

Consideration of heat stress in multiple lactation test-day models for dairy production traits

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Summary

In the previous study applying a pedigree based random regression test-day models using multiple lactation records, variance components estimated by Gibbs sampling did not converge for fat and protein (kg) when additive genetic (AG) and permanent environment (PE) effects of heat tolerance (HT) were assigned to each lactation which was treated as different traits; therefore, a common effect was assumed across lactation. In the follow-up analysis, we found many positive estimates of AG effects of HT for milk, fat, and protein (kg), and *vice versa* (negative estimates) for somatic cell score (SCS). This was expected given the nature of random regression effects applied; however, may need to study further in light of the heat stress definition (phenotypic changes per unit increase in the temperature-humidity index (THI) when THI increases above a threshold). As a simple solution, we pre-adjusted phenotypes by adding / subtracting the expected decrease / increase of phenotypes using the results of the previous study. Gibbs samplings converged for all traits with the model assigning AG / PE effects of HT to each lactation. Positive genetic trends in protein (kg) observed in the previous study disappeared and it was difficult to find trends for all traits. The finding may be reasonable as animals have never been selected for HT directly. The new methodology would provide more reasonable estimates than the previous study.

Keywords: heat stress, pre-adjustment, random regression, estimation of variance components, genetic trends, Holstein

Introduction

Considering the impact of heat stress (HS) on dairy production traits and the critical importance of improving cattle genetics, we previously conducted a parameter estimation study of random regression test-day model using first lactation records and genome wide markers (Atagi *et al.*, 2018a). Because many random regression models in practice, including that in Japan, use multiple lactation models which treat each lactation as different traits, we aimed to estimate variance components with such model; however, Gibbs samplings did not

converge for fat and protein (kg) when additive genetic (AG) and permanent environment (PE) effects of heat tolerance (HT) were assigned to each lactation; therefore, a common effect was assumed across lactation (Atagi *et al.*, 2018b). HS was defined as phenotypic changes per unit increase in the temperature-humidity index (THI) when THI increases above a common threshold for all records for each trait – lactation.

In the follow-up analysis, we found many positive estimates of AG effects of HT for milk, fat and protein (kg), and *vice versa* (negative estimates) for somatic cell score (SCS).

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Considering the multivariate normal distribution assumed in random regression effects, this result was expected; however, such estimates may need to study further as such findings could be interpreted as many cows actually possess the genetic ability to increase milk production (kg) under heat stress. The objective of this study is to identify a methodology in order to better estimate variance components and AG effects of HT.

Material and methods

Phenotypic records

Test-day records of milk, fat and protein yield (kg) and SCS (obtained from somatic cell count x (1 000 cells / ml) by $\log_2(x/100) + 3$) from purebred Holstein cows in Japan, except from those in Hokkaido where HS is minimal, collected until May 2017 and calved after January 2000, were processed according to the data editing criteria of the Japanese National Genetic Evaluation. Complete data were used to estimate the AG effects of HT. Due to limited computing resources for variance component estimations, number of records was further reduced applying the following criteria: at least 10 cows within a dairy farm – test-day – milking frequency (HTDT) and a dairy farm – calving year – lactation (1st or 2nd + 3rd) (HYP) subclasses; then divided into 3 subsets randomly. Table 1 shows the summary of the records.

Dairy farms were linked to meteorological offices according to their locales for announcements regarding weather forecasts, advisories, and warnings that reflect local climates. Each phenotype was linked to the average temperature – humidity index (THI) (NRC, 1971) of 2–4 (1–12 for SCS) days before each test-day (Hagiya *et al.*, 2019).

$$THI = (1.8 \times T_d + 32) - (0.55 - 0.0055 \times RH) \times (1.8 \times T_d - 26),$$

Where T_d is the dry bulb temperature in Celsius and RH is the relative humidity in percentage.

Statistical analysis

We pre-adjusted phenotypes, i.e., adding / subtracting expected amount of decrease / increase of phenotypes corresponding to THI

using the results of the previous study (shown in the next section). A random regression test-day model was used in the present study; the model was based on the National Genetic Evaluation as follows:

$$y_{ijklmno} = HTDT_i + \mathbf{M}'_j \mathbf{w} + \mathbf{Ag}'_k \mathbf{w} + \mathbf{hyp}'_l \mathbf{v} + \mathbf{pe}'_{mn} \mathbf{z} + \mathbf{pe}h_{mn} \cdot f(THI) + \mathbf{u}'_{mn} \mathbf{z} + \mathbf{uh}_{mn} \cdot f(THI) + e_{ijklmno},$$

where $y_{ijklmno}$ = adjusted test-day yield in the contemporary group class i , comprising the HTDT, calving month j , calving age k of cow m , and HYP class l ; $HTDT_i$ = the fixed effect of the contemporary group effect of class i ; \mathbf{M}'_j = the row vector of fixed regression coefficients of the calving month effect of class j ; \mathbf{Ag}'_k = the row vector of fixed regression coefficients of the calving age effect of class k ; \mathbf{hyp}'_l = the row vector of random regression coefficients of the HYP effect of class l ; \mathbf{pe}'_{mn} = the row vector of random regression coefficients of the general PE effect of cow m in n^{th} lactation; $\mathbf{pe}h_{mn}$ = the random linear regression coefficient of the PE effect of HT of cow m in n^{th} lactation; \mathbf{u}'_{mn} = the row vector of random regression coefficients of the general AG effect of cow m in n^{th} lactation; \mathbf{uh}_{mn} = the random linear regression coefficient of the AG effect of HT of cow m in n^{th} lactation; $e_{ijklmno}$ = heterogeneous random residuals corresponding to days in milk (DIM, t) in n^{th} lactation categories o ($t = 6-35, 36-65, 66-95, 96-125, 126-215, 216-305$);

$$\mathbf{w}' = [\phi_0(t) \ \phi_1(t) \ \phi_2(t) \ \phi_3(t) \ \phi_4(t) \ e^{-0.05t}],$$

i.e., fourth order Legendre polynomials with a coefficient of the exponential term of the Wilmlink function (Wilmlink, 1987) at DIM t ; $\mathbf{v}' = [\phi_0(t) \ \phi_1(t)]$ i.e., linear Legendre polynomials at DIM t ; $\mathbf{z}' = [\phi_0(t) \ \phi_1(t) \ \phi_2(t)]$ i.e., quadratic Legendre polynomials at DIM t ; and

$$f(THI) = \begin{cases} 0: & THI < THI_{threshold} \\ THI - THI_{threshold}: & THI > THI_{threshold} \end{cases}$$

Variance components were estimated using the “gibbs3f90” program of the BLUPF90 family (BGF90) that implements Gibbs sampling with a joint sampling of random correlated effects and traits (Miszta *et al.*, 2002). A single chain of 100 000 samples was run, with the first 50 000 samples discarded as burn-in. AG, PE,

HYP, phenotypic variances, and heritabilities were calculated for each combination of DIM and THI using the remaining 50 000 samples. Convergence was determined by a visual inspection of the plotting of Gibbs samples. We identified animals from at least four generations from cows with available phenotypic records.

Let $hypt' = [hyp'_1 \dots hyp'_l \dots]$ be the overall vector of random HYP effects;

$$pet' = [pe'_{11} \quad peh_{11} \quad pe'_{12} \quad peh_{12} \quad pe'_{13} \quad peh_{13} \\ \dots \quad pe'_{mn} \quad peh_{mn} \quad \dots]$$

be the overall vector of random PE effects; and

$$ut' = [u'_{11} \quad uh_{11} \quad u'_{12} \quad uh_{12} \quad u'_{13} \quad uh_{13} \\ \dots \quad u'_{mn} \quad uh_{mn} \quad \dots]$$

be the overall vector of random AG effects, the (co)variance structure was:

$$var \begin{bmatrix} hypt \\ pet \\ ut \\ e \end{bmatrix} = \begin{bmatrix} I \otimes Q & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ & I \otimes P & \mathbf{0} & \mathbf{0} \\ & & A \otimes U & \mathbf{0} \\ & & & R \end{bmatrix},$$

where I is an identity matrix, Q is a 2×2 matrix of (co)variances for HYP effects, A is a numerator relationship matrix, P and U are 12×12 ((3 regression coefficients of Legendre polynomials for the general effect + 1 regression coefficient for HT) \times 3) \times 12 matrices of (co)variances for PE and AG effects, and R is a diagonal matrix with residual variance corresponding to DIM in i^{th} lactation category.

AG / PE effects and variances on test-day basis were calculated as presented in Atagi *et al.*, (2018a).

THI thresholds and changes per unit THI

We used the same THI thresholds and changes per unit THI as in the previous study. They were determined with the following segmented linear regression analyses (R segmented package: Muggeo, 2008):

$$\begin{cases} y_i = c + e_i: THI_i < THI_{threshold} \\ y_i = a + b * THI_i + e_i: THI_i > THI_{threshold} \end{cases}$$

where $y_i = i^{th}$ test-day yield; and $THI_i =$ THI value linked to y_i .

These estimates are shown in Table 2.

Results and discussion

The lactation average of estimated total and HT heritability at THI = 80 are both presented in Table 3. Generally, heritabilities of HT increased in the present study, except the 1st lactation of fat (kg).

The distributions of the estimates of AG effects of HT, milk(kg) are shown in Figure 1. There were 91.5 % 62.4 % 49.6 % of cows with positive values for the 1st, 2nd, and 3rd lactation, respectively, in the previous study. At a glance, we observed more cows with positive values in the present study; however, we should note that the base overall decreased as shown in Table 2. Subtracting these overall changes, cows with positive values decreased to 71.4 % 32.0 %, and 31.8 %, respectively. We could obtain better results for other traits via this model. It would not be reasonable to double the pre-adjustment, and more studies are required to further improve these percentages.

The genetic trends of HT are presented in Figure 2. These values are lactation basis at THI = 80 continuously. Genetic base are cows born in 2010. There were positive trends in protein (kg) in the previous study. After pre-adjustment, it was difficult to find the trends of HT for the traits. Given the fact that animals have never been selected for HT directly in Japan, the results in the present study were expected.

Conclusion

The pre-adjustment provides better estimates than those derived from the previous study.

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Table 1. Summary of records.

	Traits							
	milk, fat, protein (kg)				SCS			
	Set1	Set2	Set3	Full	Set1	Set2	Set3	Full
test-day records	1 456 561	1 443 028	1 570 143	13 460 744	1 454 642	1 559 421	1 332 148	13 098 209
cows (female with records)	79 705	78 337	85 110	722 170	80 207	86 527	73 838	714 212
bulls (sire of cows)	4 621	4 621	4 697	7 311	4 594	4 746	4 495	7 283
other animals in a pedigree	112 989	105 790	109 366	663 971	107 365	113 377	106 814	660 627

Table 2. THI thresholds and changes per 1 THI

traits	lactation	Test-day records	THI _{threshold}			change / 1 THI		
			milk (kg)	fat (kg)	protein (kg)	milk (kg)	fat (kg)	protein (kg)
milk, fat, protein (kg)	1 st	8 983 199	72.246	54.356	66.008	-8.19e-2	-3.27e-3	-3.54e-3
	2 nd	7 448 202	71.886	53.444	64.368	-1.72e-1	-4.25e-3	-5.01e-3
	3 rd	5 316 403	66.521	51.167	58.788	-1.59e-1	-5.01e-3	-4.62e-3
SCS	1 st	7 690 035	63.645			1.73e-2		
	2 nd	6 361 339	64.865			1.24e-2		
	3 rd	4 509 975	59.460			1.26e-2		

Table 3 Heritabilities at THI=80

traits	lactation	total		heat tolerance	
		previous study	present study	previous study	present study
milk (kg)	1 st	0.2831±0.0063	0.2798±0.0062	0.0294±0.0014	0.0298±0.0013
	2 nd	0.2427±0.0055	0.2435±0.0056	0.0167±0.0008	0.0220±0.0010
	3 rd	0.2050±0.0070	0.2143±0.0071	0.0372±0.0019	0.0434±0.0021
fat (kg)	1 st	0.2013±0.0047	0.2148±0.0050	0.0311±0.0015	0.0254±0.0015
	2 nd	0.1962±0.0042	0.1941±0.0049	0.0191±0.0009	0.0445±0.0025
	3 rd	0.1942±0.0048	0.2053±0.0060	0.0188±0.0009	0.0459±0.0024
protein (kg)	1 st	0.2278±0.0055	0.2312±0.0077	0.0337±0.0014	0.0357±0.0050
	2 nd	0.2081±0.0053	0.2078±0.0076	0.0249±0.0011	0.0403±0.0061
	3 rd	0.2015±0.0060	0.2048±0.0085	0.0384±0.0016	0.0463±0.0063
SCS	1 st	0.1281±0.0041	0.1277±0.0041	0.0088±0.0007	0.0088±0.0008
	2 nd	0.2081±0.0053	0.1553±0.0041	0.0089±0.0005	0.0092±0.0006
	3 rd	0.2015±0.0060	0.1878±0.0060	0.0180±0.0013	0.0194±0.0013

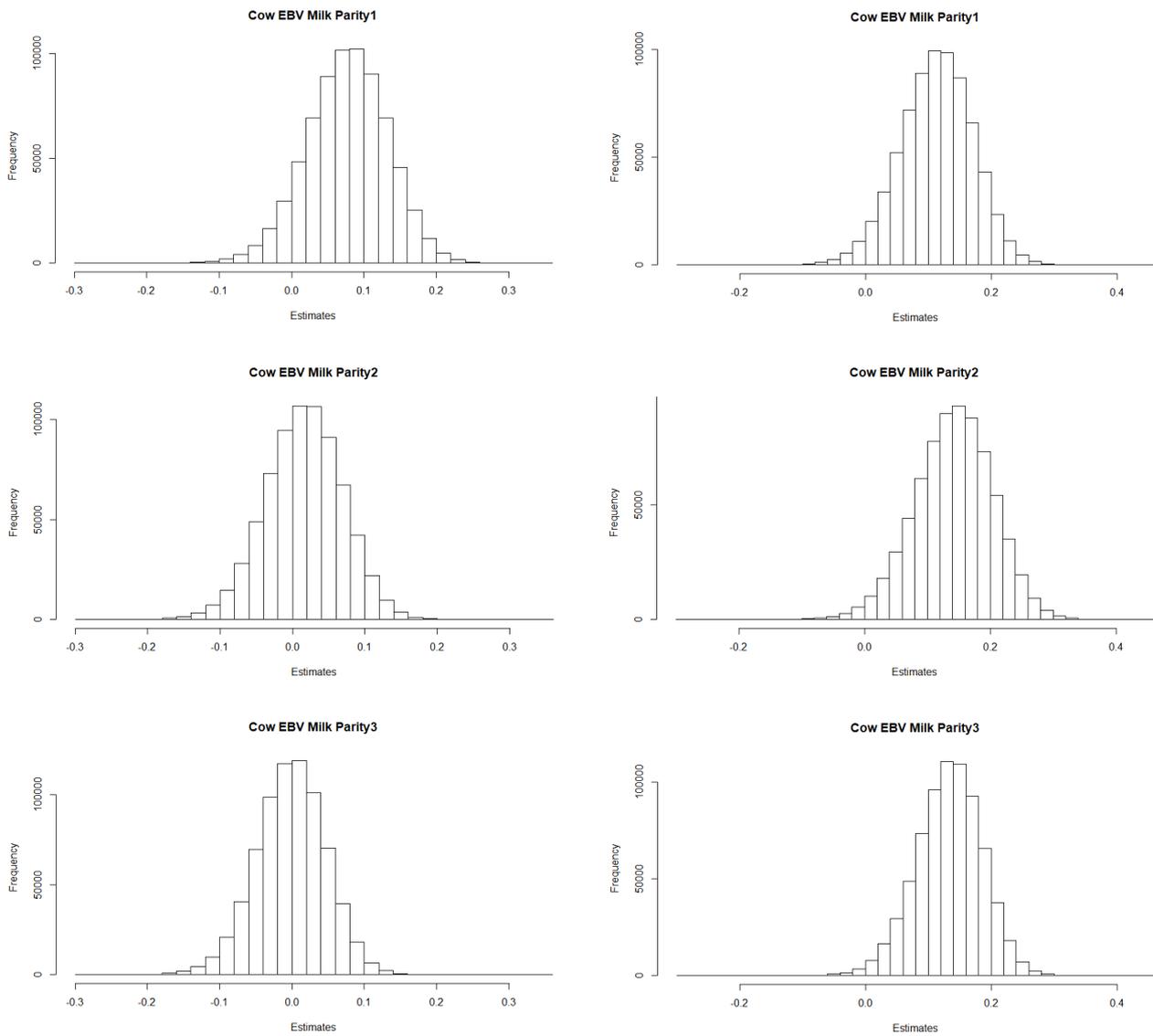


Figure 1. Distributions of additive genetic effects of heat tolerance, cow, milk (kg). Left: the previous study. Right: the present study.

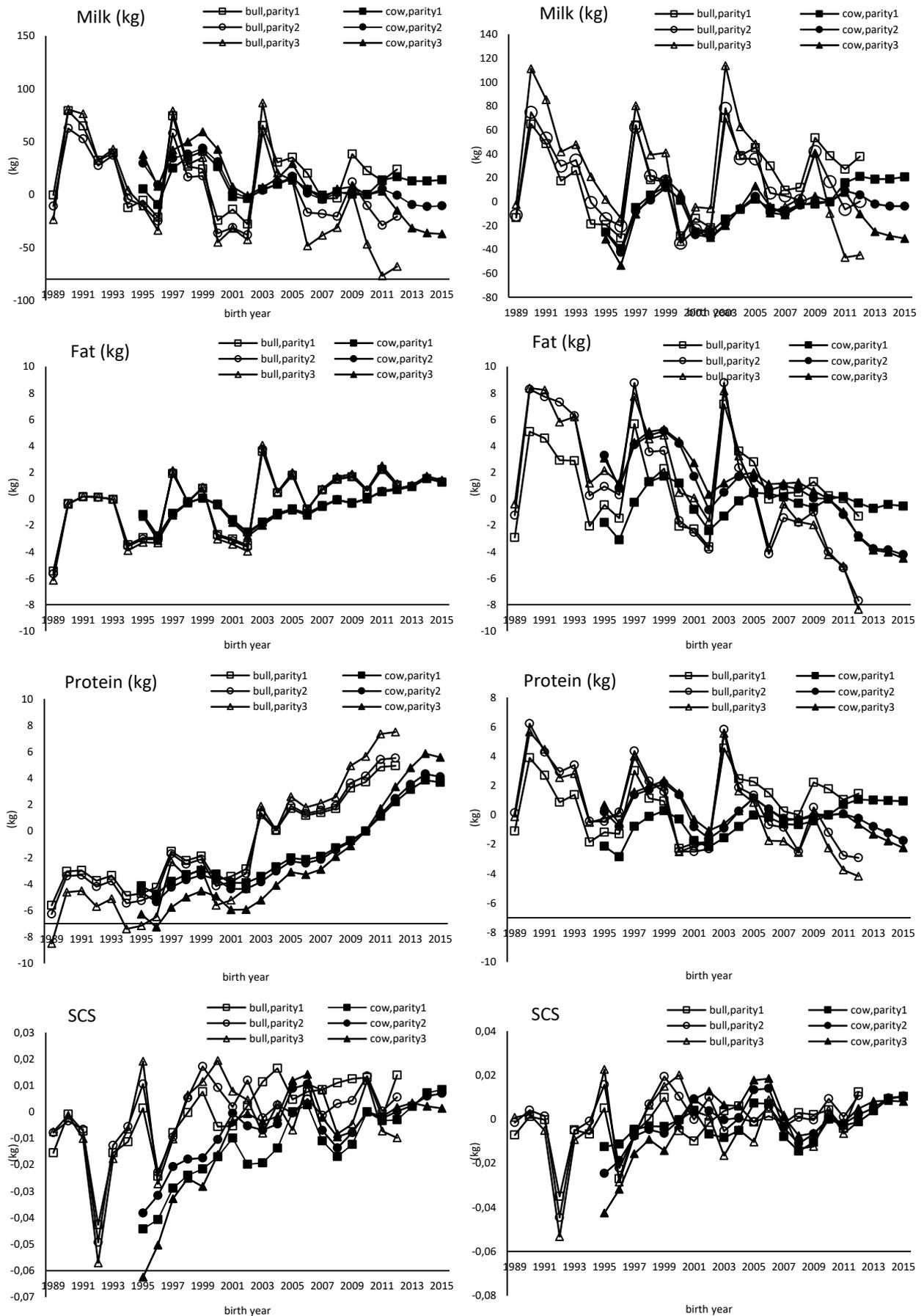


Figure 2. Genetic trends of heat tolerance. Left: the previous study. Right: the present study