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Livestock Production Science 86 (2004) 69–83

**LIVESTOCK
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Scope for a random regression model in genetic evaluation of beef cattle for growth

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Received 15 May 2002; received in revised form 10 December 2002; accepted 2 June 2003

Abstract

Potential improvement in accuracy of genetic evaluation of beef cattle for growth from replacing the current multi-trait (MT) model comprising birth, weaning, yearling and final weights as separate traits, with a random regression (RR) model analysis is examined by simulation. Maintaining the original data and pedigree structure for three beef cattle data sets, data were simulated assuming a cubic regression on polynomials of age for direct and maternal, genetic and permanent environmental effects and heterogeneous measurement error variances. Ages at weighing from birth to 730 days were considered. Data set I represented records from an experimental herd with monthly weighing of animals. Data sets II and III were field data, selecting a subset of herds in which at least 50% of animals had four or more weights recorded and records for all herds for a small breed, respectively. Simulated records were analysed fitting a MT model and RR models. Field data sets were expanded by adding a fictitious weight approximately 3 months after the original records. Accuracy of genetic evaluation was calculated as correlation between true and estimated values for each analysis. For the same subset of data, accuracies from a RR analysis were consistently higher than for a MT analysis, due to more appropriate modelling of variances and genetic parameters. Using all records available, RR accuracies for breeding value estimates for 200, 400 and 600 days in data set I were 0.023–0.034 or 4.3–5.9% higher than for MT. Corresponding gains were 3.1–3.6% for data set II and 1.5–1.7% for data set III. Expanding the field data sets by 100%, increased RR accuracies by 0.027–0.038 over those from MT analyses. While small in absolute terms, this was equivalent to a proportional increase of 5.7–8.3%. Results showed that substantial benefits could be obtained from the implementation of a RR model, if additional weight records were collected.

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Keywords: Accuracy; Genetic evaluation; Beef cattle; Growth; Random regression model

1. Introduction

Random regression (RR) models have become a popular choice for modelling of traits, which are

measured repeatedly per individual, but change gradually and continually with time. Growth of animals is a typical example for such traits, and the ‘infinite-dimensional’ model, where covariances are modelled as functions of polynomials of age has been first been presented in this context (Kirkpatrick et al., 1990).

Applications in genetic evaluation schemes so far, however, have been limited to the analysis of test-day records for dairy cattle. Genetic merit for growth of

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¹ AGBU is a joint venture of NSW Agriculture and the University of New England.

meat producing animals is generally assessed treating records taken at different ages, or ranges of ages, as different traits. BREEDPLAN, the Australian genetic evaluation scheme for beef cattle (Johnston et al., 1999), for instance, distinguishes between birth, weaning, yearling, final and mature cow weights as separate traits, allowing ranges in age at recording of 200 days or more for weaning, yearling and final weights with some pre-adjustment for differences in age at recording. A RR model appears an obvious and preferable alternative, which would not only remove current limits on the number of records per animal which can be utilised and eliminate the need for age correction, but also provide estimates of genetic merit for any age at recording.

The current 'standard' multi-trait (MT) analysis employed in BREEDPLAN has been shown to model changes in growth over time quite well, and has facilitated considerable genetic improvement in growth of beef cattle (Farquharson et al., 2002). Whilst the RR model is clearly conceptually highly appealing, it is not certain how much can be gained by its adoption. There has been concern that use of a RR model might increase computational requirements over those of a MT model, as incidence and coefficient matrices are denser and the number of effects to be estimated might be increased. Nobre et al. (2002) reported that a RR model fitting a cubic regression on age at recording for all random effects required less memory and substantially less time than a MT analysis, assigning weights from birth to 2 years of age to eight separate traits.

Simple selection index calculations suggest that the gain in accuracy of genetic evaluation due to inclusion of additional records is small for animals, which have birth, weaning, yearling and final weight recorded. However, in most breeds under performance recording, the average number of records per animal is only about two. Moreover, such calculations ignore the fact that analyses are carried out within contemporary groups, which tend to be small, and the complex utilisation of information from a range of relatives in an animal model, mixed model analysis. Theoretical values can be obtained from the inverse of the coefficient matrix in the mixed model equation or an approximation thereof, but can be inappropriate in individual cases.

This paper presents a simulation study, attempting to quantify the potential increase in accuracy of genetic evaluation for beef cattle due to implementation of a RR model.

2. Material and methods

2.1. Simulation

Data were simulated assuming a RR model for three beef cattle data sets, maintaining the original data and pedigree structure while replacing the original observations by simulated values. Simulations assumed a cubic regression on Legendre polynomials of age at recording for direct genetic, maternal genetic, direct permanent environmental and maternal permanent environmental effects, and heterogeneous measurement error variances. Changes in the latter with age were modelled as a step function with 19 classes (0, 1–30, . . . , 271–300, 301–360, . . . , 661–720 and 721–730 days). Estimates of covariance components for growth of Australian Hereford cattle (Meyer, 2002) were used as population values.

Simulations were carried out by sampling sets of RR coefficients for each level of the four random factors from appropriate multivariate normal distributions, accounting for correlations between animals for genetic effects. The resulting curves for each animal were evaluated at the ages for which it had records (direct effects) or progeny (maternal effects). Samples for the four random effects for each age were then combined and augmented by a temporary environmental effect, sampled from a normal distribution with measurement error variance corresponding to the age at recording, to form the record for each age. No systematic differences between animals were simulated.

2.2. Data sets

Data set I comprised records collected in a selection experiment carried out at the Wokalup research station in Western Australia; see Meyer et al. (1993) for details. This comprised weights from birth to 730 days of age for two herds with about 300 cows each over a period of 17 years. Animals were weighed on a monthly basis except during the calving season,

resulting in up to 25 records per animal. Records after weaning were predominantly for females, as only replacement animals remained in the herd. All pedigree information available for parents without records was extracted.

Data set II consisted of field records, obtained by extracting records up to 730 days of age for 16 herds with at least 20 animals and in which at least 50% of animals had four or more records prior to edits, from the Australian and New Zealand Hereford and Polled Hereford data base. Pedigree information for parents not in the data was collected for up to four generations backwards.

Data set III represented a larger set of field data, comprising the complete records for a less numerous breed of cattle. Data consisted of all records between birth and 730 days of age available after basic edits in the Australian Murray Grey database. Again, pedigree information up to four generations backwards was utilised.

For data sets II and III, additional, fictitious records were generated as described below to expand the data by 50 or 100%. Characteristics of the data structure are summarised in [Table 1](#).

2.3. Analysis

Up to five analyses were carried out for each data set. Mixed model equations were set up using sparse matrix storage, and solutions were obtained iteratively using a preconditioned gradient algorithm ([Stranden and Lidauer, 1999](#); [Tsuruta et al., 2001](#)).

The first analysis carried out for all three data sets was a RR analysis using all records available (RR*). The model of analysis was the same as the model under which the data were simulated, i.e. estimates of four RR coefficients corresponding to a cubic regression on Legendre polynomials of age at recording were obtained for each level of all four random effects, and population values for covariances among RR coefficients were used as input values for the mixed model analysis. Whilst no fixed effects were simulated, contemporary groups and a quartic regression on Legendre polynomials of age, where fitted as fixed effects to mimic a realistic model of analysis. Contemporary groups were defined as herd–sex–management group–year/month of weighing subclasses for birth weights, and herd–sex–management

group–date of weighing subclasses otherwise. To reduce the range of ages compared directly, subclasses in data sets II–III were divided further by applying an ‘age slicing’ similar to that employed in BreedPlan of 45–300 days, and 60 days for higher ages.

Secondly, a ‘standard’ MT analysis (MT-4) considering birth weight, 200-, 400- and 600-day weight as four separate traits was carried out. For this, a subset of data comprising up to four records per animal, namely birth weight and the weight closest to the target ages of 200, 400 and 600 days within the ranges of 80–300, 301–500 and 501–700 days, respectively, were selected. With single records per trait, permanent and temporary environmental effects could not be separated. Hence, the model of analysis fitted direct and maternal genetic, and maternal permanent environmental effects for the four traits only, i.e. included direct permanent environmental effects in the residual. Input values for covariance matrices were obtained by evaluating the covariance functions given by the population covariances between RR coefficients for ages 0, 200, 400 and 600. Fixed effects fitted were a linear regression on age at recording for each weight (except birth weight) and contemporary groups, defined as above for birth weights and as trait–herd–sex–management group–date of weighing subclasses (with the same age slicing as for the RR analysis) otherwise.

The third analysis for each data set was a RR analysis as described above, but considered only the subset of records used in the MT analysis (RR-4).

Further RR analyses considered the scenario, where up to eight records might be available per animal. For data set I with monthly weights for a large proportion of animals, another subset of the data was extracted as described above for MT-4 but including any records available close to intermediate target ages of 100, 300, 500 and 700 days in addition (RR-8). [Fig. 1](#) shows the distribution of ages at recording for the complete data and the two subsets considered.

For the two field data sets, differences between the complete data and the subset utilised in MT analyses were small. Hence, expanded data sets (RR×2) were created by adding a fictitious record for each record available, doubling the total number of records. First, weighing dates and year–months of birth dates were

Table 1

Characteristics of the data structure for complete data sets (RR*), subsets considering the same records as standard MT analyses (RR-4) and up to eight records per animal (RR-8), respectively, and expanded data sets adding about 50% (RR×1.5) and 100% records (RR×2)

Analysis	Data set I			Data set II				Data set III			
	RR*	RR-8	RR-4	RR*	RR-4	RR×1.5	RR×2	RR*	RR-4	RR×1.5	RR×2
Total number of animals ^a		8443				22 670				173 126	
Number of sires ^b		364				578				6936	
Number of dams ^b		2646				5007				50 254	
Number of records	75 829	33 556	18 765	44 328	38 887	66 749	88 656	227 219	214 964	340 561	454 438
Number of animals in data	7305	7305	7305	12 839	12 835	12 839	12 839	117 977	117 900	117 977	117 977
Number of animals in data with one record	800	800	864	837	1083	398	10	58 396	59 778	29 425	209
Number of animals in data with two records	545	603	3817	2154	2993	941	827	26 840	28 805	35 871	58 187
Number of animals in data with three records	158	1151	229	2769	3218	1447	125	19 795	19 692	16 155	647
Number of animals in data with four records	271	2184	2395	5254	5541	2041	2030	10 776	9625	14 710	26 200
Number of animals in data with ≥5 records	5531	2567	–	1868	–	8012	9847	2170	–	21 816	32 734
Number of records—0 days	7288			10 229				74 406			
Number of records—80–300 days	33 096	15 535	6435	12 519	10 555	19 885	26 811	71 988	68 270	114 326	155 988
Number of records—301–500 days	14 026	5147	2625	10 941	9367	16 428	21 863	47 826	4349	82 529	118 168
Number of records—501–700 days	12 791	4840	2417	10 112	8736	16 919	23 308	28 192	25 796	49 507	70 446
Number of CG-RR ^c	11 417	7543	4876	5682	5198	10 131	11 263	54 263	51 980	92 825	108 503
Number of CG-MT ^d			4878		5350				52 941		

^a Including parents without records.

^b With progeny in data.

^c Contemporary groups in RR analysis.

^d Contemporary groups in MT analysis.

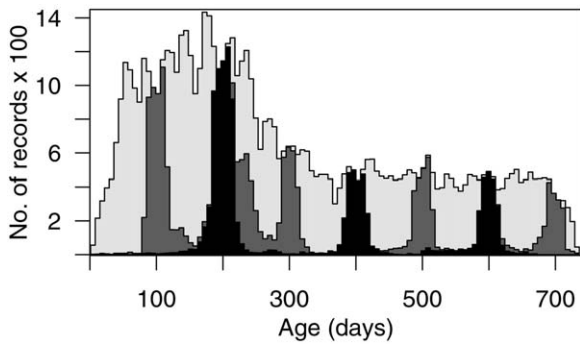


Fig. 1. Distribution of records over ages at recording (in 7-day intervals) for data set I (□: all records, ■: subset with up to eight records per animal (RR-8), and ■: subset as for MT analysis (MT-4), birth weights not shown).

collected for each herd. Second, a corresponding fictitious weighing date was determined for each. For this, a random interval between 65 and 125 days for birth weight and 80–110 days for the other weights was sampled from a uniform distribution. The new date was then derived as original date plus interval, setting day to 15 for each original year–month of birth.

Contemporary groups for the ‘new’ records were derived assuming the same management groups as for the corresponding original records. This strategy ensured a contemporary group structure for the new records similar to that for the original data. In addition, a subset expanded by only 50% ($RR \times 1.5$) rather than 100% was formed from $RR \times 2$ by randomly deleting half of the ‘new’ records. The relationship

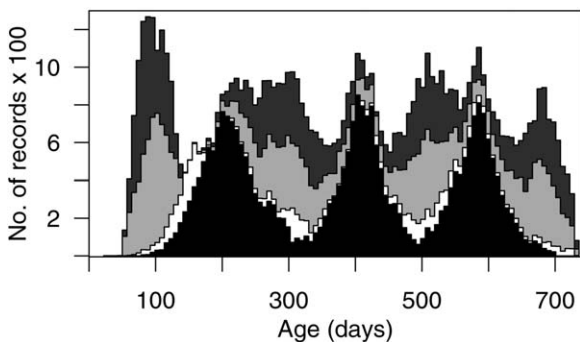


Fig. 2. Distribution of records over ages at recording (in 7-day intervals) for data set II (white bars: all records, ■: subsets as for MT analysis (MT-4) □: data set expanded by 50% ($RR \times 1.5$), and, ■: data set expanded by 100% ($RR \times 2$)); birth weights not shown.

between records used in the different analyses for data sets II and III is illustrated in Figs. 2 and 3, respectively. Both data sets (original records) show the typical distribution of records around the target ages of 200, 400 and 600 days. For data set II, however, the usual decline in numbers of records with age found in field data (see Fig. 3) is absent, due to selecting only herds with a high proportion of animals with at least four records.

2.4. Criteria

Accuracies of evaluation for each analysis were calculated as correlations between simulated and estimated effects, across all animals and for selected groups of animals. For RR analyses, point estimates corresponding to the estimates from the MT analysis were derived by evaluating the estimated regression curves at the target ages of 0, 200, 400 and 600 days.

A total of 800 replicates were carried out for data sets I and II, and 150 replicates were performed for data set III. Mean accuracies and proportional increases in accuracy for RR over MT analyses and their empirical standard deviations (S.D.) across replicates were calculated. In addition, average bias and mean square errors across replicates were determined.

2.5. Expected accuracy

Selected elements of the inverse of the coefficient matrix in the mixed model equations, namely the

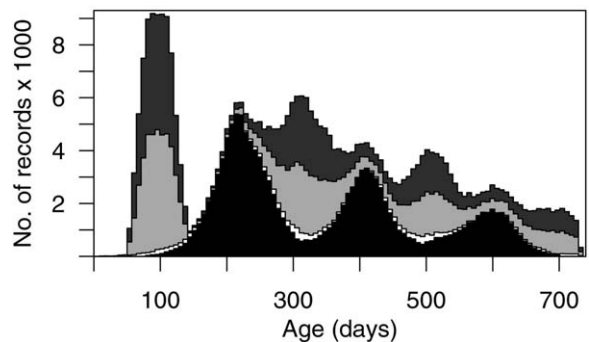


Fig. 3. Distribution of records over ages at recording (in 7-day intervals) for data set III (white bars: all records, ■: subset as for MT analysis (MT-4) □: data set expanded by 50% ($RR \times 1.5$), and ■: data set expanded by 100% ($RR \times 2$)); birth weights not shown.

diagonal blocks pertaining to sets of RR coefficients for direct and maternal genetic effects, were estimated for each data set and analysis using a Gibbs sampling algorithm as described by Harville (1999). A total of 400 000 samples were drawn, discarding the first 20 000 samples as burn in. This involved matrices to be inverted of size up to 118 769, 264 011 and 2 166 439 for data sets I, II and III, respectively. Due to computational demands, only inverses for analyses RR×2 and MT-4 were obtained for data set III.

For RR analyses, the diagonal block for each set of RR coefficients provided an estimate of the prediction error covariances among the coefficients for an animal. Breeding value estimates were obtained by evaluating the estimated regression for the target ages desired. Whilst this was a polynomial function of age, it was linear for the estimated RR coefficients. Hence, corresponding prediction error variances (PEV_i) of breeding values at age i was obtained from the estimated covariances among RR coefficients simply as the variance of a linear function. The expected accuracy was then calculated as $\sqrt{(1 - PEV_i/Var_i)}$, with Var_i the genetic variance for age i . This was done for each animal, and an average accuracy was calculated omitting any cases for which the estimate of PEV_i was larger than the corresponding Var_i . In addition, a second estimate of the expected average accuracy was determined by averaging PEV_i over animals before calculating the corresponding accuracy as above.

3. Results

3.1. Expected gain in accuracy

Phenotypic variances and genetic parameters resulting from the population values assumed for covariances between RR coefficients are given in Table 2 for ages in 100 day intervals. Values were estimates obtained for Hereford data (Meyer, 2002), resulting in direct heritabilities for weaning weight somewhat lower and the proportion of variance due to maternal permanent environmental effects (not shown) substantially higher than in most other breeds. Whilst genetic correlations assumed between birth weights and later weights were only low to moderate, the remaining correlations were high (>0.75) and close to unity for weights recorded 100 days apart.

Simple index calculations to assess the potential benefit of including additional weights for the accuracy of genetic evaluation are summarised in Table 3. For a single record per animal, the accuracy is equal to the square root of the heritability. Hence, for birth weight with a high heritability and moderate genetic correlations to later weights, accuracies increase little when adding additional records. Conversely, for 200 day weight with a low direct heritability and high genetic correlations with other, more highly heritable weights, increasing the number of records to two or four yields a marked increase in accuracy, equivalent to 15.6% on average. However, comparatively little accuracy is gained for any trait by adding four additional records.

Table 2

Genetic correlations together with heritabilities (in bold) and phenotypic variances (σ_p^2 , in kg^2) for selected ages implied by the population covariance functions, for direct (lower triangle) and maternal (upper triangle) effects

Age (days)	Age (days)									σ_p^2
	0	0	100	200	300	400	500	600	700	
0	0.399	0.071	0.294	0.251	0.268	0.310	0.362	0.409	0.423	17.1
100	0.682	0.122	0.084	0.993	0.966	0.902	0.813	0.760	0.785	342.0
200	0.605	0.962	0.145	0.091	0.988	0.941	0.862	0.805	0.808	655.6
300	0.567	0.869	0.968	0.182	0.074	0.981	0.926	0.872	0.851	936.3
400	0.546	0.781	0.911	0.984	0.237	0.058	0.980	0.941	0.894	1168.3
500	0.553	0.741	0.870	0.954	0.989	0.304	0.049	0.985	0.930	1368.0
600	0.576	0.746	0.842	0.906	0.943	0.977	0.359	0.044	0.970	1696.3
700	0.579	0.753	0.784	0.799	0.820	0.875	0.956	0.389	0.041	2521.2

Table 3

Accuracy of genetic evaluation for additive genetic effects based on a single record for a trait, two records (the trait plus one of the remaining records from 0, 200, 400 and 600 days; averaged over the three possibilities), records at four ages (0, 200, 400, 600 days) and eight ages (0, 100, . . . , 700)

Trait	h^{2a}	Direct genetic			
		Single	Two	Four	Eight
Birth weight	0.399	0.632	0.636	0.646	0.650
200-day weight	0.145	0.381	0.475	0.549	0.557
400-day weight	0.237	0.487	0.527	0.589	0.599
600-day weight	0.359	0.599	0.607	0.625	0.646

^a Heritability.

These calculations assume that records are taken at the target ages, i.e. are assigned their correct variances. If this is not the case, a RR analysis achieves higher accuracies than a MT analysis, as it accounts for changes in covariances with age. For instance, consider an index of 200- and 600-day weights to select for 200 days weight with an accuracy of 0.5113. If records were taken at 100 and 700 days, but treated as if they were taken at 200 and 600 days, respectively, the expected accuracy would still be 0.5113 whilst the true accuracy of the index would be only 0.4981. This is the scenario of a MT analysis. If the correct covariances were used to derive index weights, the equivalent of a RR analysis, the accuracy would be 0.5003. Similarly, an index of four weights at 0, 300, 500 and 700 days would have expected and true accuracies of 0.5488 and 0.5449 whilst, using correct covariances, the accuracy would be 0.5537. For eight records at 0, 180, 280, . . . , 680 days, corresponding values would be 0.5488, 0.5473 and 0.5566. Whilst differences on an individual level, as shown here, are small they compound in a genetic evaluation scheme, where information from progeny and parents is taken into account.

Similar calculations for the potential increase in accuracy of selection for 190-day weight in pigs considered the animals' own performance as well as four full and 45 half sibs. Using two weights at the beginning and end of the fattening period only, taken between 55 and 95 and around 190 days of age, Huisman et al. (2002) reported an expected increase in accuracy from a RR analysis of 7%, which increased to 12% if an additional record at 130 days was

available, and 13% if three records at 100, 130 and 160 days were included in the analysis.

3.2. Accuracy of random regression coefficients

Table 4 gives mean accuracies of evaluation for all RR coefficients estimated for data set I. Results for the other data sets showed a similar pattern. Whilst estimated RR coefficients are of secondary interest in their own right, the table emphasises the effect of the amount of information available for each animal on the accuracy of estimation.

Considering only records used in a MT analysis (MT-4), there were on average 2.6 records per animal and only 32.8% of animals in the data had four records (see Table 1), i.e. the minimum number of points to fit a cubic polynomial. Records on relatives are expected to provide information for additional ages, and thus facilitate accurate estimation at the genetic level for animals with less records than the order of polynomial fit, and, in turn, allow genetic and permanent environmental effects to be separated. Data set I originated from closed, experimental herds with considerable relationships between animals. Even so, estimates of the quadratic and cubic, direct regression coefficient, both genetic and permanent environmental, showed low accuracies when only records corresponding to MT analyses were used.

Considering up to eight records per animal increased the average number of records to 4.6 and the proportion of animal with four or more records to 65.0%, and thus yielded a substantial increase in accuracy for these coefficients. Results suggest that some of the 'end of range' problems observed in the estimation of covariance components for RR models might be alleviated if a large proportion of animals had a minimum number of records equal to the order of polynomial fit for direct, permanent environmental effects. Using all records, with 10.4 records per animal and 79.4% of animals with at least four records, increased accuracies for all coefficients further, but effects were less marked.

Differences between analyses for maternal RR coefficients were less pronounced, as dams with multiple progeny were more likely to have information for at least four ages than individuals. Relatively high accuracies for cubic maternal coefficients were an artefact of the assumed covariance structure among

Table 4
Accuracy (ρ) of estimates of RR coefficients together with empirical S.D., bias and mean square error (MSE) for data set I

Coefficient ^b		Analysis ^a	Additive genetic				Permanent environmental			
			0	1	2	3	0	1	2	3
<i>Direct effects</i>										
ρ	RR*		0.617	0.586	0.486	0.465	0.646	0.447	0.473	0.563
	RR-8		0.608	0.572	0.445	0.418	0.628	0.420	0.405	0.473
	RR-4		0.586	0.529	0.308	0.283	0.589	0.359	0.279	0.351
S.D.	RR*		0.018	0.021	0.028	0.028	0.007	0.010	0.008	0.008
	RR-8		0.018	0.021	0.030	0.031	0.007	0.010	0.009	0.008
	RR-4		0.019	0.024	0.038	0.036	0.008	0.010	0.010	0.009
Δ^c			5.2	10.9	59.4	66.5	9.8	24.6	69.8	60.6
			1.0	1.9	14.7	18.4	0.7	2.0	5.0	3.4
Bias	RR*		-0.018	0.006	0.030	0.015	-0.025	-0.016	-0.007	-0.004
	RR-8		-0.015	0.000	0.024	0.014	-0.025	-0.016	-0.007	-0.004
	RR-4		0.003	0.022	0.044	0.023	-0.025	-0.016	-0.007	-0.004
MSE	RR*		358.8	151.7	49.0	12.2	454.2	226.2	107.8	33.6
	RR-8		365.3	155.5	51.5	12.8	472.5	232.8	116.1	38.2
	RR-4		380.0	166.4	58.2	14.3	509.4	246.3	128.2	43.2
<i>Maternal effects</i>										
ρ	RR*		0.366	0.256	0.193	0.353	0.618	0.382	0.276	0.594
	RR-8		0.361	0.251	0.174	0.339	0.607	0.372	0.265	0.579
	RR-4		0.353	0.241	0.140	0.320	0.584	0.352	0.241	0.553
S.D.	RR*		0.032	0.036	0.041	0.033	0.011	0.017	0.017	0.011
	RR-8		0.032	0.037	0.039	0.033	0.011	0.017	0.018	0.011
	RR-4		0.034	0.038	0.040	0.035	0.011	0.016	0.018	0.012
Δ			3.9	6.8	48.4	10.8	5.8	8.5	15.0	7.5
			2.9	7.4	107.7	5.3	1.0	1.9	5.1	1.1
Bias	RR*		-0.032	-0.006	-0.010	-0.020	-0.026	-0.003	0.002	-0.006
	RR-8		-0.020	-0.004	-0.011	-0.017	-0.026	-0.003	0.002	-0.006
	RR-4		-0.020	-0.003	-0.009	-0.016	-0.026	-0.003	0.002	-0.006
MSE	RR*		105.0	15.0	4.7	5.1	170.2	9.2	8.0	10.5
	RR-8		105.4	15.0	4.7	5.2	174.2	9.3	8.1	10.8
	RR-4		106.2	15.1	4.8	5.3	181.4	9.4	8.2	11.3

^a RR*, all data; RR-8, subset with up to eight records per animal, and RR-4, subset as for MT analyses.

^b RR coefficient, 0: intercept, 1: linear, 2: quadratic, and 3: cubic.

^c Increase in accuracy from RR* over RR-4, in % of RR-4, first line mean, second line S.D.

RR coefficients, in particular strong correlations between intercept and cubic terms. A large S.D. in the percentage increase in accuracy for the quadratic coefficient for maternal genetic effects was explicable by a number of replicates with very low estimates for this coefficient for analysis RR-4.

Empirical S.D. of accuracies were similar for all analyses with a slight increase for direct coefficients as the number of records decreased. Similarly, mean square errors increased with decreasing size of the data set, in essence being a different measure of the accuracy of estimation. Average biases were close to 0 throughout.

3.3. Accuracy of breeding value estimates

Mean correlations between true and estimated genetic effects, calculated across all animals, for 0, 200, 400 and 600 days for direct effects and 200 days of age for maternal effects are summarised in Tables 5–7, together with corresponding expected values.

On the whole, mean empirical accuracies show excellent agreement with expected values derived from the inverse of the coefficient matrix in the mixed model equations, differences being well within the range of S.D. over replicates. Expected values calculated as the average of correlations for individual

Table 5
Accuracy (ρ) of breeding value estimates, and increase in accuracy from RR over MT analyses, for data set I

Analysis ^a	Expected ρ^b		Empirical ρ				Increase (in %)				Bias	MSE
	A	B	Mean	S.D.	Minimum	Maximum	Mean	S.D.	Minimum	Maximum		
<i>Birth weight—direct</i>												
RR*	0.629	0.641	0.639	0.017	0.583	0.717	2.0	0.5	0.5	3.4	0.001	3.87
RR-8	0.621	0.634	0.631	0.018	0.575	0.711	0.7	0.3	-0.6	1.5	0.002	3.93
RR-4	0.617	0.630	0.627	0.018	0.570	0.709	0.1	0.1	-1.4	0.7	0.003	3.97
MT-4	0.617	0.630	0.627	0.018	0.570	0.709					0.003	3.97
<i>200 day weight—direct</i>												
RR*	0.571	0.587	0.583	0.020	0.525	0.639	4.3	1.0	1.3	7.3	-0.003	61.4
RR-8	0.563	0.579	0.576	0.021	0.519	0.633	2.9	0.8	0.7	6.1	0.003	62.3
RR-4	0.549	0.563	0.561	0.021	0.501	0.621	0.3	0.4	-4.0	2.5	0.006	63.8
MT-4	0.550	0.564	0.560	0.021	0.498	0.619					0.005	64.0
<i>400 day weight—direct</i>												
RR*	0.586	0.603	0.600	0.018	0.532	0.652	5.6	1.2	1.3	9.9	-0.025	169.6
RR-8	0.575	0.592	0.590	0.019	0.521	0.647	3.7	1.0	0.3	7.7	-0.020	173.0
RR-4	0.557	0.573	0.571	0.020	0.496	0.628	0.4	0.5	-6.5	2.9	-0.022	178.8
MT-4	0.557	0.574	0.569	0.020	0.487	0.628					-0.024	179.5
<i>600 day weight—direct</i>												
RR*	0.597	0.614	0.613	0.018	0.563	0.667	5.9	1.2	2.4	10.1	-0.030	361.1
RR-8	0.589	0.605	0.603	0.018	0.552	0.661	4.1	1.0	1.1	8.1	-0.028	368.2
RR-4	0.566	0.582	0.582	0.020	0.524	0.640	0.5	0.6	-5.3	3.8	-0.013	382.5
MT-4	0.569	0.586	0.579	0.020	0.520	0.639					-0.013	384.7
<i>200 day weight—maternal</i>												
RR*	0.363	0.373	0.386	0.034	0.277	0.487	4.9	3.0	-2.6	17.6	-0.030	50.8
RR-8	0.360	0.370	0.380	0.034	0.274	0.483	3.1	2.4	-4.2	14.9	-0.020	51.1
RR-4	0.347	0.356	0.369	0.035	0.258	0.473	0.2	0.7	-4.3	6.1	-0.020	51.6
MT-4	0.341	0.349	0.368	0.035	0.255	0.469					-0.021	51.6

^a RR*: all data, RR-8: subset with up to eight records per animal, RR-4: subset as for MT analyses, and MT-4: multi-trait.

^b From inverse of coefficient matrix, A: average of individual accuracies, B: accuracy computed from average diagonal elements.

animals tended to be lower than their counterparts derived from the average of PEVs. This could be attributed to the fact that animals which had estimated PEVs higher than the genetic variance were omitted. The proportion of such animals was small and decreased somewhat with increasing length of the Monte-Carlo chain in the Gibbs sampler used to estimate the required elements of the inverse coefficient matrix. This indicates some problems with the inversion procedure due to high correlations between RR coefficients—the Gibbs sampler used was scalar, i.e. sampled for one row at a time (Harville, 1999, Eqs. (8) and (9)). A block-wise procedure, sampling for sets of RR simultaneously, might reduce such problems but was not tried.

RR analyses utilising the same subset of records as the MT analyses (RR-4) were, on average, consistently more accurate than MT (MT-4) analyses. This could be attributed to more appropriate modelling of variances and genetic parameters in the RR analysis. Whilst MT-4 analyses treated all records within the range of permissible ranges for a trait as if they had variances and genetic parameters equal to those of the target age, RR-4 assumed the correct variances for each record.

For example, RR analyses assumed records taken at 100 and 300 days of age to have appropriate phenotypic variances of 342 and 936 kg², direct heritabilities of 0.122 and 0.182 and maternal heritabilities of 0.084 and 0.074, respectively. In contrast,

Table 6
Accuracy (ρ) of breeding value estimates, and increase in accuracy from RR over MT analyses, for data set II

Analysis ^a	Expected ρ^b		Empirical ρ				Increase (in %)				Bias	MSE
	A	B	Mean	S.D.	Minimum	Maximum	Mean	S.D.	Minimum	Maximum		
<i>Birth weight—direct</i>												
RR×2	0.501	0.530	0.533	0.020	0.473	0.593	1.4	0.9	-0.9	6.0	0.010	4.91
RR×1.5	0.498	0.527	0.533	0.020	0.483	0.603	1.3	0.9	-1.3	7.4	0.007	4.92
RR*	0.497	0.526	0.531	0.020	0.480	0.601	0.8	0.9	-1.4	8.0	0.009	4.94
RR-4	0.496	0.524	0.530	0.020	0.471	0.601	0.6	0.9	-1.8	7.8	0.009	4.94
MT-4	0.485	0.526	0.527	0.020	0.460	0.600					0.009	4.97
<i>200 day weight—direct</i>												
RR×2	0.492	0.506	0.506	0.022	0.458	0.576	5.7	3.3	0.2	21.2	-0.006	71.2
RR×1.5	0.486	0.498	0.501	0.022	0.435	0.583	4.9	3.0	-1.7	27.2	-0.035	71.6
RR*	0.480	0.492	0.493	0.023	0.426	0.568	3.1	2.2	-1.3	20.8	-0.025	72.3
RR-4	0.474	0.485	0.492	0.023	0.417	0.579	2.7	2.8	-2.8	24.9	-0.017	72.5
MT-4	0.469	0.490	0.479	0.025	0.382	0.563					-0.018	73.9
<i>400 day weight—direct</i>												
RR×2	0.524	0.538	0.538	0.019	0.481	0.612	6.0	2.8	0.4	18.7	-0.033	197.5
RR×1.5	0.517	0.529	0.532	0.019	0.475	0.600	5.4	2.6	0.5	19.6	-0.057	199.0
RR*	0.509	0.520	0.522	0.020	0.461	0.588	3.4	2.0	-0.2	16.0	-0.009	201.7
RR-4	0.499	0.510	0.520	0.021	0.457	0.597	2.7	2.5	-1.3	17.3	-0.030	202.6
MT-4	0.494	0.515	0.506	0.022	0.429	0.588					-0.034	206.8
<i>600 day weight—direct</i>												
RR×2	0.546	0.557	0.558	0.018	0.512	0.620	6.7	2.7	1.8	20.4	-0.018	420.1
RR×1.5	0.536	0.545	0.550	0.018	0.495	0.612	5.9	2.4	1.5	17.2	-0.021	424.8
RR*	0.525	0.534	0.535	0.019	0.478	0.603	3.6	2.2	-0.4	18.0	0.074	433.9
RR-4	0.516	0.525	0.534	0.020	0.468	0.605	2.6	2.3	-1.9	17.0	0.022	435.5
MT-4	0.507	0.530	0.520	0.021	0.442	0.596					0.013	444.8
<i>200 day weight—maternal</i>												
RR×2	0.332	0.332	0.348	0.033	0.256	0.457	5.7	3.9	-4.8	32.3	0.012	53.1
RR×1.5	0.322	0.322	0.342	0.034	0.243	0.452	4.6	3.7	-5.3	32.4	0.018	53.1
RR*	0.330	0.330	0.336	0.033	0.220	0.452	2.5	2.5	-11.3	16.2	-0.023	53.4
RR-4	0.324	0.324	0.333	0.034	0.206	0.445	1.8	2.5	-9.4	16.5	0.007	53.5
MT-4	0.319	0.321	0.328	0.033	0.211	0.439					0.007	53.7

^a RR×2, data expanded by 100%; RR×1.5, data expanded by 50%; RR*, all data; RR-4, subset using the same records as MT analyses, and MT-4 multi-trait.

^b From inverse of coefficient matrix, A: average of individual accuracies, B: accuracy computed from average diagonal elements.

MT-4 analyses assigned values for the target age of 200 days, namely 656 kg², 0.145 and 0.091, to both records. Hence, differences between MT4 and RR-4 were smallest for birth weights and for data set I, for which records for 200, 400 and 600 days were clustered closer to the target age than in the two field data sets. In addition, the total number of contemporary groups for RR-4 was somewhat smaller than for MT-4 for all data sets (see Table 1), i.e. the 'effective number of records' was slightly increased.

Clearly, this superiority relies on the RR model describing the covariance structure in the data better than the MT model. Whilst a RR model which assumes continuously increasing variances and covariances is more plausible than a MT model, it might only provide an approximation to the covariance structure in real data. Hence, simulation results where the RR model is the true model provide an estimate of the maximum increase in accuracy, which can be achieved.

Table 7

Accuracy (ρ) of breeding value estimates, and increase in accuracy from RR over MT analyses, for data set III

Analysis ^a	Expected ρ^b	Empirical ρ				Increase (in %)			
	B	Mean	S.D.	Minimum	Maximum	Mean	S.D.	Minimum	Maximum
<i>Birth weight—direct</i>									
RR×2	0.539	0.539	0.019	0.505	0.612	1.6	0.9	0.5	4.5
RR×1.5	—	0.537	0.019	0.500	0.607	0.9	0.5	0.4	3.4
RR*	—	0.535	0.020	0.502	0.604	0.3	0.2	0.0	0.8
RR-4	—	0.535	0.018	0.502	0.603	0.3	0.3	-0.2	2.8
MT-4	0.535	0.534	0.019	0.497	0.608				
<i>200 day weight—direct</i>									
RR×2	0.517	0.521	0.016	0.494	0.572	8.3	4.6	2.2	22.3
RR×1.5	—	0.507	0.018	0.480	0.554	4.3	3.0	1.4	19.0
RR*	—	0.496	0.020	0.454	0.559	1.5	1.2	0.4	6.3
RR-4	—	0.495	0.018	0.451	0.557	1.5	1.7	-0.2	16.2
MT-4	0.489	0.488	0.021	0.424	0.555				
<i>400 day weight—direct</i>									
RR×2	0.530	0.535	0.016	0.510	0.592	8.1	4.0	3.3	22.4
RR×1.5	—	0.521	0.018	0.493	0.571	4.6	2.5	2.1	15.1
RR*	—	0.509	0.021	0.472	0.572	1.7	1.0	0.4	5.3
RR-4	—	0.507	0.018	0.471	0.570	1.5	1.5	0.2	12.0
MT-4	0.499	0.500	0.021	0.441	0.568				
<i>600 day weight—direct</i>									
RR×2	0.537	0.542	0.017	0.510	0.613	7.6	3.3	3.8	18.6
RR×1.5	—	0.527	0.019	0.490	0.592	4.7	2.2	2.0	14.4
RR*	—	0.513	0.023	0.476	0.591	1.7	0.8	0.4	3.9
RR-4	—	0.509	0.020	0.475	0.589	1.4	1.2	0.2	10.8
MT-4	0.502	0.505	0.021	0.460	0.587				
<i>200 day weight—maternal</i>									
RR×2	0.410	0.420	0.023	0.371	0.472	7.6	3.4	2.8	17.7
RR×1.5	—	0.402	0.025	0.342	0.484	4.4	2.9	1.1	20.6
RR*	—	0.382	0.026	0.324	0.443	1.1	0.6	-0.5	3.6
RR-4	—	0.381	0.026	0.324	0.473	1.2	1.6	-0.6	17.9
MT-4	0.376	0.380	0.026	0.319	0.469				

^a RR×2, data expanded by 100%; RR×1.5, data expanded by 50%; RR*, all data; RR-4, subset using the same records as MT analyses, and MT-4 multi-trait.

^b From inverse of coefficient matrix, B: accuracy computed from average diagonal elements.

Considering all records available (RR*) increased accuracies only slightly compared with RR-4 for data sets II and III, as there were only a small number of additional records (see Table 1). Hence, at the current data structure, the main benefit from a RR analysis to be expected for field data is due more appropriate modelling of covariances.

However, as results for the experimental data set (I) show, overall increases in accuracy of genetic evaluation of 0.023, 0.031, 0.034 and 0.018, equivalent to average percentage increases of 4.3, 5.6, 5.9 and

4.9%, for 200, 400 and 600 day weights and 200 day maternal effects, respectively, can be achieved by switching from a MT to a RR analyses (RR* vs. MT-4), provided a sufficiently large number of additional records was available. Whilst monthly weighing as in data set I is clearly not practical for commercial breeders, producers might consider recording 'repeated' records obtained some 3–4 months after the standard weights already reported, such as a marking weight, a heifer weight at joining or 300, 500 and 700 day weights. This scenario has been examined by

Table 8

Accuracy of estimates for direct genetic effects for 200, 400 and 600 day and maternal genetic effects for 200 (M 200) day weights for selected categories of animals, in Data set II

Analysis ^a	Females								Males							
	200 days		400 days		600 days		M 200 days		200 days		400 days		600 days		M 200 days	
	ρ^b	Δ^c	ρ	Δ	ρ	Δ	ρ	Δ	ρ	Δ	ρ	Δ	ρ	Δ	ρ	Δ
	All (N=12 870)								All (N=8270)							
RR×2	0.477	5.0	0.508	5.3	0.528	6.0	0.354	5.4	0.537	5.1	0.566	5.3	0.586	5.8	0.347	5.0
RR×1.5	0.474	4.3	0.504	4.7	0.521	5.2	0.348	4.7	0.537	4.3	0.564	4.5	0.581	5.0	0.341	4.2
RR*	0.467	2.8	0.495	3.0	0.507	3.0	0.339	2.8	0.529	2.6	0.554	2.8	0.566	2.7	0.331	2.3
MT-4	0.455		0.482		0.496		0.332		0.516		0.540		0.553		0.327	
S.D. ^d	0.022	2.6	0.021	2.0	0.020	1.9	0.030	2.9	0.026	2.7	0.023	2.1	0.022	1.9	0.040	3.8
	Females with 1 record (N=413)								Males with own records (N=5372)							
RR×2	0.565	6.2	0.587	5.9	0.603	6.1	0.385	5.6	0.630	4.9	0.664	5.1	0.687	5.7	0.400	4.9
RR×1.5	0.554	4.9	0.579	5.0	0.591	5.3	0.388	4.5	0.631	4.0	0.662	4.3	0.682	4.7	0.394	4.0
RR*	0.538	2.9	0.560	3.0	0.569	3.1	0.378	2.4	0.621	2.3	0.649	2.4	0.664	2.3	0.383	2.2
MT-4	0.530		0.552		0.562		0.370		0.607		0.635		0.651		0.378	
S.D.	0.049	4.3	0.046	3.7	0.045	3.5	0.063	5.6	0.026	2.6	0.023	2.0	0.021	1.8	0.045	3.8
	Females with two records (N=1052)								Males with 1–10 progeny (N=2753)							
RR×2	0.607	5.3	0.634	6.1	0.650	6.3	0.403	5.6	0.244	6.4	0.259	6.9	0.268	7.6	0.171	5.8
RR×1.5	0.602	4.8	0.627	5.6	0.639	5.6	0.394	4.8	0.238	5.8	0.251	6.2	0.259	6.6	0.170	5.2
RR*	0.590	3.0	0.610	3.1	0.619	3.2	0.383	2.5	0.237	4.2	0.249	4.7	0.254	5.0	0.165	2.9
MT-4	0.577		0.596		0.606		0.377		0.227		0.239		0.245		0.162	
S.D.	0.036	3.7	0.034	2.9	0.032	2.6	0.053	4.7	0.029	4.9	0.027	4.5	0.028	4.9	0.032	5.6
	Females with three records (N=1450)								Males with 11–20 progeny (N=153)							
RR×2	0.638	4.8	0.678	5.0	0.701	5.4	0.435	5.5	0.686	6.2	0.727	6.5	0.748	7.1	0.444	4.5
RR×1.5	0.633	4.2	0.671	4.8	0.690	5.1	0.427	4.9	0.693	5.8	0.731	6.3	0.749	6.6	0.439	4.5
RR*	0.624	2.7	0.660	3.0	0.672	2.8	0.414	2.6	0.684	5.4	0.719	6.0	0.732	6.5	0.427	1.9
MT-4	0.609		0.643		0.659		0.408		0.653		0.686		0.699		0.423	
S.D.	0.032	2.8	0.028	2.4	0.027	2.1	0.051	4.2	0.049	5.3	0.045	5.2	0.043	5.2	0.078	5.3
	Females with four records (N=3023)								Males with 21–50 progeny (N=139)							
RR×2	0.654	4.7	0.696	4.8	0.726	5.5	0.456	5.1	0.769	5.9	0.808	6.0	0.827	6.6	0.503	4.8
RR×1.5	0.653	3.8	0.692	3.8	0.718	4.4	0.450	4.0	0.765	6.1	0.802	6.2	0.820	6.9	0.496	4.1
RR*	0.645	2.2	0.682	2.1	0.701	2.0	0.438	2.1	0.755	4.9	0.792	5.3	0.804	6.2	0.485	2.5
MT-4	0.630		0.667		0.689		0.432		0.725		0.759		0.769		0.475	
S.D.	0.026	2.6	0.022	1.9	0.020	1.7	0.042	3.3	0.042	5.3	0.037	4.9	0.035	5.5	0.074	5.4
	Female with one to five offspring (N=8948)								Males with 60+ progeny (N=56)							
RR×2	0.398	5.0	0.426	5.3	0.444	6.0	0.329	5.8	0.862	3.6	0.895	3.1	0.911	3.1	0.670	4.8
RR×1.5	0.396	4.3	0.423	4.6	0.439	5.2	0.323	5.0	0.865	3.3	0.897	3.1	0.911	3.2	0.666	3.8
RR*	0.392	3.0	0.416	3.2	0.428	3.2	0.315	3.1	0.856	2.1	0.887	1.8	0.899	1.9	0.651	2.1
MT-4	0.380		0.404		0.417		0.307		0.838		0.871		0.885		0.641	
S.D.	0.022	2.7	0.021	2.2	0.020	2.0	0.026	2.7	0.041	2.8	0.032	2.3	0.029	2.2	0.083	4.5
	Female with six to ten offspring (N=534)															
RR×2	0.621	4.5	0.676	4.7	0.706	4.9	0.555	4.0								
RR×1.5	0.622	3.5	0.673	3.9	0.702	3.9	0.554	3.2								
RR*	0.615	2.1	0.661	2.3	0.684	2.0	0.545	1.8								
MT-4	0.603		0.648		0.674		0.537									
S.D.	0.040	3.4	0.035	2.5	0.033	2.2	0.048	3.0								

^a RR×2: data expanded by 100%. RR×1.5: data expanded by 50%. RR*: all data, and MT-4: multi-trait.^b Average correlation between true and estimated genetic value; means over 400 replicates.^c Increase in accuracy relative to MT analyses; in %.^d Empirical S.D., averaged over analyses.

considering data sets II and III expanded by 50% (RR \times 1.5) or 100% (RR \times 2).

As shown in Tables 6 and 7, doubling the number of records per animal could yield markedly increased accuracies of genetic evaluation due to RR analyses in field data. Increases possible are similar in absolute terms and higher in relative terms to those found for the experimental data with monthly weight recording. For data set III, for instance, proportional increases for breeding values for later weights range from 7.6 to 8.3% (RR \times 2 vs. MT-4), however, with large S.D. of 3.3–4.6%. Increasing the number of weights recorded by about 50% could give corresponding values of 4.6–5.9% for data set II, and 4.3–4.6% for data set III. Gains in accuracy appear to depend on the original data structure. Analyses RR-8 for data set I and RR \times 2 should be roughly comparable, but differences to MT-4 are larger for the field data sets. Encouragingly, increases in accuracy are largest for data set III that represents a typical field data set.

3.4. Accuracies for particular animals

Results above considered all animals in the analysis, including parents without records themselves. Benefits from a RR analyses for individual animals clearly depend on the amount of information available for each. Table 8 gives accuracies for selected categories of animals in data set II. With few widely used bulls, patterns for males and females were similar. Animals were grouped according to the number of records available in the MT analysis (MT-4). Hence, as expected, accuracies increased most for estimates of direct effects of animals with only one or two records initially, with relative increases of 5% or more for cows with single records when expanding the data by 50%. Conversely, accuracies for maternal genetic effects increased most for cows with few offspring, 0.014 or 6.9%, 0.019 or 6.0% and 0.019 or 5.5% for RR \times 2 compared with MT-4 for cows with one, two and three progeny, respectively (not shown). For bulls with many progeny, cumulative information on offspring of female sibs and progeny resulted in increases in accuracy for 200-day maternal effects of up to 0.031.

An important criterion in a livestock improvement programme is the accuracy of evaluation of young animals to be selected. Fig. 4 shows the average

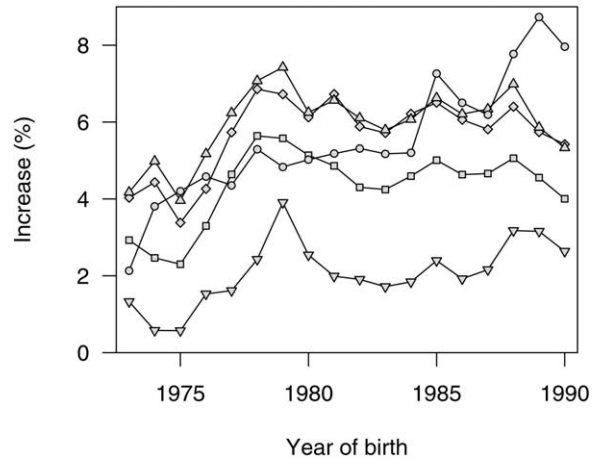


Fig. 4. Proportional increase (in %) in accuracy of genetic evaluation for data set I from a RR analysis using all data (RR*) over a MT analysis (MT-4) (▽: birth, □: 200-day, ◇: 400-day, △: 600-day, and ○: maternal 200-day weight).

proportional increase in accuracy from a RR analysis using all records over a MT analysis, according to animals' year of birth for data set I. Animals born in the last year only had records until weaning. Averages (\pm S.D.) for these animals, which were candidates for selection, were 2.6 ± 1.9 , 4.0 ± 3.0 , 5.4 ± 3.7 , 5.3 ± 3.5 and $8.0 \pm 15.5\%$ for breeding values for birth, 200, 400, 600 and 200 day maternal, respectively, i.e. comparable to averages for all animals for direct effects and somewhat higher, albeit with large S.D. across replicates, for maternal effects.

The average accuracy for animals in data set III for individual sexes and years of birth are shown in Fig. 5, again comparing RR \times 2 and MT-4. On the whole, there was little difference between males and females. Accuracies increased gradually with year of birth, reflecting the accumulation of records and information on progeny and parents, until an 'equilibrium' value was reached. For direct effects, this was about 1991. Mean accuracies then declined again for the youngest animals without progeny information and particularly for animals born in the last year (1999) and with few records for later weights. Notably, differences between RR \times 2 and MT-4 remained almost the same, close to 0.04 for direct effects for 200 and 600 day weight for the last 10 years of birth, i.e. with mean accuracies after 1988 being lowest for 1999, proportional increases were largest for animals in the last

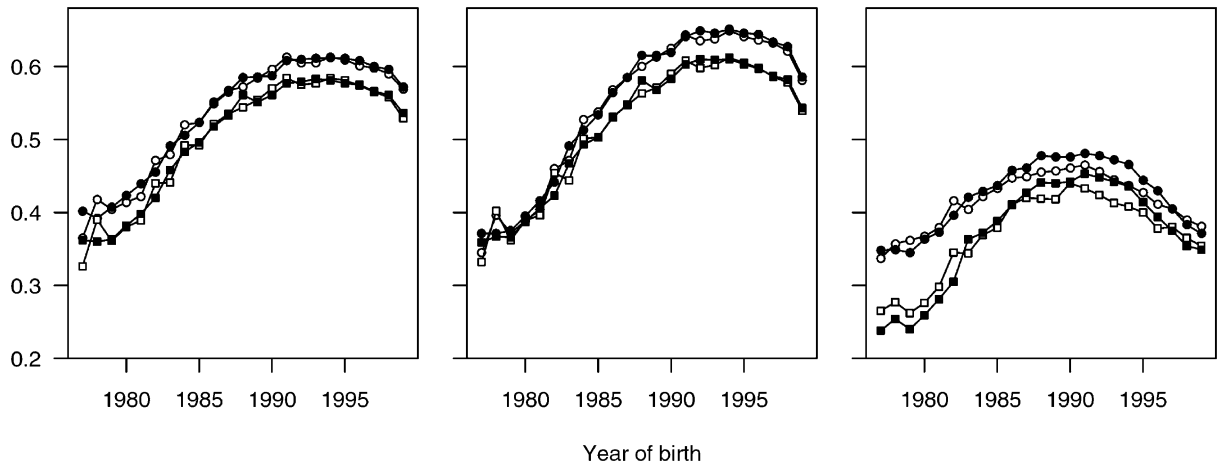


Fig. 5. Accuracy of genetic evaluation for 200-day weight (left), 600-day weight (middle) and 200-day maternal genetic effects (right) (circle: RR analyses using data expanded by 100% (RR \times 2), square, MT analysis (MT-4)) for animals in data set III, according to year of birth and sex (females: closed symbols, males: open symbols).

year of birth, representing candidates for selection. The pattern for 200-day maternal effects was somewhat different, due to the lag in time for availability of information for maternal genetic effects, and showed more fluctuations. Again though, differences in accuracy between analyses within sex remained reasonably constant for the last 10 years considered.

4. Discussion

Results show that there is substantial scope for a RR model to yield more accurate estimates of genetic merit for growth than the four trait, multivariate models. As with any simulation study, results are highly dependent on the assumptions made, both for the genetic parameters and variances, and the data and pedigree structure. The latter is clearly demonstrated by differences in results for the three data sets examined.

The RR model achieves somewhat higher accuracies than the MT model for currently available field data due to better modelling of variances and genetic parameters. Improvements shown represent an upper limit, as they rely on the assumption that the RR model describes the covariance structure in the data correctly. The full potential of the RR approach, however, can only be realised if additional, 'repeated' records are available. As results demonstrate, the effects of such additional information disseminates

to all animals in the analysis, though clearly are most beneficial to animals with least information available in a MT scenario.

If the number of weights recorded were to be doubled, for instance by weighing calves at marking and obtaining a 'repeated' record for weaning, yearling and final weights, accuracies of estimated breeding values for 200, 400 and 600 days in field data can be expected to increase by 6–8% across all animals, with a corresponding increase in response to selection based on these estimates. Even if the current data were only expanded by 50%, relative gains in accuracy across all animals of 4% or more could readily be achieved.

Other advantages of the RR model, in particular the fact that adjustments for age at recording are no longer required, have not been addressed in this study. This eliminates an important potential source of bias due to inadequate adjustment factors. Furthermore, BREEDPLAN includes mature cow weights as a fifth weight trait in addition to weights at the four target ages examined, considering repeated records per cow. Future work should extend the RR model to include such records, and examine the scope for estimating genetic growth curves for lifetime growth.

Computational requirements of the RR model are higher than those of the four-trait MT model, but, as reported by (Nobre et al., 2002), substantially lower than for an eight-trait multivariate analysis. The latter

encountered problems with accuracy and convergence when solving the mixed model equations in a RR analysis. No corresponding problems were noted in this study. For practical applications, computing resources needed could be reduced by fitting an equivalent model which does not estimate animals' permanent environmental effects explicitly, including them in the residual error instead while still modelling the within animal covariances via the corresponding covariance function (Meyer, 2001). Covariances matrices for RR coefficients often have one or more small eigenvalues. Hence, the number of effects to be estimated could be reduced through a reparameterisation which considers only the linear combinations of RR coefficients corresponding to non-negligible eigenvalues (Misztal et al., 2000). This is equivalent to estimating effects for the most important eigenfunctions only, and, typically, causes little loss of information. In addition, it may alleviate problems of poor convergence for the RR model (Nobre et al., 2002).

5. Conclusions

Accuracy of genetic evaluation for growth of beef cattle can be improved by replacing a four-trait model with a RR model. Benefits for the current data structure in commercial beef herds would arise mainly from more appropriate modelling of variances and genetic parameters and the elimination of age adjustments. However, if more records per animal were collected, considerable additional gains due to increased amounts of information utilised could be achieved.

Acknowledgements

This work was supported by grant BFGEN.002 of Meat and Livestock Australia Ltd (MLA).

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