

<sup>1</sup>Martin-Luther-University Halle-Wittenberg, Institute of Agricultural and Nutritional Sciences, Germany,

<sup>2</sup>Res. Inst. Anim. Prod., P.O.Box 1, Uhřetěves 10401, Czech Rep.

HANA KREJČOVÁ<sup>1</sup>, NORBERT MIELENZ<sup>1</sup>, JOSEF PŘIBYL<sup>2</sup> and LUTZ SCHÜLER<sup>1</sup>

## **Estimation of Genetic Parameters for Daily Gains of Bulls with Multi-Trait and Random Regression Models\***

### **Abstract**

The average daily gains of 6,420 Czech Pied bulls (dual-purpose, Simmental type) from 7 breeding stations were analyzed using single-trait animal models, a multi-trait animal model and random regression models. The effects of station, year and season were taken into account by creating herd-year-season classes (HYS) with the season being defined as a 3-month class starting with December. Legendre polynomials of the 1<sup>st</sup> to the 4<sup>th</sup> degree were used to describe the daily gains within the HYS classes as well as to model bull-specific gain curves. The comparison of the  $h^2$ -values estimated with single-trait models and those gained with a multi-trait model returned only insignificant differences. The comparison of genetic parameters based on the multi-trait model to those from different random regression models shows that polynomials of at least the 2<sup>nd</sup> degree are to be used for the genetic analysis of daily gains.

**Key Words:** bulls, daily gain, random regression, heritability

### **Zusammenfassung**

**Titel der Arbeit: Schätzung von genetischen Parametern für die tägliche Zunahme von Bullen mit Mehrmerkmals- und Random-Regression Modellen**

Die durchschnittlichen täglichen Zunahmen von 6420 Fleckvieh Bullen aus 7 Zuchtstationen wurden mit Hilfe von Einmerkmals-Tiermodellen, einem Mehrmerkmals-Tiermodell und mit Random-Regression Modellen ausgewertet. Die Effekte von Station, Jahr und Saison wurden durch Bildung von Herden\*Jahr\*Saison-Klassen (HYS) berücksichtigt, wobei die Saison als Dreimonatsklasse beginnend mit Dezember definiert wurde. Zur Beschreibung der täglichen Zunahmen innerhalb der HYS-Klassen als auch zur Abbildung tierspezifischer Zunahmekurven wurden Legendre Polynome 1. bis 4. Ordnung verwendet. Zwischen den  $h^2$ -Werten geschätzt mit Einmerkmalsmodellen und jenen geschätzt mit einem Mehrmerkmalsmodell wurden nur unerhebliche Unterschiede gefunden. Ein Vergleich der genetischen Parameter basierend auf dem Mehrmerkmalsmodell und verschiedenen Random-Regression- Modellen zeigte, dass für die genetische Analyse von täglichen Zunahmen mindestens Polynome 2. Grades verwendet werden müssen.

**Schlüsselwörter:** Fleischrindbullen, tägliche Zunahme, Random-Regression, Heritabilität

### **Introduction**

Growth traits, such as bodyweight and particularly average daily gains, are important performance indicators for dual-purpose cattle breeds (GOYACHE et al., 2003; CANTET et al., 2003). For such growth traits, there is an increased availability of repeated records per animal gathered over a certain test period. FITZHUGH (1976) analyzed the possibility to modify the shape of growth curves. LEGARRA et al. (2004) developed a methodology for the conversion of parameters of multi-trait and random regression models. They suggested using cubic Legendre polynomials in order to assure the sufficient fit of the models with minimal artifacts. MEYER (1999a, b) and ALBUQUERQUE and MEYER (2001) calculated genetic and phenotypic covariance functions for different growth stages of beef cattle. They described the

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covariance structure between the effects of the animal and of the permanent environment. Genetic parameters for beef cattle cows were estimated by ARANGO et al. (2002). BOHMANOVÁ et al. (2003) used the random regression methodology for the description of differences in the growth curves of beef cattle.

Since the average daily gains are calculated from three successive observations of the bodyweight, this trait requires not the test day but the test month (or in even broader terms, the test season) to be taken into account as environmental effect when composing the model. Due to the continuous sending of bulls to test stations over several years, the animals differ in their age on the test day. As a result, models are to be preferred which directly take into account not only the systematic environmental effects of the test months but also the growth stage of the animals when describing the test-day performance in mathematic-statistical terms (MEYER, 2001; MALOVRH, 2003). Similarly to the conditions prevailing for dairy cows, it appears to be a suitable approach to model the growth curves of, for example, members of a herd with the help of covariates with fixed regression coefficients. These so-called fixed regression models (FRM) exclusively employ covariates with fixed regression coefficients to take the different age of animals on the test day into account. While FRMs only estimate a fixed deviation per animal for the whole growth period, random regression models (RRM) can be used to map animal-specific performance deviations for any age with the help of individual growth curves (SCHAEFFER and DEKKERS, 1994; SWALVE, 1995; JAMROZIK and SCHAEFFER, 1997). NOBRE et al. (2002) analyzed the live weights for a large population of beef cattle using random regression models and then compared their calculations to results based on a multi-trait model.

The objective of this paper is to adjust random regression models suited for the analysis of average daily gains. Due to special data preparations, it became possible to use a multi-trait model as reference model. The time-dependent heritability values and the genetic correlations estimated with various RR models, which differed in their polynomial degree, were compared to the results from the reference model.

### Material and Methods

The growth data analyzed in this study were gathered from more than 6,000 bulls of the Czech Pied breed. In particular, dual-purpose cattle of Simmental type (medium to large body size) were used. The data were collected at 7 breeding stations over a period of 20 years. The tested bulls are descendants of a total of 253 sires. On average, every bull had 26 half-sibs. In order to be able to evaluate the performance data with a multi-trait model, 8 age periods were defined: from day 12 to day 62, from day 63 to day 113, from day 114 to day 164, from day 165 to day 215, from day 216 to day 266, from day 267 to day 317, from day 318 to day 368, and from day 369 to day 420. As average daily gain (DG1 to DG8) of a certain animal within these 50-day age periods, the performance with the smallest temporal distance to the middle of the age period (i.e. day 37, 88, 139, 190, 241, 292, 343 and 394) was selected. The other records from these age periods were omitted. As a result, every bull disposed of a minimum of 4 and a maximum of 8 records on the average daily gains (DG) of the bodyweight during the test period. The descriptive statistics for traits DG1 to DG8 are contained in Table 1. The analysis of the modified data was carried out:

- a) with single-trait models (STM)

- b) with an 8-trait model (multi-trait model, MTM)
- c) with random regression models (RRM) (when describing the individual daily gains of the bodyweight with Legendre polynomials).

The effects of station, year and season were taken into account through the creation of Herd\*Year\*Season classes (HYS) with 3-month intervals chosen for the season.

Table 1

Number of records (N), means and standard deviations (SD) for the average daily gain (Anzahl Beobachtungen, Mittelwerte und Standardabweichungen für das Merkmal tägliche Zunahme)

Trait	Age (in days)	Middle of the interval	N	Mean (g/day)	SD
DG1	(12 – 62)	37	978	743.7	196.2
DG2	(63 – 113)	88	3948	930.1	213.9
DG3	(114 – 164)	139	5236	1144.3	249.1
DG4	(165 – 215)	190	6052	1242.8	218.5
DG5	(216 – 266)	241	6095	1288.3	206.3
DG6	(267 – 317)	292	5610	1249.5	214.7
DG7	(318 – 368)	343	4593	1124.9	229.0
DG8	(369 – 420)	394	1729	955.7	247.0
DG	(12 – 420)	216	34241	1156.3	261.4

Per HYS class, at least 40 records were required to be available. The occasional difference of age of the animals within an age period was corrected with the help of a square regression of the age within the 8 age periods. Let  $y_{ijk}$  be the record of animal  $j$  in HYS-class  $i$  for trait  $k$  gathered at age  $t_{ijk}$ . For the multi-trait model, we then obtain the following shape:

$$(MTM) \quad y_{ijk} = \beta_{0,ik} + \beta_{1,ik}t_{ijk} + \beta_{2,ik}t_{ijk}^2 + a_{ijk} + p_{ijk} + e_{ijk}$$

Here,  $\beta_{m,ik}$  denotes fixed regression coefficients (with  $m=0,1,2$ ),  $a_{ijk}$  is the additive-genetic effect of animal  $j$  in HYS-class  $i$  for trait  $k$ ,  $p_{ijk}$  represents the permanent environmental effect of animal  $j$ , and  $e_{ijk}$  is the random residual effect. Let  $a = (a_1, \dots, a_N)'$  with  $a_j = (a_{j1}, \dots, a_{jn})'$  be the vector of additive-genetic effects of all animals, and let  $A$  denote the numerical relationship matrix; it follows:

$$Var(a) = A \otimes G_a \quad \text{with} \quad Var(a_j) = G_a$$

Furthermore, let  $p_j$  be the vector of the permanent environmental effects, and let  $e_j$  be the vector of random residual effects of animal  $j$  with  $\sigma_{e_k}^2 = Var(e_{ijk})$ . If animal  $j$  has records for all traits, it follows:

$$Var \begin{bmatrix} p_j \\ e_j \end{bmatrix} = \begin{bmatrix} G_p & 0 \\ 0 & R_e \end{bmatrix} \quad \text{with} \quad R_e = diag(\sigma_{e_k}^2)$$

Permanent effects and residual effects of different animals are assumed uncorrelated. Since this study does not allow to record two traits at the same time for the same animal, matrix  $R_e$  is diagonal. The permanent effects in the MTM serve to take into account that environmental effects or other circumstances might permanently affect the performance of an animal.

During the evaluation with RR models, Legendre polynomials of the 2<sup>nd</sup> to the 4<sup>th</sup> degree were fitted with fixed regression coefficients within the HYS classes (MIELENZ et al., 2007). For the description of individual gains, Legendre polynomials with random regression coefficients were used with the polynomial degree being increased step-wise from 1 to 4.

The following random regression model was used for the analysis of average daily gains:

$$(RRn) \quad y_{ijk} = \sum_{m=0}^{n_1} \beta_{im} \phi_m(t_{ijk}) + \sum_{m=0}^{n_2} \alpha_{jm} \phi_m(t_{ijk}) + \sum_{m=0}^{n_2} \gamma_{jm} \phi_m(t_{ijk}) + e_{ijk} \quad n_1, n_2 \in \{1, \dots, 4\}$$

With:

- $y_{ijk}$  = gain at age  $k$  of animal  $j$  in Herd\*Year\*Season  $i$ ,
- $t_{ijk}$  = the standardized age in interval  $(-1, 1)$ ,
- $\phi_m(\cdot)$  = the orthogonal Legendre polynomial of degree  $m$ ,
- $\beta_{im}$  = fixed regression coefficients within Herd\*Year\*Season  $i$ ,
- $\alpha_{jm}$  = the additive-genetic random regression coefficient of animal  $j$ ,
- $\gamma_{jm}$  = the permanent environmental regression coefficient of animal  $j$
- $e_{ijk}$  = random residual effect.

Let  $\alpha_j$  and  $\gamma_j$  be the vectors of the random regression coefficients of animal  $j$  with  $Var(\alpha_j) = K_a$  and  $Var(\gamma_j) = K_p$ . Furthermore,  $\phi_k = (\phi_0, \phi_1(t_k), \dots, \phi_n(t_k))'$  shall denote the vector of the covariates at age  $t_k$ . Then, the genetic and phenotypic covariance functions are of the following structure:

$$(cf1) \quad cov(g(t_k), g(t_{k'})) = \phi_k' K_a \phi_k$$

$$(cf2) \quad cov(y(t_k), y(t_{k'})) = \phi_k' (K_a + K_p) \phi_k + \delta_{kk} \sigma_e^2 \quad \text{with} \quad \sigma_e^2 = Var(e_{ijk})$$

Here,  $\delta_{kk'} = 1$  for  $k = k'$ ; otherwise, it is zero. Formulas (cf1) and (cf2) can be used for the estimation of the genetic and phenotypic correlations between daily gains at a different age (for details, see ALBUQUERQUE and MEYER, 2001).

The statistical analysis of the data was performed with the program package SAS, whereas the estimation of variance components made use of the REML method of the program VCE5 (KOVAC et al., 2002).

## Results

The heritability values estimated with the single-trait models (STM) and with the multi-trait model (MTM) are provided in Table 2. For all traits, there are only slight differences between the heritability values of the models with one variable and those of the respective MTM. The highest  $h^2$ -values were found for trait DG1 (i.e. the gain for the age of 37 days), whereas the age of 394 days showed the lowest estimates. When considering the heritability values of the two estimations over all age periods, very similar trends could be observed.

From Table 2, it becomes obvious that the gains for an age of 37 and 88 days as well as the gains for older animals are very weakly or even negatively correlated. The larger the temporal distance between observations, the smaller the genetic correlations between DG3 and DG4 up to DG8. The only phenotypic correlations with rather moderate values between 0.19 and 0.48 are those between directly adjacent traits. Phenotypic correlations between non-adjacent observations are close to zero and lie between -0.03 and 0.16. For the heritability values of traits DG1 and DG8, the MTM returned standard errors of 0.03 and 0.02 respectively. In contrast, the standard errors for the  $h^2$ -values of traits DG2 to DG7 were found between 0.006 and 0.009. The

estimated standard errors for the genetic correlations of the 8 traits varied between 0.02 and 0.10.

Table 2

Heritability values, genetic correlations (above the diagonal) and phenotypic correlations (below the diagonal) estimated with the multi-trait model. (Heritabilitäten, genetische Korrelationen (oberhalb) und phänotypische Korrelationen (unterhalb der Diagonale) geschätzt mit einem Mehrmerkmalsmodell)

	Trait							
	DG1	DG2	DG3	DG4	DG5	DG6	DG7	DG8
DG1	<b>0.290</b>	0.156	-0.131	-0.117	0.033	-0.013	0.208	0.045
DG2	0.503	<b>0.100</b>	0.717	0.177	0.269	0.067	0.290	0.203
DG3	0.157	0.335	<b>0.132</b>	0.742	0.693	0.439	0.418	0.366
DG4	0.162	0.120	0.229	<b>0.168</b>	0.903	0.531	0.451	0.403
DG5	-0.012	0.038	0.046	0.227	<b>0.203</b>	0.706	0.654	0.542
DG6	-0.021	0.002	0.016	0.081	0.187	<b>0.167</b>	0.864	0.808
DG7	0.020	0.022	-0.002	0.020	0.059	0.213	<b>0.130</b>	0.959
DG8	0.127	0.052	0.073	0.071	0.049	0.073	0.419	<b>0.045</b>
<sup>1</sup> STM	<b>0.320</b>	<b>0.069</b>	<b>0.125</b>	<b>0.173</b>	<b>0.225</b>	<b>0.165</b>	<b>0.120</b>	<b>0.025</b>

<sup>1</sup>estimates from single-trait model

Two statistics were used to measure the quality of fit for the different models: the correlation between observed and predicted values ( $r_{y,\hat{y}}$ ) and the correlation between the values predicted with random regression models and those predicted with the MTM ( $r_{\hat{y},\hat{y}(MTM)}$ ). The number of model parameters, the model fitting statistics, and the smallest and largest eigenvalues of matrices  $K_a$  and  $K_p$ , transformed to percentage values, are given in Table 3. As expected, the most complex model yielded the strongest correlations with values of 0.86 and 0.95. Even though the number of parameters differs strongly between the models in question, quite similar correlations could be found between the predicted values of the MTM and those of models RR2, RR3 and RR4.

Table 3

Number of fixed effects ( $p$ ), number of variance components ( $q$ ), correlations between observed and predicted values, and minimum and maximum genetically conditioned and permanent environmentally conditioned eigenvalues given in % (Anzahl fixe Effekte, Anzahl Varianz-komponenten sowie genetisch und umweltbedingte minimale und maximale Eigenwerte)

Model	$p$	$q$	$r_{y,\hat{y}}$	$r_{\hat{y},\hat{y}(MTM)}$	$\lambda_{\min}(K_a)$	$\lambda_{\max}(K_a)$	$\lambda_{\min}(K_p)$	$\lambda_{\max}(K_p)$
RR1	561	7	0.755	0.899	24.7	75.3	12.9	87.1
RR2	561	13	0.798	0.916	21.0	45.9	0.0	67.3
RR3	648	21	0.829	0.937	0.0	57.1	0.0	61.6
RR4	825	31	0.856	0.954	2.1	60.0	0.0	46.2

Since RR2, RR3 and RR4 differ in their number of fixed effects, no information criteria can be used for the selection of an appropriate model. The leading eigenvalue of model RR1 reveals that its associated eigenvector accounts for over 75% of the additive-genetic variation (KIRKPATRICK et al., 1990). The top genetic eigenvalues corresponding to the constant coefficients of the polynomials explain more than 45%, 57% and 60% of the genetic variation for models RR2, RR3 and RR4 respectively. Eigenvalues close to zero reveal the possibility to reduce the order of the polynomials. The estimates of the heritability based on the RR models at the 8 points of measurement are listed in Table 4.

With values of 0.26, 0.16 and 0.07, the comparison of the  $h^2$ -values estimated with the MTM and those estimated with models RR2, RR3 and RR4 showed a significant

underestimation for trait DG1. For the models with polynomials of the 3<sup>rd</sup> and 4<sup>th</sup> degree, the strongest underestimations were found at the beginning of the test period (i.e. for an age of less than 88 days). The estimated average heritability values for the total test period from day 12 to day 420 when using models RR1, RR2, RR3 and RR4 are 0.125, 0.140, 0.124 and 0.127 respectively.

Table 4

Comparison of heritability coefficients for varying age estimated with different models (Vergleich der Heritabilitätskoeffizienten für verschiedene Altersabschnitte)

Model	DG1	DG2	DG3	DG4	DG5	DG6	DG7	DG8
MTM	0.290	0.100	0.132	0.168	0.203	0.167	0.130	0.045
RR1	0.127	0.113	0.104	0.102	0.109	0.125	0.146	0.169
RR2	0.261	0.115	0.104	0.147	0.164	0.134	0.094	0.129
RR3	0.164	0.071	0.115	0.148	0.162	0.156	0.120	0.073
RR4	0.069	0.083	0.112	0.180	0.190	0.148	0.129	0.076

The MTM and models RR2 to RR4 differed only slightly in their  $h^2$ -values for traits DG2 to DG8. With model RR1 excluded from the considerations, the  $h^2$ -values from the RR models for traits DG2, DG3, DG4, DG5, DG6 and DG7 lie between 0.07 and 0.12, between 0.10 and 0.12, between 0.15 and 0.18, between 0.16 and 0.19, between 0.13 and 0.16, and between 0.09 and 0.13 respectively.

The trends in the heritability estimates over the age for the comparison of RR1 and RR3 with the MTM as well as for the comparison of RR2 and RR4 with the MTM are shown in Figures 1 and 2 respectively. Figure 1 indicates that the estimates with model RR1 and those with the MTM are not equivalent.

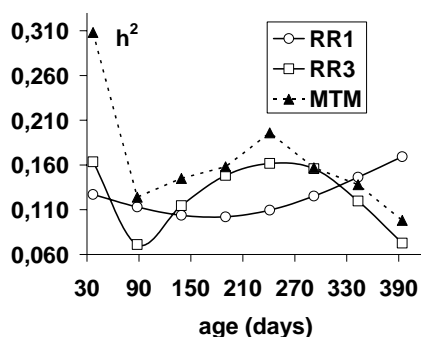


Fig. 1: Estimated heritability function of RR1 and RR3 compared to the MTM estimates (Mit RR1 und RR3 geschätzte  $h^2$ -Funktionen im Vergleich zu den Schätzungen mit MTM)

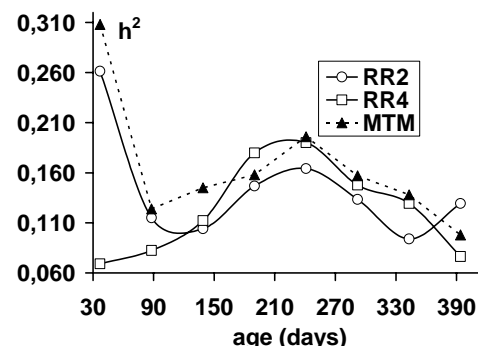


Fig. 2: Estimated heritability function of RR2 and RR4 compared to the MTM estimates (Mit RR2 und RR4 geschätzte  $h^2$ -Funktionen im Vergleich zu den Schätzungen mit MTM)

For lower age values, the heritability estimates based on models RR3 and RR4 do not match with those from the MTM. For intermediate and high age values, the estimates of models RR3, RR4 and the MTM are very similar. The trend in the heritability estimates for the MTM (shown in Fig. 1) can quite easily be modeled with the help of the estimated  $h^2$ -curves of models RR2 and RR3. The best visual match with the estimates of the MTM were returned by the RR model based on polynomials of the 2<sup>nd</sup> degree. The estimated standard deviations of the environmental components over all age periods are shown in Figures 3 and 4.

The environmental variance ( $V_E$ ) was calculated as the sum of the permanent ( $V_{EP}$ ) and the temporary environmental variance ( $V_{ET}$ ) for a given age. The estimates of the

environmentally conditioned standard deviation of the MTM increase for young animals (age of 37 to 139 days), decrease for intermediate age values (day 139 to day 241) and increase again for high age values (day 241 to day 394). The largest differences between estimates of the environmentally conditioned standard deviation of the RR models and those based on the MTM were found for extreme age differences. Respective extreme differences were obtained with the comparison of the MTM to RR2 and of RR3 to RR4 for the high age of 394 days, and with the comparison of the MTM and all RR models for the young age of 37 days. Similar estimates of the environmentally conditioned standard deviation were returned by all models for the age period between 139 and 343 days.

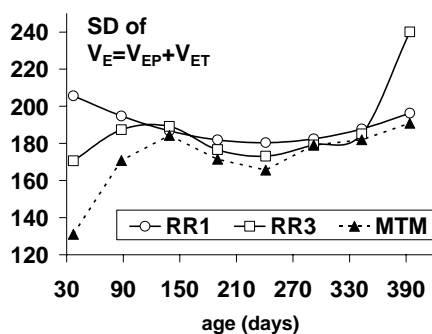


Fig. 3: Estimated function of the environmentally conditioned standard deviation (SD) for RR1 and RR3 compared to the estimates from the MTM (Mit RR1, RR3 und MTM geschätzte umweltbedingte SD)

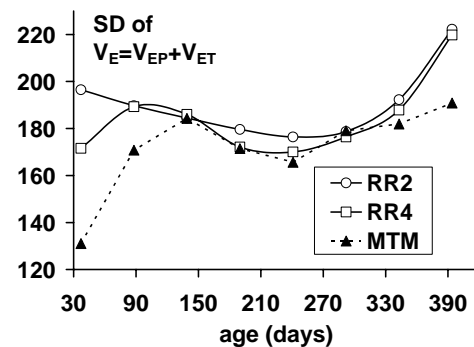


Fig. 4: Estimated function of the environmentally conditioned standard deviation (SD) for RR2 and RR4 compared to the estimates from the MTM (Mit RR2, RR4 und MTM geschätzte umweltbedingte SD)

The average correlations as a function of the length of the time interval (lag) between two repeated observations per animal are illustrated in Figures 5 and 6. Between two successive observations, there is a temporal distance of 51 days. If the interval of 51 days is set to 1, the temporal distance (d) in the MTM can only lie between values from 0 to 7. For  $d=0$ , the average correlation is equal to 1. For  $d=1$  and  $d=2$ , the average correlation can be calculated with 7 and 6 values from Table 2 respectively. The average correlations of the RR models as a function of  $d$  were estimated using the covariance function (cf2). Figures 5 and 6 show that the average correlations tend to decrease with increasing temporal distance. For  $d=6$  and  $d=7$ , the largest differences were found between all RR models and the MTM. The trend in the correlation estimates of the MTM can be modeled adequately using RR2 (Fig. 6).

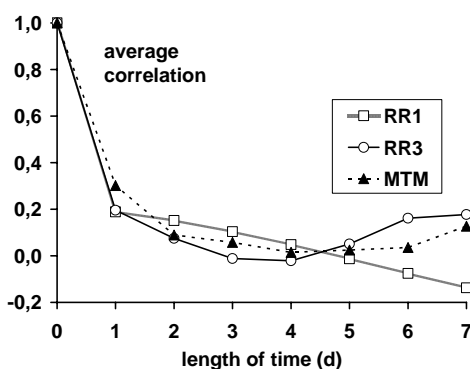


Fig. 5: Average phenotypic correlations estimated with RR1, RR3 and MTM (Mittlere phänotypische Korrelationen geschätzt mit RR1, RR3 und MTM)

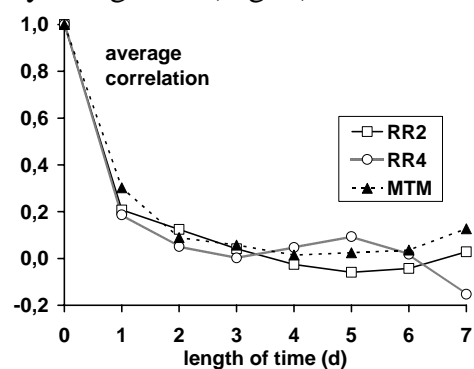


Fig. 6: Average phenotypic correlations estimated with RR2, RR4 and MTM (Mittlere phänotypische Korrelationen geschätzt mit RR2, RR4 und MTM)

### Discussion

For the period from day 12 to day 420, the heritability values for the average daily gains of bodyweight estimated with the MTM are relatively low with values between 0.06 and 0.31. Excluding the beginning of the test period, the highest  $h^2$ -values fall into the period from day 267 to day 317. Except for the beginning of the test period, the heritability values estimated with the MTM were reflected quite well with RR models using polynomials of the 2<sup>nd</sup> to the 4<sup>th</sup> degree. If the average daily gains for the age are calculated over all bulls, the result will be a curve that can be described very well with the help of a square function. As a consequence, the RR models should be based on polynomials of at least the 2<sup>nd</sup> degree as well.

The heritability estimates and the environmentally conditioned standard deviations for the beginning and end of the test period, estimated with the MTM and models RR2 to RR4, partially exhibit significant differences. One reason for this might be the relatively low number of records for the age periods at the beginning and end of the test period. For the RR models, at least 40 records per HYS class were available. When using a multi-trait model, the number of observations within the HYS classes must be additionally divided by the number of traits. Since there were considerably fewer observations available for trait DG1, the number of observations can turn out quite low for some of the HYS classes. Therefore, additional genetic calculations with the MTM under the assumption of random HYS effects were performed. The genetic parameters based on fixed and random HYS effects showed highly similar values. Thus, the only results presented in this study are those from the multi-trait analysis with fixed HYS effects.

Partially significant differences were found between the correlations estimated with the MTM and those obtained with the RR models. The latter allow the calculation of correlations between two arbitrary points in time. In contrast, the MTM is only used to estimate the correlations between time periods. Not every animal disposes of a record for the exact middle of the 8 time periods. As a result, inevitable differences between the genetic parameters of the MTM and those of the RR models are to be expected.

For the analyzed RR models, the polynomial degree of the fixed and random regression matches. Additionally, variants were analyzed for which the degree of the fixed regression was below the polynomial degree of the random regression. In these cases, the resulting  $h^2$ -values were considerably less adjusted to the estimates of the MTM. In model (RRn), it is assumed that the expected values of all random effects are equal to zero. Therefore, the polynomial degree of the fixed regression should not be lower than the degree of the polynomials with random coefficients. As a consequence, the polynomial degrees had to be adjusted with the result that the 4 analyzed RR models sometimes differed strongly in their number of fixed model parameters. The likelihood function of the REML method is independent from the fixed model parameters. Thus, the information criteria of Akaike (AIC) or those of Bayes (BIC) based on the restricted likelihood function can only be used for the optimization of the covariance structure of the random model effects for respective identical structures of expected values. In this study, the fixed regression parts of models RR2, RR3 and RR4 were modeled with increasing order of the polynomials; therefore, AIC and BIC could not be used during the selection of the best covariance structure. This is why the selection of suitable RR models in this study focuses on the comparison of the estimates from RR models with those from the MTM. Model RR2 returned the best



visual match with the heritability values estimated with the MTM. The disadvantage of RR2 lies in the inadequate modeling of the environmental variance for low age. In order to improve the model fitting based on RR2, the residual variance should not be considered invariable but instead should be modeled with the help of square or cubic functions.

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Corresponding Author

Dr. NORBERT MIELENZ

Institute of Agricultural and Nutritional Sciences

Martin-Luther-University Halle-Wittenberg

Adam-Kuckhoff-Straße 35

06108 HALLE / GERMANY

E-Mail: [norbert.mielenz@landw.uni-halle.de](mailto:norbert.mielenz@landw.uni-halle.de)