Comparison of different traits to evaluate the growth of bulls

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ABSTRACT: The live weights of 8 243 performance-tested bulls from 100 to 400 days of age were analysed using random regression (RR) and single-trait animal models. Evaluations were done for live weight at 400 days of age and gains from 100 to 400 days of age at various monthly intervals. Estimates of variance components differed depending on the trait definition and model of analysis. Systematic environmental effects explained a higher proportion of variability in the RR for gains than for other definitions of growth. The expected average reliability of estimated breeding values was similar for all methods from 0.42 to 46, but the rankings of animals differed. Determinations (r^2) of breeding values between methods ranged from 0.64 to 0.94. Correlations of the breeding values of progeny at performance-test stations with parents were highest for the evaluation of gains in consecutive intervals evaluated by RR. Correlations of the breeding values of sires from their growth at performance-test stations with the breeding values of groups of progeny at progeny-test stations were from 0.26 to 0.38. Correlations were the highest for RR evaluations of gain using consecutive short intervals. Evaluation of the growth of animals according to daily gains in short consecutive intervals was preferred because more animals and more observations per animal were included in the evaluations, and the growth curve was separated into genetic and non-genetic parts. Simple evaluation of growth according to the final weight or daily gain in a long interval is not entirely correct, since environmental compensatory growth can occur.

Keywords: bulls; daily gains; random regression; breeding values; variances

The growth of animals of different categories and different species in nutritional experiments (Bartoň et al., 2007) or in genetic evaluations for breeding purposes (Přibyl et al., 2003; Wolf et al., 2005; Maxa et al., 2007) is usually evaluated on the basis of recorded live weights at different ages, or by average daily gains over specified periods, assuming linear growth. Single- or multiple-trait animal models (AM) have been used for genetic evaluation most frequently.

The assumption of linearity is not frequently valid. Animals follow different growth patterns (Krejčová et al., 2008) due to different environments, management restrictions, and compensation from changing environments. Animals with high growth potential are negatively affected by unfavourable environmental factors more than animals with poor growth capability.

Growth can be evaluated by repeated weighings of each animal and by modelling the growth trajectory. Different methodologies of linear and nonlinear growth curves have been used (Hyánek and Hyánková 1995; Nešetřilová, 2005; Vuori et al., 2006). The evaluation of longitudinal data has

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been done by Random Regression Animal Models (RR), which account for systematic environmental factors and also genetic and non-genetic factors, including functional dependences between repeated measurements on the same animal. RR methodology for the evaluation of live weight was used in cattle by Albuquerque and Meyer (2001), Nobre et al. (2003), Legarra et al. (2004), Bohmanová et al. (2005), Cantet et al. (2005), Meyer (2005) and Přibyl et al. (2007, 2008). Different types of growth functions and comparisons of RR with multiple-trait AM methodology were examined. Both direct and maternal genetic effects were considered. Average growth curves for groups of animals of the same breed kept under the same conditions, herd-year-seasons of weighings, and the genetic and permanent environmental effects of animals are usually taken into account. Heterogeneous residual variances, which change with the age of the animal, are also considered. Consequently, heritability is not constant over the time period and changes with the age of the animal for the direct and maternal parts.

Live weights of cattle at different ages are highly correlated because weight is a cumulative trait, and the subsequent weight includes previous weights at younger ages (Bouška et al., 2003; Přibyl et al., 2007, 2008). Live weights accumulate the history of systematic external and internal factors which are difficult to separate accurately at the moment of evaluation. When animals change environments, such as going from the herd of birth to a test station or to a new group of animals, or the restriction of nutrition for diverse reasons takes place, compensatory growth can occur.

Besides the evaluation of live weights, daily weight gains from one age to another can be evaluated by an RR. The change in weight from one age to the next one does not depend on the previous accumulation of effects so much but it depends much more on the environmental effects during that current period. Krejčová et al. (2007a) compared RR methodology with multiple-trait AM when daily gains in different phases were considered as different traits. A high degree of similarity of results between both methodologies was found.

Krejčová et al. (2008) reported the culmination of daily gain at 250 days of age for performance-tested young bulls of Czech Fleckvieh cattle kept under standardized conditions. Heritability of daily gains was very low due to the high random fluctuations of daily gains and random errors of production records in short intervals. Heritability of cumulative gain was very high, corresponding to the reliability of the composite trait according to the length of the period. Daily gains in consecutive segments of the growth curve have high genetic but low, even negative, phenotypic and permanent environmental correlations. The genetic potential persists over the growth period, and environmental compensations in growth also exist. The separation of genetic and environmental components is essential for the correct evaluation of growth.

Repeated daily gains for a longitudinal analysis could be calculated from live weights taken every month. From 100 to 400 days of age there would be 10 intervals of 30 days, 5 intervals of 60 days, 3 intervals of 90 days or 2 intervals of 150 days. Long intervals tend to average out the environmental fluctuations over time, but give fewer records per animal than short intervals and fewer points for modelling the growth trajectory. Short intervals may contain too much environmental variability. A balance between interval length and number of records per animal must be achieved.

Growth for breeding purposes can be evaluated according to several sources of information, such as own individual animal performance, progeny tests, and general field tests under farm conditions. Performance tests of own individual growth are usually time-limited and do not cover the period to optimal slaughter weight (Bouška et al., 2003). The performance test of the daily gains of young Czech Fleckvieh bulls was evaluated using BLUP AM by Konstantinov and Váchal (1985). Live weights of the same bulls were evaluated using RR by Přibyl et al. (2007, 2008). Mielenz et al. (2007) and Krejčová et al. (2007a,b, 2008) evaluated daily gains for repeated 50-day or 1-month intervals of each animal by RR methodology.

Objectives

The purpose of this paper was to compare different expressions of growth records for the genetic evaluation of young performance-tested bulls evaluated by different models.

MATERIAL AND METHODS

The live weights of young, dual-purpose Czech Fleckvieh bulls at performance-test stations, taken at 1-month intervals from approximately 1 to 17 months of age, were used for the study. The bulls were the progeny of highly selected mothers and sires of sires from the entire national population. Therefore, each mother usually had only one son at the stations, and there were only weak ties among the mothers. Bulls enter test stations throughout the year, usually at an early age, and are selected for use in artificial insemination (AI) at 14 months. Thus, bulls of different ages are present at the test station at any given time. Nutrition was regulated for a maximum daily gain of 1.3 kg. The individual consumption of nutrients was not recorded.

The weights at 1-month intervals were designated as W1m. Gains from month to month were calculated as the difference between two consecutive weights and were designated as G1m. In addition, gains were calculated in consecutive 2 and 3 month intervals (designated as G2m and G3m), and one gain for the period from 100 to 400 days of age (designated as Gp). From the analysis of W1m, the difference in live weight at 400 and 100 days of age (designated as W1mD) was calculated. Finally, let W400 designate the live weight at 400 days of age, which was derived by interpolation of the weights between 350 and 450 days of age.

The data consisted of bulls with more than two weighings, with more than 4 paternal half-sibs and with more than 4 contemporaries in the station-year-3month season of birth classes (SY3), and station-year-3month season of weighing classes (TDS3). After editing of the data, there were 8 243 bulls within 303 TDS3 classes, representing the progeny of 349 sires. There was an average of 27 G1m observations within TDS3 classes, and an average of 24 sons per sire. The number of observations per animal differed according to the trait under evaluation (Table 1). The highest number of animals and observations was for test-day records with one month intervals.

The monthly gains and weights were analysed using random regression (RR), while Gp and W400 were analysed by a single-trait animal model (AM). For the reasons already mentioned above – that calves enter the stations at a very early age, that there are only weak ties among mothers, and that each mother has practically only one son at the station – the maternal effects were not therefore considered in the evaluation.

For the RR model the analysis was done according to the following equation:

$$y = X_{SY3} f_{LP} + X_{TDS3}\, tds + Z_G f_G + Z_{PE} f_{PE} + e$$

where:

y = measured values of weight or gain

X_{SY3} = the incidence matrix for station-year-3month season of birth ($SY3$) classes

f_{LP} = the average growth curve according to groups of bulls within $SY3$ classes (fixed effect)

X_{TDS3} = the incidence matrix for station-year-3month season of weighing (TDS3) classes

tds = the vector of station-year-3month season of weighing classes (fixed effects)

Z_G, Z_{PE} = incidence matrices for the animal

f_G = the function for the genetic deviation of the individual growth curve of the animal (random effect with additive relationship matrix)

f_{PE} = the function for the deviation of the individual growth curve under the effect of the permanent environment of the animal (random effect)

e = random residuum

In the case of longitudinal analysis of daily gains (G1m, G2m and G3m) Legendre polynomials were used for f_{LP}, f_G and f_{PE} effects. In the case of live weight (W1m) linear spline functions were used for f_G and f_{PE}. All the functions had 5 parameters. A detailed description of the methodology is in Přibyl et al. (2007, 2008) and Krejčová et al. (2008).

In the case of single traits (Gp and W400), a linear model with only one fixed effect ($sy3$) and additive animal genetic effects (a) with relationship matrix was used.

$$y = X_{SY3}\, sy3 + Z_G a + e$$

Calculations of RR were done for the entire observed period from 6 to 520 days of age of the bulls. The polynomial curves show generally rather high variability and no logical values at the beginning and the end of the observed period. The results are therefore formulated for a part of the growth curve without boundary values, in this case from 100 to 400 days of age only.

Variance components were estimated by REML (REMLF90 Program, Misztal et al., 2002). Heterogeneous variability in the course of growth was dealt with by weighted analysis. Coefficients of weights for weighted analysis were relative reciprocal values of the variance of a trait at a given age.

The variance components for Gp and W400 from AM analysis were available directly from REML calculations. For traits from RR analysis (G1m, G2m, G3m, W1m and W1mD) the variance components for traits were derived from the covariance matrix of random regression coefficients (Přibyl et al., 2007; Krejčová et al., 2008).

Estimates of genetic (G) and permanent environmental (PE) components for each day during the test period were obtained by

$$VC_{t,t'} = p_t{}'C\,p_{t'}$$

where:

$VC_{t,t'}$ = genetic ($VG_{t,t'}$) or the animal's permanent environment ($VPE_{t,t'}$), covariance of growth trait between age (t) and (t')

$p_t, p_{t'}$ = vectors of parameters of the curves at age (t) and (t')

C = covariance matrix of regression coefficients for the genetic or permanent environmental effect of the animal

The values for cumulative gain have the abbreviation ending "cel". Cumulative (co)variance components up to the times (j) and (j') ($CVC_{j,j'}$) were calculated according to the sum of the vectors of parameters from the age of bulls 100 days to the given age.

$$CVC_{j,j'} = \Big(\sum_{t=100}^{j} p_t\Big)'\, C\Big(\sum_{t=100}^{j'} p_t\Big)$$

The residual (RE) variances were estimated as the ratio of the average REML estimate of the residual variance to the weight factor depending on the age. The residuals for each day of age were assumed to be independent of all other days of age, and therefore the overall residual variance was the sum of the estimates for each day.

Breeding values from RR of daily gain or live weight for animal (i) at age (t) were

$$BV(t)_i = g_i{}'p_t$$

where:

g_i = the vector of genetic regression coefficients for animal (i) from the function f_G

The breeding value of cumulative gains is just the sum of daily breeding values for a period from 100 to 400 days of age.

For animals with production records (not for ancestors in the pedigree), correlations of breeding values (*BV*) between the different methods of evaluation were calculated for the traits of cumulative gains, live weights, and differences in live weight.

For each method of evaluation, correlations between progeny and parents that reflected the Mendelian sampling and prediction error were calculated (Schaeffer et al., 1996; Miglior and Van Doormaal, 2000).

The correlations of *BV* of sires' own individual growth at performance-test stations with the net gain of groups of sons at progeny-test stations were also calculated. The *BV* of tested progenies was taken from the official national evaluation performed by "Plemdat". The Sire- Maternal Grand Sire Model is the official method of progeny test evaluation.

RESULTS AND DISCUSSION

Fitness of the model

The fixed effects included in the models were tested prior to this study by GLM/SAS procedures and were statistically significant for all evaluated traits and statistical models (Přibyl et al., 2007; Krejčová et al., 2008).

The error terms from REML calculations by RR and AM methods are summarized in Table 1. There were parameters predicted for each animal in the AM method (traits Gp, W400) and 10 parameters per animal in the RR method (traits G1m, G2m, G3m, and W1m). The estimation of 2 covariance parameters in the AM method and 31 covariance parameters in the RR method corresponds to them.

Residual standard deviations (Se) for daily gains decreased with the length of the interval (1 m, 2 m, 3 m, and 300 days for trait Gp), being the highest for the shortest interval. Daily gain within a given interval is an average value according to the length of the interval. The variability of averages was lower than that of individual observations and eliminated random fluctuations. Longer intervals are averages of more daily gains, but at the same time there is a decrease in the number of observations per animal and in the total number of animals (Table 1). For trait G1m there were nearly 10 observations per animal, while for trait Gp there was only 1 observation. G1m and W1m allowed the greatest number of animals to be evaluated.

Residual standard deviation for live weight evaluated by the RR model (W1m) was 6.39 kg on average during the entire period observed and 10.12 kg at 400 days of age. Residual variability for live weight in the case of ST-AM (W400) was higher than in the RR model. In RR the great changes in variability with the age of the animal (Přibyl et al., 2007)

Table 1. Data sets for Random Regression (RR) and Single Trait Animal Models (AM) analysis

Trait and methods	Animals with records	Animals in pedigree	Records	Mean	SD	REML Se
Gp (g/day)	7 461	15 065	7 461	1 217.27	121.21	78.42
G1m (g/day)	8 243	16 488	79 796	1 188.23	352.74	294.13
G2m (g/day)	7 916	15 765	40 225	1 182.57	285.97	208.95
G3m (g/day)	7 504	15 021	25 655	1 182.80	248.34	162.51
W400 (kg)	7 461	15 065	7 461	499.14	42.42	28.64
W1m (kg)	8 243	16 488	79 796	290.02	130.16	6.39 (10.12[a])

G – daily gain (g/day); W – live weight (kg)

1 m, 2 m, 3 m – repeated average daily gains or weights in 1-, 2- or 3-month consecutive intervals between weighings

Gp – average daily gain from 100 to 400 days of age; W400 – live weight at 400 days of age

SD – average standard deviation of records; Se – average residual standard deviation from REML calculation

[a] at 400 days of age

were corrected by the growth function. A part of residual variability in W400 from the simple AM is included in the animal's permanent environment effects in the RR model.

Components of variance

Covariance components were calculated for daily gains, cumulative daily gains, live weight, and difference in live weights. In RR analysis components are calculated from covariance matrices of random effects (Přibyl et al., 2007; Krejčová et al., 2008). Table 2 shows standard deviations for separate components according to the trait and method of evaluation.

Daily gains (g/day)

All components changed with the age of the animal. Consequently, heritability also changed. The highest heritability was in the middle of the observed period at about 250 days of age (Krejčová et al., 2007a, 2008). Table 2 shows only average values over days 100 to 400. ST-AM gave higher genetic components (G) than the RR models and lower residual components (SRE). In the RR models genetic components between methods were more similar. The smallest was for the 2-month interval.

In the RR models, the longer the consecutive intervals (1 m, 2 m, 3 m), the lower the residual com-

Table 2. Standard deviations of variability components and heritability; SG is the genetic component, SPE is the permanent environmental component, SRE is the residual component, and SP is the total phenotypic SD

	Gp	G1m	G2m	G3m	W400	W1m	W1mD
Daily gain, average during the period from 100 to 400 days of age (g)							
h^2	0.36	0.03	0.05	0.09			
SG	58.99	52.66	49.61	55.21			
SPE		10.45	20.52	41.22			
SRE	78.42	300.74	213.65	166.17			
SP	98.13	305.67	220.69	180.47			
Cumulative gain from 100 to 400 days of age and live weight at 400 days of age (kg)							
h^2cel	0.36[b]	0.87	0.91	0.94	0.36	0.34	0.34
SGcel	17.70[b]	13.68	12.89	13.97	21.64	21.86	17.70
SPEcel		1.39	3.29	5.04		29.03	23.14
SREcel	23.52[b]	5.23	3.71	2.89	28.63	10.12	8.98
SPcel	29.44[e]	14.66	13.52	14.40	35.89	37.72	30.48

cel – cumulative values from 100 to 400 days of age; [b] average daily gain multiplied by 300

W1mD – deviation (weight at 400 days of age – weight at 100 days of age) calculated from the RR model ponents. Longer intervals contain a higher number of daily gains averaged together. In the RR models, a decrease in SRE with the length of repeated consecutive intervals was partly compensated by an increase in the permanent environmental component (SPE).

Phenotypic variability changed with residual variability. A reduction in residual variability caused heritability to increase with the length of the interval in the RR models. Heritability in the RR models was much lower than that for a long, 300-day period, evaluated by ST-AM (Gp). Differences in heritability were caused by differences in residual variability. The genetic components between methods were more similar than residual and phenotype variability.

Cumulative gains from 100 to 400 days of age (kg)

The cumulative value for Gp is calculated on the basis of 300 times the average daily gain for the entire period. The cumulative values for traits G1m, G2m and G3m are calculated from covariance matrices of each method, as noted in methodology. The value for W1mD was derived from RR covariance matrices for trait W1m.

The values of standard deviations for cumulative components have the ending “cel”. ST-AM for gains from 100 to 400 days of age (Gp) and deviations of weight according to RR (W1mD) have much higher genetic components (SGcel) than the cumulative gains at 400 days of age according to the RR models for gains in short intervals (G1m G2m and G3m). The cumulative values according to RR for gains at 400 days of age for permanent environment (SPEcel) and random environment (SREcel) were very low. The accumulation in the RR models for gain was much higher for the genetic component (SGcel) than for other components. This accumulation is practically the selection index with summation of everyday breeding values (economic values for all partial breeding values are constant = 1). The components of variance express variability of the index in this case. The RR models for daily gains yielded much lower cumulative phenotype standard deviations (CPcel) than ST-AM for gain over a long period and than evaluations of live weight. This documents that systematic environmental effects in the RR models for gain in short consecutive intervals explain the much higher proportion of variability than in ST-AM for a simple trait covering a long period. Cumulative phenotypic standard deviation (SPcel) was slightly higher for RR of deviation in weight (W1mD) than for ST-AM methods. A reduction in variability in the RR models for gain in comparison with the models of weight evaluation or ST-AM for gain over a long period was much greater in environmental components than in the genetic one.

The values of (h^2cel) in RR for gain represent the ratio of components after linear combination of traits into the complex selection index. It is not a question of the heritability of a simple trait, but rather the reliability of a composite trait.

Weight at 400 days of age

Our selection criterion was live weight at 400 days of age. Covariance components for live weight develop notably with the age of the animal (Albuquerque and Meyer, 2001; Meyer, 2001; Nobre et al., 2003; Legarra et al., 2004; Bohmanová et al., 2005; Cantet et al., 2005; Přibyl et al., 2007, 2008).

The values of the genetic component for live weight (SGcel) according to ST-AM and RR at 400 days of age were nearly similar. The phenotypic standard deviation (SPcel) for the RR method was a little higher than for ST-AM. The heritability of live weight, deviation of live weight and daily gain according to the simple trait (Gp) for the period from 100 to 400 days yielded similar values. The values of heritability were comparable with those reported by other authors (Pulkrábek et al., 1983; Kirkpatrick et al., 1990; Albuquerque and Meyer, 2001; Meyer, 2001; Bouška et al., 2003).

Variability of cumulative breeding values.

Cumulative breeding values (*BV*) were calculated in different ways from recorded traits (Table 1) by the RR and AM methods. From the RR analysis, cumulative BV were from repeated gains of 1-month, 2-month, and 3-month intervals; from the ST-AM analysis, cumulative BV were for gain from 100 to 400 days (Gp), and breeding values for live weight at 400 days; and from the RR analysis, cumulative BV were calculated from repeated weighings at 1-month intervals, and from deviations of live weight (weight at 400 days of age – weight at 100 days of age). Recorded live weight (W400) (Table 1) and cumulative gain (CG) recorded for the same animals (Gp records multiplied by the length of the period, 300 days) correspond to these values.

Standard deviations of cumulative *BV* are summarised in Table 3. The highest values were for evaluation of weight, lower for evaluation of a difference in live weight and daily gain over a long interval

Table 3. Standard deviations of cumulative breeding values (*BV*) and of production records in kg at 400 days of age and the ratio of variability

Variable	SD of *BV*		Ratio V_{All}/V_{Prod}	SGcel	Ratio V_{Prod}/V_G
	all	production			
CG [b]		36.92			
BVGp	9.78	11.70	0.71	17.70	0.44
BVG1m	8.02	8.94	0.82	13.68	0.43
BVG2m	7.93	8.58	0.86	12.89	0.44
BVG3m	8.46	9.19	0.86	13.97	0.43
W400		42.78			
BVW400	11.84	14.01	0.71	21.64	0.42
BVW1m	12.42	14.33	0.76	21.86	0.43
BVW1mD	10.37	12.04	0.76	17.70	0.46

[b]average daily gain in kg from Table 1 multiplied by 300

all – all animals in pedigree file

production – animals with production records only

V_{All}/V_{Prod} – ratio of the variability of *BV* of all animals and only animals with production records

V_{Prod}/V_G – ratio of the variability of *BV* of animals with production records and genetic variability

(BVW1mD, BVGp) and the lowest for evaluation of short consecutive intervals of gain.

Standard deviations of breeding values for all animals included in the pedigree file were smaller than for animals having production records. The ratios of this variability (V_{All}/V_{Prod}) were highest for the RR models of gains (BVG1m, BVG2m, BVG3m), lower for the RR model of weight (BVW1m, BVW1mD), and the lowest for ST-AM (BVGp, BVW400). The RR models maintain a higher variability of parents in the pedigree file, which should correspond to the higher precision of genetic evaluation of parents without production records.

The differences between standard deviations of breeding values (SD) in Table 3, according to the method of evaluation, correspond to the differences between genetic standard deviations for cumulative traits (SGcel) from Table 2. Although methods differed in the variability of breeding values, the ratio of variability V_{Prod}/V_G was quite similar for all methods, ranging from 0.42 to 0.46. The ratio of variability V_{Prod}/V_G represents the average reliability of breeding value estimation.

The standard deviations of *BV* of daily gains calculated by RR were in a smaller proportion from standard deviations of measured cumulative records (CG), about 1/4, compared to standard deviations of *BV* of live weight from live weight records (W400), about 1/3. Systematic environmental effects in the RR model for gain accounted for a higher proportion of variability than in ST-AM.

Correlations between cumulative breeding values (only animals with production records)

Correlations between *BV* were calculated only for animals with production records and are summarised in Table 4. All the correlations were highly significantly different from zero. The correlation between production records of weight at 400 days of age (W400) and gain from 100 to 400 days of age (CG) was 0.89. *BV* for daily gain in consecutive intervals with the RR models according to the length of the interval gave similar variability (BVG1m, BVG2m and BVG3m from Table 3). Correlations between the methods were high and ranged from 0.94 to 0.97 (Table 4).

ST-AM for gain (BVGp) yielded lower correlations with the other methods according to RR for gain (0.88 to 0.90) than were the correlations between the RR methods for gain themselves. The correlation of breeding values of live weight evaluated by the AM (BVW400) and RR (BVW1m) methods was 0.94.

Daily gain for the entire period of 100–400 days of age evaluated by ST-AM (BVGp) and for the same interval evaluated by RR for weight (BVW1mD) was correlated at 0.92. ST-AM of weight and ST-AM of gain for the entire period gave a correlation of 0.90. Production records of weight (W400)

Table 4. Correlations of *BV* for cumulative values at 400 days

	CG	BVGp	BVG1m	BVG2m	BVG3m	W400	BVW400	BVW1m	BVW1mD
CG	1	0.79	0.65	0.64	0.68	0.89	0.70	0.64	0.72
BVGp		1	0.88	0.88	0.90	0.73	0.90	0.83	0.92
BVG1m			1	0.97	0.94	0.61	0.80	0.83	0.94
BVG2m				1	0.96	0.61	0.81	0.85	0.94
BVG3m					1	0.63	0.82	0.84	0.94
W400						1	0.80	0.77	0.69
BVW400							1	0.94	0.84
BVW1m								1	0.90
BVW1mD									1

and production records of gain for the entire period (CG) yielded higher correlations with evaluation by ST-AM than with evaluation by the RR models.

Particular methods handle environmental factors and dependences between growths in different phases differently. Therefore, the similarity between methods is only partial.

Parents – progeny correlations (Mendelian sampling) of cumulative breeding values

Correlations of *BV* for cumulative growth between generations are influenced by Mendelian sampling and by the error of evaluation (Schaeffer et al., 1996). Mendelian sampling was similar in our study for all methods; therefore, differences between methods in parent – offspring correlations depend mainly on the reliability of *BV* estimation of both groups of animals. Parent – progeny correlations of *BV* for cumulative growth (sum of breeding values for daily gain from 100 to 400 days of age, average daily gain from 100 to 400 days, live weight at 400 days of age, difference between live weights at 400 and 100 days of age) are summarized in Table 5. They were calculated (a) for all animals in the pedigree file, and (b) only for animals where the sire had his own production records at a performance-test station. In the latter case, the numbers of progeny and numbers of sires for calculation of correlations were much smaller.

Three generations of ancestors were available. The methods differ partly in the number of sires (Sires), in the number of progeny with known sires (N_S), and also in the number of progeny with both parents known (N_{SD}).

In the entire data set, correlations between sires and sons were from 0.69 to 0.81. The highest were for RR of daily gain, lower for RR of weight, and the lowest for the ST-AM methods. Correlations between the averages of both parents with their sons were much higher (from 0.90 to 0.96), but the rank of the methods was similar to the previous case. The highest correlations were again for RR of daily gain, lower for RR of weight, and the lowest for the ST-AM methods. The RR methods for gain in short consecutive intervals were the most precise for evaluating the growth.

Comparisons of correlations with restriction only to sires with production records were lower than for correlations using all animals in the pedigree file. Calculations were performed in two ways. “Correlation 1” is in the case where sires and progeny were evaluated in the same run. Only sires with their own production records and their progeny were selected from results. In “Correlation 2”, the sires were from evaluation without progeny (*BV* of sires based only on own individual production and pedigree). In the next step progeny in the complete data set were evaluated. In both calculations, correlations were lower than in the entire data set. The values in “Correlation 2” were lower than those in “Correlation 1”.

In all cases the rank of the methods was similar. The best methods were for BVG2m and BVG1m using an RR analysis.

Correlation with progeny at progeny-test stations

The objective of the study was to determine the best prediction method for the growth potential

Table 5. Correlations of cumulative *BV* of parents with progeny (animal-A, sire-S, dam-D)

	All animals in pedigree file					Only if sire has production records					
				correlation				correlation 1		correlation 2	
	sires	N_S	N_{SD}	A × S	A × (S + D)/2	sires	N_{SD}	A × S	A × (S + D)/2	A × S	A × (S + D)/2
BVGp	1 582	13 218	7 806	0.72	0.91	43	279	0.63	0.87	0.27	0.65
BVG1m	1 670	15 018	9 000	0.81	0.95	59	377	0.70	0.94	0.52	0.83
BVG2m	1 599	14 853	8 868	0.80	0.96	58	364	0.72	0.94	0.55	0.83
BVG3m	1 541	14 721	8 762	0.80	0.95	55	349	0.68	0.93	0.49	0.81
BVW400	1 582	13 218	7 806	0.69	0.90	43	279	0.67	0.87	0.42	0.72
BVW1m	1 670	15 018	9 000	0.73	0.91	59	377	0.63	0.88	0.45	0.76
BVW1mD	1 670	15 018	9 000	0.76	0.92	59	377	0.62	0.89	0.42	0.77

correlation 1 – sires and progeny evaluated in the same run

correlation 2 – two runs, the first only with sires without progeny, the second with complete data set, sires from the first run, progeny + dam from the second run

N_S – number of progeny with known sire; N_{SD} – number of progeny with both parents known

Table 6. Correlations of *BV* according to the own individual performance test of sire with *BV* according to sons in progeny-test; 387 performance-tested sires were evaluated; the minimum number and average number of progeny per sire are 11 and 11.79

BVGp	0.33
BVG1m	0.37
BVG2m	0.38
BVG3m	0.37
BVW400	0.30
BVW1m	0.26
BVW1mD	0.30

of future progeny up to optimal slaughter weight, which corresponds to final live weights of 650 to 700 kg and age of 18–20 months. Table 6 shows the correlations of *BV* of sires according to own individual growth at performance-test stations (gain from 100 to 400 days of age, live weight at 400 days of age) and *BV* according to the net gain of groups of their sons at progeny-test stations. The sons were slaughtered at live weight of about 600 kg and 500 days of age.

From the file of *BV* of progeny test performed by the institution responsible for national evaluation, "Plemdat", only sires with 11 or more progeny were used. The set comprised 387 sires (bulls in our database of performance test) with 11.79 sons on the average. Correlations ranged from 0.26 to 0.38. The highest value was for BVG2m. All RR methods for gain in short consecutive intervals were better for the prediction of net gain of progeny than the other methods. The lowest values of correlations were for the evaluation of sires according to their own live weight. The magnitudes of correlation coefficients should depend on the selected data sample, but the tendency of comparison of methods prefers the RR evaluation of daily gains in short, repeated consecutive intervals for each animal.

CONCLUSIONS

The comparison of methods was on the basis of cumulative daily gains from 100 to 400 days of age or live weight at 400 days of age. The evaluation of growth according to the final live weight or average daily gain for the entire test period by simple AM allows the determination of *BV* only on the basis of one observation per animal. The evaluation of daily gains by RR allows different growth curves for each animal and yields *BV* for each day during the growth period. However, in this case a greater number of parameters must be estimated for each animal. The cumulative value is, in reality, a selection index with the same weights placed on all combined traits (all partial *BV*). According to the breeder's decision, the weights in the index can be changed and an emphasis is placed not only on total growth but also on differences in growth in separate phases.

Some methods appear similar and yield similar reliability, but they partly differ in the selection of animals. The reliability of prediction of the results of one method by another one is the square of correlations between the methods. Determination (r^2) between methods ranged from 64 to 94%.

Methods differed in the prediction of genetic variability for cumulative gain from 100 to 400 days of age. The RR models for daily gain in short consecutive intervals showed the lowest genetic variability. The genetic component of variability for live weight or daily gain over a long interval probably includes some artefact that also covers the non-genetic part deriving from the accumulation and compensation in consecutive periods of growth.

The methods differed in phenotypic variability. The RR models for daily gain at short consecutive intervals gave the lowest phenotypic variability of cumulative value to 400 days of age. Therefore, the RR models for daily gains over short consecutive intervals better deal with the systematic influences of external and internal environments during the entire period of the growth of animals.

The results of *BV* from the RR models differed more from production records than the results of *BV* from ST-AM. The RR model with the shortest consecutive intervals allowed the evaluation of the largest number of animals by exploiting all the available records of the animal. Correlations between parents and offspring were the highest for the RR methods for gain in short consecutive intervals. The variability of parents without their own individual production records in the pedigree file in comparison with animals with production records was also proportionately higher for these procedures.

Correlations of breeding values according to two independent data sets – own individual growth of sires at performance-test stations and progeny test with sons at progeny-test stations – favoured RR evaluation of growth according to daily gain in short, repeated consecutive intervals.

The best overall results were for the evaluation of growth according to daily gains in repeated consecutive 2-month intervals. Close behind them were the results for daily gains in repeated consecutive 1-month intervals, which allowed utilizing the maximum number of production records.

Simple evaluation of growth according to the final weight or daily gain over a long interval is not entirely correct. The results seem to be generally acceptable for all species and categories of animals.

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