals would be beneficial. In the Czech Republic, the breeding goal was also expanded upon. In addition to the number of piglets born and those born alive, piglet survival, expressed as the number of piglets weaned, was included (Krupa and Wolf 2013). Furthermore, the number of teats was incorporated to enhance the sow's maternal abilities (Krupa et al. 2016). Additional updates of the breeding goal were implemented in 2021, primarily involving modifications of the selection indexes applied.

Nevertheless, breeders continue to seek traits that further strengthen balanced breeding objectives. One possible approach is to incorporate traits derived from individual piglet birth weights. The present study aims to evaluate data obtained from litter weighing and to assess its potential for selection purposes.

MATERIAL AND METHODS

Data and data processing. Individual piglet weights were collected in Large White (LW) and Landrace (L) nucleus herds between 2018 and 2024. Herd staff weighed liveborn piglets within 12 h after birth with an accuracy of 10 g. A total of 6 632 weighed litters were available in the database. Following outlier detection, 569 (8.6%) litters were excluded from subsequent analyses, including those with fewer than 10 total born piglets (TNB), a farrowing interval shorter than 130 days or longer than 182 days, and from sows whose age at first farrowing was below 11 months. Since not all litters were weighed in the herds, only those for which it was possible to merge them into herd–year–season (HYS) groups based on farrowing date were retained in the dataset. Each HYS group was required to contain at least 20 litters and to cover the shortest possible period. First, we divided litters into preliminary clusters, which, if too small, were iteratively merged with neighbouring clusters under progressively relaxed maximum length thresholds. The final HYS length could not exceed 210 days. The grouping of records into HYS resulted in a total of 122 HYS levels, with an average time span of 102 ± 46.2 days and an average number of records of 45.4 ± 20.8.

In total, 5 536 litters with 86 241 individually weighed piglets from 2 049 LW and 665 L sows were included in the analysis. Litters were either purebred (75%) or crossbred, and the service sires (424 in total) were exclusively of maternal LW or L breeds. From the available piglet weights, the following traits were derived: arithmetic mean of piglet weight within litter (MBW), standard deviation of piglet weight within litter (SDBW), coefficient of variation in piglet weight within litter (CVBW), and proportion of small piglets among liveborn (SMALL), calculated as the percentage of piglets weighing less than 1.1 kg. Next, the number of liveborn piglets (NBA) and the number of piglets weaned at 18–24 days (NW) were additional traits used in the analyses. Other available litter-level information included parity (PAR), gestation length (PREG), and breed of dam (BREEDD) and sire (BREEDS). PAR was coded as first to fifth parity, and ≥ sixth parity, while PREG was grouped into eight levels (<113, 113–118 by day, and >118 days). Since HYS was constructed solely to ensure sufficient data within as short a time period as possible, and thus does not reflect seasonal effects, a year–season factor (YS) was added. The descriptive statistics of the data are presented in Table 1.

SNP genotype data were available for 1 631 animals with a call rate of at least 0.90. Genotyping was performed using the PorcineSNP60 v2 BeadChip (61 565 SNPs) and the GGP Porcine 50K arrays (50 697 SNPs). In total, genotypes of 975 sows (751 LW and 224 L) with weighed litter data were available. Only SNPs present in both fields, loci with a minor allele frequency (MAF) >0.05, and

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Table 1. Descriptive statistics of the data

Parameter	Mean	SD	Min	Max
Total number of piglets born (TNB)	16.70	2.70	10.0	28.0
Number of piglets born alive (NBA)	15.58	2.22	10.0	24.0
Number of piglets weaned (NW)	13.60	2.13	9.0	23.0
Proportion of stillborn	0.07	0.08	0.0	0.60
Proportion of losses until weaning	0.13	0.10	0.0	0.50
Mean of piglet weight within litter (MBW, g)	1 308	142.8	665	2 059
SD of piglet weight within litter (SDBW, g)	128.4	62.6	5.0	566
Coefficient of variation of piglet weight within litter (CVBW)	9.97	5.06	0.35	44.54
Minimal piglet weight within litter (g)	1 068	210.9	500	1 800
Maximal piglet weight within litter (g)	1 515	186.1	1 000	2 500
Proportion of piglets <1.1 kg (SMALL, %)	10.2	16.45	0.0	100.0
Length of pregnancy (PREG, days)	114.8	1.58	110.0	125.0

polymorphic loci without missing genotypes were retained for further analysis (31 003 SNPs).

Statistical analysis. First, we performed an analysis of variance to evaluate the effects of factors on the traits using R software (R Core Team 2022). The relative importance of each factor was assessed by sequentially excluding it from the full model and evaluating the reduced model using likelihood ratio tests and changes in explained variance. The main systematic effects influencing the evaluated piglet-weight traits were, in order of importance, HYS, litter size (TNB), YS, and PAR. Piglet-weight traits, except MBW, were also significantly influenced by PREG. The breed of the sow ranked last among the explanatory variables in terms of importance.

Genetic parameters were estimated using both BLUP and ssGBLUP methods. The pedigree was traced back for 20 generations and included 10 338 animals. Initially, each trait was analysed with a univariate repeatability model, and bivariate repeatability models were subsequently implemented, pairing each piglet-weight trait (MBW, SDBW, CVBW, and SMALL) with a litter-size trait (NBA and NW). The general statistical model was expressed as follows:

$$Y = X\beta + Zu + e \tag{1}$$

where:

Y – the vector of phenotypes (piglet-weight or litter-size traits);

X, Z – incidence matrices for fixed and random effects, respectively;

β – the vector of fixed effects;

u – the vector of random animal effects;

e – the residual.

The random animal effects were assumed to follow a multivariate normal distribution $u \sim N\left(0, A\sigma_u^2\right)$, where A is the numerator relationship matrix and σ_u^2 is the additive genetic variance. The residual effects were assumed to be normally distributed as $e \sim N\left(0, I\sigma_e^2\right)$.

Univariate models for piglet-weight traits included fixed effects (HYS, YS, PAR, BREEDD, and, except for MBW, PREG) and the sow's additive genetic effect as a random factor. Models were fitted with or without the sow's permanent environmental effect (PE) and litter size (NBA). For litter-size traits, fixed effects included HYS, YS, PAR, BREEDD, and BREEDS; random effects included the sow's additive genetic effect and PE. Bivariate models followed the univariate structure, excluding NBA for piglet-weight traits.

Genetic parameters were estimated using the AI-REML algorithm implemented in the BLUPF90 family of programmes (Misztal et al. 2014), and standard errors of estimates were approximated following the BLUPF90 tutorial (Masuda 2018).

Model performance was compared based on realised accuracy (rEBV), assessed as the correlation between breeding values predicted from a reduced dataset, in which validation animals were represented only by pedigree, and breeding values obtained from the complete dataset, where the same validation animals also had phenotypic records.

RESULTS AND DISCUSSION

Phenotypic data. Despite a relatively large average litter size (16.7 piglets born), the mean piglet birth weight in our population reached 1 309 g (Table 1), which is comparable to values reported by Sell-Kubiak et al. (2015) for litters of similar size (1.21 and 1.31 kg in litters of 16.3 and 15.2 piglets born, respectively). In contrast to most published studies, the variability of piglet birth weight observed in our dataset was markedly lower, as indicated by a coefficient of variation of 10% and a standard deviation of 128 g. Previous studies typically reported CVBW values ranging from 18% to 22%, with extremes up to 27.2% in litters with 17 piglets born (Sell-Kubiak et al. 2015; Declerck et al. 2017; Matheson et al. 2018; Camargo et al. 2020). Only one study (Boonkum et al. 2025) reported CVBW at a similar level of 11%, albeit with a much lower litter size (11.4 TNB).

The threshold used to define small piglets was set empirically at 1.1 kg, corresponding approximately to the 15th percentile of birth weights in our dataset. A similar cut-off was applied by Romero et al. (2022), who demonstrated that such piglets had a markedly higher mortality rate compared with heavier individuals (32% vs 10%). Mbuthia et al. (2025) reported a slightly higher threshold of 1.18 kg, below which survival probability at birth was reduced.

Heritability estimates. Overall, the heritability estimates for all traits (Table 2) were low and, except for SDBW and CVBW, statistically significant at $P < 0.05$. The highest heritability was found for SMALL (0.070 ± 0.021 and 0.165 ± 0.020 in the models with and without PE, respectively), followed by MBW (0.059 ± 0.019 and 0.101 ± 0.018 in the models with and without PE). The proportion of variance explained by the permanent environmental effect of the sow was statistically significant ($P < 0.05$) for all traits except SDBW and CVBW. For traits reflecting variability in piglet weights within litters, the exclusion of PE from the models appears justified. An exception was SMALL, which also represents variability but was adjusted for the number of piglets weighed. For this trait, the proportion of PE in the total variance was the highest among all traits studied (0.09), and when PE was excluded from the model, almost all of this variance was shifted to the genetic component. A similar tendency was observed for MBW, although the variance explained by PE was lower (0.054), and when PE was excluded, part of this variance was absorbed by the residual. The highest repeatability was found for SMALL (up to 0.169), followed by MBW (0.113), NW (0.101), and NBA (0.095). For the other traits, repeatability was below 6%.

The heritability estimates for MBW in this study were lower than those reported by other authors: values of 0.30–0.36 were reported by Matheson et al. (2018) and Camargo et al. (2020), and even the lowest estimate of 0.183 published by Boonkum et al. (2025) was approximately three times higher than those obtained in our study. In those studies, litter size was included as one of the explanatory variables. Similarly, in our study, analysis of the phenotypic data confirmed a strong influence of litter size at birth (after accounting for environmental effects, HYS and YS, litter size was the most important explanatory variable). However, the inclusion of litter size in the model, whether as a fixed factor or as a covariate, tended to further reduce the heritability of MBW. This outcome is consistent with the results of bivariate models with litter size, where the proportion of variance in piglet weight explained by the genetic factor did not increase.

The heritability estimates of piglet-weight variability traits within litters (SDBW and CVBW) were low (0.01–0.07) in published studies (Matheson et al. 2018; Camargo et al. 2020), which is consistent with the values reported here. The proportion of variance explained by the permanent environmental effect of the sow, as reported in the literature, ranged from 0.01 to 0.06, with a median of 0.05, and is therefore comparable to the level observed in the current study.

Heritability estimates for litter size were lower than those previously reported in studies on LW and L data in Czechia. Krupa and Wolf (2013) published heritability rates of 0.10 and 0.09 for TNB and 0.09 and 0.07 for NW in LW and L breeds, respectively. Similar values were found by Ogawa et al. (2019): 0.09 for L and 0.08 for LW. In the present study, heritability for both traits was approximately 70% of the values reported by those authors. Lin et al. (2024) reported heritability rates of 0.170, 0.115, and 0.077 for TNB, NBA, and stillborn, respectively. However, Zaalberg et al. (2023) found heritability rates ranging from 0.04 to 0.08 for NBA and NW, which is comparable with our results (see Table 2).

The low heritability estimates observed in this study are likely attributable to a combination of the

Table 2. Estimates of variance, heritability, proportion of permanent environmental effect on total variance, and realized accuracy for litter-size traits, average piglet birth weight, and uniformity of piglet birth-weight traits from BLUP and ssGBLUP univariate models[1]

Trait	Model	Genetic variance	PE variance	Residual variance	h^2	pe^2	rEBV
NBA	G	0.190**	0.216**	3.87***	0.045**	0.050**	0.609
	B	0.194**	0.197*	3.87***	0.046**	0.046*	0.535
NW	G	0.197***	0.163*	3.20***	0.055***	0.046*	0.768
	B	0.211***	0.135*	3.20***	0.060***	0.038*	0.698
MBW	G	616**	569**	9 311***	0.059**	0.054**	0.724
	Gwpe	1 077***	–	9 551***	0.101***	–	0.631
	Gnba	496**	448*	8 796***	0.051**	0.046*	0.677
	B	323*	764***	9 319***	0.031*	0.073***	0.681
	Bwpe	846***	–	9 660***	0.080***	–	0.611
	Bnba	220	623	8 809***	0.023	0.065	0.586
SDBW	G	62.2*	13.2	1 925***	0.031*	0.006	0.680
	Gwpe	69.9**	–	1 932***	0.035**	–	0.673
	Gnba	70.2*	20.8	1 877***	0.035*	0.010	0.707
	B	49.3	20.7	1 924***	0.025	0.009	0.520
	Bwpe	61.4*	–	1 935***	0.031**	–	0.502
	Bnba	56.2	28.9	1 876***	0.029	0.014	0.568
CVBW	G	0.596**	0.191	12.8***	0.044**	0.014	0.636
	Gwpe	0.705***	–	12.9***	0.051***	–	0.631
	Gnba	0.605**	0.113	12.7***	0.045**	0.008	0.644
	B	0.602**	0.156	12.8***	0.044**	0.011	0.552
	Bwpe	0.695***	–	12.9***	0.051***	–	0.576
	Bnba	0.568**	0.119	12.7***	0.043**	0.008	0.586
SMALL	G	10.9***	13.7***	113.7***	0.079***	0.090***	0.658
	Gwpe	23.6***	–	118.8***	0.165***	–	0.599
	Gnba	9.4***	7.69***	108.5***	0.075***	0.061***	0.617
	B	9.5***	14.0***	113.8***	0.070***	0.101***	0.595
	Bwpe	21.5***	–	118.6***	0.154***	–	0.514
	Bnba	8.0***	8.19***	108.6***	0.065***	0.065***	0.575

[1] Significance of estimated parameters as superscripts: *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$

Models: G = ssGBLUP; B = BLUP (wpe: without permanent environmental factor; nba: NBA included as a factor); Traits: NBA = number of piglets born alive; NW = number of piglets weaned; MBW = mean piglet weight within the litter (g); SDBW = standard deviation of piglet weight within the litter (g); CVBW = coefficient of variation of piglet weight within the litter (%); SMALL = proportion of piglets below 1.1 kg from NBA (%); (–) = model did not include the permanent environmental factor

h^2 = proportion of variance explained by the genetic factor; pe^2 = proportion of variance explained by the permanent environment of the sow; rEBV = realised accuracy (correlation between EBV from the reduced and complete datasets)

biological complexity of the traits, a moderate data size, and characteristics of field data recording. In particular, residual variance may be increased by imprecision in piglet weighing and by variability in the timing of recording liveborn piglets in large litters, where early postnatal mortality can contribute to random variation.

Relationship between traits. Estimated correlations (of phenotypic and genetic/genomic data from models with PE included) among litter-size and piglet-weight traits are presented in Table 3. Moderate positive genetic correlations of NBA with NW (0.54 and 0.59) indicate a favourable genetic relationship between litter size at birth and subsequent survival

Table 3. Genetic and phenotypic correlations between litter-size traits and piglet-weight traits[1]

Trait	Type	NW	MBW	SDBW	CVBW	SMALL
	G	0.540**	–0.390	0.150	0.196	0.300
NBA	B	0.586*	–0.175	0.055	0.084	0.251
	P	0.665***	–0.287***	0.049***	0.122***	0.231***
	G	–	0.162	–0.315	–0.324	–0.234
NW	B	–	0.389	–0.642	–0.474	–0.249
	P	–	–0.160***	–0.133***	–0.090	0.078***

[1] Significance of estimated parameters as superscripts: $^{*}P < 0.05$; $^{**}P < 0.01$; $^{***}P < 0.001$

Type: G = ssGBLUP correlations; B = BLUP correlations; P = Pearson phenotypic correlations. Traits: NBA = number of piglets born alive; NW = number of piglets weaned; MBW = mean piglet weight within the litter (g); SDBW = standard deviation of piglet weight within the litter (g); CVBW = coefficient of variation of piglet weight within the litter (%); SMALL = proportion of piglets below 1.1 kg from NBA (%)

to weaning. Overall, the genetic correlations between litter-size and piglet-weight traits were low to moderate and mostly nonsignificant, although they followed the expected direction of association. For piglet-weight traits, genomic correlations with NBA were two or three times stronger than the corresponding genetic correlations, whereas the opposite pattern was observed for NW.

Genomic correlations suggested that larger litters (NBA) tend to be genetically less uniform (ranging from 0.15 for SDBW to 0.30 for SMALL) and have lower mean birth weights (–0.39). In contrast, for NW, a positive relationship with MBW indicates that litters with higher average piglet weight tend to have more surviving piglets (correlations of 0.16 and 0.39), while litters with higher weight variability have fewer surviving piglets (correlations ranging from –0.23 to –0.64), although this was not significant. Differences between genomic and genetic correlations were likely due to partial confounding of the sow's permanent environmental effects with the genetic effect. For example, the genetic correlations between MBW and NBA in models without PE were stronger (up to –0.53) and more similar to the genomic correlations. A significant challenge in the bivariate models, including litter size and birth-weight variability traits (mainly SDBW), was the difficulty in partitioning variance between the genetic and permanent environmental effects, which led to convergence issues and high standard errors. For more robust conclusions, a larger dataset with a better data structure is needed. In our dataset, almost 23% of sows had only a single weighed litter.

The findings of other authors are broadly comparable to ours, although some differences in the strength of correlations have been reported. Camargo et al. (2020) observed stronger genetic correlations between NBA and MBW (–0.73) and between NBA and CVBW (0.64), while Boonkum et al. (2025) found negative correlations between litter size and MBW (–0.30 for TNB and –0.15 for NBA) and positive correlations with SDBW (0.18) and CVBW (0.30) when analysing a dataset of different breeds.

Models used. Different models provided slight changes in the estimated heritability (Table 2) and covariance rates among traits (not shown). Realised accuracies were at a similar level across all traits, ranging from 0.50 to 0.72 for piglet-weight traits and from 0.54 to 0.77 for litter-size traits, with generally higher values in genomic models. Compared with BLUP, ssGBLUP generally increased the proportion of variance explained by the genetic effect (except for CVBW and litter size traits). These increases were mostly small, except for MBW, where both genetic variance and heritability almost doubled. Nevertheless, realised accuracy across traits increased under ssGBLUP by approximately 4% (MBW) to 15% (SDBW). Although only a subset of animals was genotyped, a substantial proportion of phenotyped animals had genotyped parents (among animals with performance records, 41% had a genotyped dam and 67% had a genotyped sire). Nevertheless, the moderate size of the genotyped reference population may have limited the increase in genetic variance and heritability estimates for some traits.

Including litter size (number of weighed piglets) as a factor in the model generally reduced total variance, and for most traits, it also reduced the sow's genetic and permanent environmental components (except for SDBW, where both increased).

Overall, heritability or the proportion of PE did not change. Changes in realised accuracy were inconsistent across traits.

Omitting PE produced the most pronounced changes in SMALL, where almost the entire variance, which was initially explained by PE, was attributed to the genetic effect, leading to a substantial increase in heritability, but realised accuracy decreased (by about 0.08). A similar but less pronounced effect was observed for MBW, with a comparable decrease in realised accuracy. For SDBW and CVBW, excluding PE only caused small changes, but in bivariate models, omitting PE substantially improved model convergence, particularly in models including NBA.

In this study, piglet weights were analysed using a repeatability model at the sow's litter level. This approach allows the estimation of both the characteristics of birth weight and its variability. An alternative approach is to analyse piglet birth weights and the direct genetic effects of the piglet, with the sow's influence modelled through maternal genetic effects. For example, Lee et al. (2022) reported direct and maternal heritability rates of 0.108 and 0.237, respectively, with a correlation of −0.757, while Boonkum et al. (2025) estimated direct additive heritability as 0.119 ± 0.02 and maternal heritability as 0.072 ± 0.01. Alves et al. (2018) reported a heritability of 0.15 ± 0.03 for piglet birth weight, with significantly low-to-moderate negative correlations between direct and maternal additive effects (−0.25 to −0.41 for b.w.). Furthermore, Sell-Kubiak et al. (2015) proposed the use of a heteroscedastic (canalising selection) model, which assumes that both MBW and residual variance are affected by systematic and random effects, with residual variance being heterogeneous and partially under genetic control. Using this approach, they found that the direct genetic effect of the piglet on body weight was low, whereas maternal genetic effects were crucial for both body weight and its variability. They concluded that selection for uniformity (reduction in residual variance) is more efficient than joint selection for both traits (e.g. mean and uniformity). Formoso-Rafferty et al. (2016) applied a similar methodological approach in a long-term selection experiment with two divergent mouse lines. They found that selecting for greater uniformity was feasible and yielded specific benefits: low-variability lines had higher litter size, there was better survival at weaning, and total litter weight at birth/weaning was improved. Although individual birth and weaning weights were slightly lower in the low-variability line, the higher litter size and improved survival resulted in greater overall litter performance.

CONCLUSION

This study provides estimates of genetic parameters for piglet birth-weight traits and their relationships with litter-size traits in Czech Large White and Landrace populations. Heritability estimates for piglet-weight traits were generally low, with the highest values obtained for mean birth weight and the proportion of small piglets. Heritabilities for litter-size traits were also low. Genetic correlations between piglet born and piglet-weight traits were mostly unfavourable. In contrast, correlations involving the number of piglets weaned tended to be favourable. However, none of the correlations between litter size and piglet-weight traits were statistically significant. The use of ssGBLUP consistently improved realised accuracy of prediction across traits. It also led to a slight increase in the proportion of variance explained by genetic effects for selected piglet-weight traits, most notably for mean birth weight and proportion of small piglets, whereas changes for litter-size traits were negligible.

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Conflict of interest

The authors declare no conflict of interest.

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