

Use of Multitrait Evaluation Procedures to Improve Reliability of Early Prediction of Survival

T. DRUET,^{*,†} J. SÖLKNER,[‡] and N. GENGLER,^{*,†}

^{*}National Fund for Scientific Research, B-1000 Brussels, Belgium

[†]Animal Science Unit, Gembloux Agricultural University,
B-5030 Gembloux, Belgium

[‡]Department of Livestock Science,
University of Agriculture, A-1180 Vienna, Austria

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ABSTRACT

Multitrait, across-country evaluation procedures were adapted to improve reliability of survival breeding values by combining direct information with yield and functional traits: milk persistency, somatic cell count, fertility (male and female), and calving ease (direct and maternal). A set of bulls was selected from the Austrian Simmental population based on mean original reliabilities of at least 0.50 for yield traits or of at least 0.20 for functional traits. Only breeding values above these limits were retained. The breeding values were deregressed, assuming that they were obtained by single-trait, sire-maternal grandsire models. An expectation-maximization restricted maximum likelihood algorithm based on the multitrait, across-country evaluation equations was used to compute genetic correlations among all of these traits. These equations were solved, and the reliabilities of the solutions were estimated. Mean rank correlation between direct and combined breeding values was 0.85 with values as low as 0.67 for the group of youngest bulls. Direct (original), indirect, and combined reliabilities were compared to appreciate the impact of our procedures on improvement of reliability of survival breeding values. This improvement, dependent on the level of reliability of direct and indirect information, could be up to 0.24 for animals with low direct reliability and high indirect reliability. For young bulls born in 1992 without reliable direct survival information but with already reliable information on yield and functional traits, mean reliability improvement was 0.13. For all bulls this value was still 0.06.

(**Key words:** multitrait, across-country evaluation; survival; functional traits; genetic correlations)

Abbreviation key: **DYD** = daughter yield deviation; **MACE** = multitrait, across-country evaluation; **MAPE** = multitrait, a posteriori evaluation; **PEV** = prediction error variance.

INTRODUCTION

Many studies, as the one by Congleton and King (4), have shown that selection for longevity has a positive economic impact. The replacement costs are lower, fewer health problems are expected, and more cows are in high lactation ranks. But there are two major obstacles for selecting on such a trait: low heritability and late availability (e.g., 22). Many different methods to express longevity have been proposed: for example, herd life (e.g., 2, 3, 4), productive life (e.g., 25), and stayability (e.g., 2). A comparative study of these methods can be found in Vollema and Groen (27). Ducrocq (6) proposed survival analysis as a method that allows getting earlier information by the optimal use of censored (not yet finished) records. However, the breeding value of a bull when his daughters are at the end of first lactation is not very reliable, as the number of daughters that are actually culled is limited.

The multitrait, across-country evaluation (**MACE**) procedure was developed for international sire comparisons (19, 20). This multitrait model considers genetic evaluations in different countries for the same yield as different traits between which genetic correlations are not unity (19, 20). In this method, residual covariances are assumed to be zero (19) because different daughters produce in different countries. Weigel (29) pointed to the similarities in the use of information from correlated traits to improve the accuracy of prediction of breeding values for longevity (herd life) as suggested earlier (e.g., 3) and the international evaluation of dairy sires. Sire evaluation data of correlated traits from different sources are combined in an optimal manner. Weigel suggested, therefore, the use of the MACE to improve early prediction of productive life. Current MACE procedures can be used to combine information for different traits in the same country under the assumption that breeding values were obtained from different sets of daughters. This procedure is called multitrait, a posteriori genetic evaluation (**MAPE**), as MACE no longer applies to such an evaluation. The accuracy of the prediction will be higher because a multitrait model combines information from different traits. Also, like all multitrait models, MAPE can accommodate missing traits and can be used to predict breeding values for them. In this way, the use of MAPE could reduce some problems of the selection for herd life, productive life, or survival and could improve the accuracy of these early predictions by combining information available on other traits without requiring that all those traits are known. Jairath et al. (13) applied MACE procedures, called MAPE here, to improve genetic evaluation for herd life in Canada by using information on yield and conformation traits. The objective of this study was to use MAPE approaches to combine survival values with yield and functional traits in the Austrian (dual purpose) Simmental population. A second objective was to estimate needed (co)variance components also using MAPE.

MATERIALS AND METHODS

Data

The data used for this study were provided by the Zentrale Arbeitsgemeinschaft österreichischer

Rinderzüchter and consisted of the breeding values available in January 1998 for 564868 Austrian Simmental bulls. Ten traits were considered: milk, fat, and protein yields, survival, milk persistency, somatic cell count, fertility (male and female), and calving ease (maternal and direct). Models, heritabilities, and key references for the methods to compute the breeding values for these traits are given in [Table 1](#). All bulls born between 1985 and 1995 were selected if the mean of the official reliabilities for the yield traits was greater than or equal to 0.50 or if the mean of the official reliabilities for the functional traits was greater than or equal to 0.20. The male ancestors in the pedigrees of those 6918 bulls were also included in the estimates. A total of 9712 bulls was involved in this study. Breeding values for all bulls were only retained in the computations if their reliabilities were greater than or equal to 0.50 for the yield traits or at least 0.20 for functional traits. [Table 2](#) shows how many bulls with breeding values were kept for each trait and the number of animals who had values for two specific traits, permitting estimation of genetic correlations. This number varied from 1384 between survival and direct calving ease to 7291 between somatic cell count and milk persistency.

TABLE 1. Traits considered in this study and models used in Austria for genetic evaluation of these traits.

Trait	Trait definition and model	Used or assumed heritability	Reference
Milk, fat, and protein yields	Multiple lactation ¹ AM ²	Milk 0.29 Fat 0.30 Protein 0.28	Fuchs (8)
Survival	Cox regression AM corrected for relative milk production	0.10	Egger-Danner (7)
Milk persistency	AM for standard deviation on test day yields	0.15	Sölkner and Fuchs (23)
Somatic cell count	AM for test-day records (higher values more desirable)	0.14	Reents et al. (17)
NRR90 ³	AM for repeated records including male (service bull) and female (cow) effects	Male 0.02 Female 0.02	Thaller et al. (24)
Calving ease	AM for repeated records including direct and maternal effects	Direct 0.05 Maternal 0.05	Gierdziewics et al. (9)

¹ Three-lactation model in which first lactation yields were split into three traits: 1 to 100, 101 to 200, and 201 to 305 DIM.

² AM = animal model.

³ NRR90 = nonreturn rate at 90 d.

TABLE 2. Number of bulls with breeding values for each trait (diagonal) and for combination of two traits.

	Yields	Survival	Persistence	Somatic cell count ¹	NRR90 (s) ²	NRR90 (f) ³	Calving ease (d) ⁴	Calving ease (m) ⁵
Yields	6385	3713	6018	5951	3101	4567	2607	5000
Survival		3715	3417	3529	1778	2684	1384	2863
Persistence			7741	7291	3763	5710	3698	6301
Somatic cell count ¹				8012	4027	5891	3959	6516
NRR90 (s) ²					4579	3681	3613	4183
NRR90 (m) ³						6272	3781	6237
Calving ease (d) ⁴							4490	4211
Calving ease (m) ⁵								7026

¹ For this trait greater values were desirable.

² NRR90 (s) = male (service bull) component of nonreturn rate at 90 d.

³ NRR90 (f) = female (cow) component of nonreturn rate at 90 d.

⁴ Calving ease (d) = direct component of calving ease score.

⁵ Calving ease (m) = maternal component of calving ease score.

Table 3 describes the means of our sample for each of these traits. For the functional traits, the breeding values were standardized to a mean of 100 and 12 points representing a genetic standard deviation. For all functional traits higher values were more desirable. For young bulls, information for all traits was not available, so some of these bulls had information for only a few traits. Male fertility and direct calving ease are available when a bull is used for the first time, whereas performances for female fertility and maternal calving ease are available when the first daughters of these bulls are inseminated or calving. Fertility traits are obtained 9 mo earlier than calving ease traits. Yield traits are only available after the first 100 d of lactation. Data for fertility and calving ease were only available after 1992, so old bulls did not necessarily have performances for these traits.

TABLE 3. Descriptive statistics of official evaluations included milk yield traits expressed as estimated breeding values on an absolute scale (in kilograms) and functional traits expressed as

standardized breeding values with a mean of 100 and a genetic standard deviation represented by 12 points.

Trait	Number of animals	Mean	SD	Minimum	Maximum
Milk yield	6385	-22.8	271.6	-961	1523
Fat yield	6385	-2.5	12.4	-48	63
Protein yield	6385	-1.5	7.5	-31	35
Survival	3715	99.4	8.2	63	131
Milk persistency	7741	99.5	8.4	61	127
Somatic cell count ¹	8012	99.5	7.5	57	130
NRR90 (s) ²	4579	99.2	8.1	45	153
NRR90 (f) ³	6272	100.0	6.4	74	122
Calving ease (d) ⁴	4490	99.7	7.5	24	154
Calving ease (m) ⁵	7026	100.6	7.1	55	138

¹ For this trait greater values were desirable.

² NRR90 (s) = male (service bull) component of nonreturn rate at 90 d.

³ NRR90 (f) = female (cow) component of nonreturn rate at 90 d.

⁴ Calving ease (d) = direct component of calving ease score.

⁵ Calving ease (m) = maternal component of calving ease score.

Methods

The MACE programs were provided by B. Klei (Holstein Association of America, Brattleboro, VT) and G. Banos (Interbull Center, Uppsala, Sweden). These programs deregressed the breeding values and computed genetic correlations between all of the traits and the solutions of the MAPE model. The MAPE models require daughter yield deviations (**DYD**) of the bulls. If these are not available, breeding values may be deregressed to get similar information ([1](#)). For this study, four steps were necessary:

- estimation of daughter equivalents,
- deregression of sire breeding values,
- estimation of sire variances and genetic correlations with an expectation-maximization

- REML procedure, and
- evaluation of new breeding values and their reliabilities by a multitrait analysis.

Numbers of daughters were not available; therefore, the concept of daughter equivalents was used (26) and included information from relatives as suggested by Schaeffer (19):

$$DE = REL(1 - REL)^{-1} (4 - h^2)/h^2 \quad [1]$$

where DE = daughter equivalent, REL = original reliability (defined between 0 and 1), and h^2 = heritability. The correct weighting of DYD or deregressed breeding values should be proportional to the inverse of their relative residual variances; the values obtained by [1] were obviously only approximate, as was the number of daughters used by the International Bull Evaluation Service (INTERBULL, Uppsala, Sweden).

The deregression was realized by an iterative process accounting for the mean and including phantom parent groups as described by Jairath et al. (13), assuming that the breeding values were obtained by single-trait, sire-maternal grandsire models. The aim of using deregression was to regenerate the right-hand side of the mixed model equations. These regenerated values with the fixed effects absorbed and adjusted for the mean were a measurement of the DYD (15) or the corrected mean deviation of a daughter group. Each trait was deregressed separately. Rogers et al. (18) reported some problems with the deregression process for traits with low heritability. To check efficiency of deregression and evaluation procedures, breeding values were first deregressed and then new solutions were estimated with no genetic correlations among traits. This procedure was done without limits on reliability for all selected bulls. Correlations between original breeding values and new solutions were not unity as expected but were even less than 0.90. With a restriction on reliabilities of the breeding values, this problem could be limited. Therefore the only breeding values that were kept were greater than or equal to 0.50 for yield and 0.20 for functional traits.

Once all of the breeding values were deregressed, MAPE procedures were applied. Deregressed values from all of the traits were combined, and the expectation-maximization REML algorithm described by Sigurdsson and Banos (21) was used to estimate the genetic correlations between all traits.

The classic MACE model by Sigurdsson and Banos (21) was used:

$$\mathbf{y} = \mathbf{Xc} + \mathbf{ZQg} + \mathbf{Zs} + \mathbf{e} \quad [2]$$

where \mathbf{y} = vector of deregressed breeding values, \mathbf{c} = vector of fixed effects for each trait (mean), \mathbf{g} = vector of genetic group effects, \mathbf{s} = vector of random bull effects, \mathbf{X} = incidence matrix linking \mathbf{y} and \mathbf{c} , \mathbf{Z} = incidence matrix linking \mathbf{y} and \mathbf{s} , \mathbf{Q} = matrix assigning bulls to phantom parent groups, and \mathbf{e} = vector of random residuals.

Mixed model equations associated with model [2] were

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{0} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{0} & \mathbf{Q}'\mathbf{A}^{-1}\mathbf{Q} \otimes \mathbf{G}^{-1} & -\mathbf{Q}'\mathbf{A}^{-1} \otimes \mathbf{G}^{-1} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & -\mathbf{A}^{-1}\mathbf{Q} \otimes \mathbf{G}^{-1} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{A}^{-1} \otimes \mathbf{G}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{c}} \\ \hat{\mathbf{g}} \\ \hat{\mathbf{g}} + \hat{\mathbf{s}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{0} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix} \quad [3]$$

where \mathbf{R} = diagonal matrix of residual variances, \mathbf{A} = additive relationship matrix among bulls, \mathbf{G} = matrix of genetic variance-covariances among traits, and \otimes = Kronecker operator. The \mathbf{R} diagonal was only an approximation, but Jairath et al. (13) deducted from selection index results that impact of this assumption should be relatively low for traits with low to moderate residual correlation. This was obviously not true for all of the traits involved in our study, so the results should be interpreted carefully.

Approximately 3500 animals and 6 traits could be used at the same time to estimate variance components. Four samples were drawn from the 6918 bulls born between 1985 and 1995. The bulls were sorted by identification number, and one bull of four was chosen. Afterward, the male ancestors of the bulls in the pedigrees were added to every sample. The size of the samples were between 3358 and 3415 bulls.

Four groups of traits were created: milk, fat, and protein yields; survival, milk persistency, and somatic cell count; male or direct components of fertility and calving ease; female or maternal components of the same traits. All of these groups were combined two by two resulting in six runs per sample for a total of 24. For a sample, the genetic correlations matrix of the 10 traits was built by calculating the mean correlations from the six runs among all the traits. These correlation matrices were positive definite. The results for the four samples were then averaged. Empirical standard errors were computed as observed standard deviation among the four samples. At the end, the mean variances obtained by a similar procedure were used to compute the variance-covariance matrix necessary for the computation of the MAPE solutions.

The MAPE equations were solved by an iterative Gauss-Seidel approach as described by Klei (14). After convergence, new variances-covariances were estimated, keeping the heritabilities and genetic correlations constant.

To approximate multitrait reliabilities the following method was used. Equation [1] can be rewritten for all of the traits as

$$\mathbf{D} = \mathbf{C}_{st} (\mathbf{I} - \mathbf{C}_{st})^{-1} \text{diag}\{\mathbf{G}\}^{-1} \mathbf{R} \quad [4]$$

where \mathbf{D} = diagonal matrix of daughters equivalents, \mathbf{C}_{st} = diagonal matrix of single-trait reliabilities, $\text{diag}\{\mathbf{G}\}$ = matrix of diagonal elements of the genetic (co)variance matrix of sire effects, and \mathbf{R} = diagonal matrix of residual variances. Multitrait reliabilities could then be approximated by estimating a matrix \mathbf{P} of multitrait prediction error variances (PEV) (10). For a given animal, PEV was

$$\mathbf{P} = \text{diag} \{(\mathbf{D}\mathbf{R}^{-1} + \mathbf{G}^{-1})^{-1}\} = \text{diag} \{(\mathbf{C}_{st}(\mathbf{I} - \mathbf{C}_{st})^{-1} \text{diag}\{\mathbf{G}\}^{-1} + \mathbf{G}^{-1})^{-1}\} \quad [5]$$

Multitrait reliabilities were then approximated as

$$\mathbf{C}_{mt} = \mathbf{I} - \mathbf{P} (\text{diag} \{\mathbf{G}\}^{-1}) \quad [6]$$

after substitution of [Equation \[5\]](#) into [Equation \[6\]](#)

$$\mathbf{C}_{mt} = \mathbf{I} - \text{diag} \{(\mathbf{C}_{st} (\mathbf{I} - \mathbf{C}_{st})^{-1} \text{diag} \{\mathbf{G}\}^{-1} + \mathbf{G}^{-1})^{-1}\} \text{diag} \{\mathbf{G}\}^{-1} \quad [7]$$

where \mathbf{C}_{mt} = diagonal matrix of multitrait reliabilities.

[Equation \[7\]](#) considered animals unrelated, which was not necessarily a bad approximation, as parent and progeny information were already contained in \mathbf{C}_{st} .

Two types of multitrait reliabilities were obtained: indirect, considering only the contributions from correlated traits, and combined, considering both direct and indirect contributions.

RESULTS AND DISCUSSION

Genetic Correlations

Correlations among the 10 traits are presented in [Table 4](#) with empirical standard errors estimated as the standard deviations of the four subsamples. Empirical standard errors were in general low with values close to 0.01 or even lower, except for some correlations involving functional traits with low heritabilities in which the empirical standard errors were up to 0.06.

Correlations among yield traits were all high, as expected (0.78 and above); the highest were between milk and protein. Correlations among functional traits were in general rather low. Relationships between yield traits and functional traits also were rather low. Two functional traits had stronger relationships with other traits, female component of fertility and persistency. The first trait had a negative correlation with milk, fat, and protein yields. In other studies the negative relationship with milk yield is stronger for high-producing breeds like Holstein or Red Holstein ([5](#), [11](#)). For example, Hoekstra et al. ([12](#)) found a value of -0.24 for Holsteins. However Hodel ([11](#)) estimated correlations from 0.08 to -0.25 for Simmental so that our value of -0.22 was not far from what might have been expected for Simmental. Male and female fertility traits showed a moderate antagonistic relationship (-0.16), indicating that the progeny of a fertile bull should be more difficult to get pregnant. This surprising result remains difficult to explain. A potential reason could be the vague definition of male fertility as raw male contribution to cow insemination results (uncorrected for sperm conditioning or straw batch differences). Milk persistency showed low to moderate correlations to other traits. Strongest correlations for persistency were between 0.12 and 0.17 for female component of fertility, maternal calving ease, and somatic cell count, stressing the importance of persistency on general health of the cows. A small, positive correlation between persistency and direct calving ease (0.14) was also noticed. This relation was rather difficult to explain, suggesting that when a cow is born from a difficult calving, it can have an impact later on her general health and affect her persistency. Druet ([5](#))

found that this relationship was not consistent across breeds.

The most interesting correlations were among functional survival and the other traits. Correlations with yield traits were small but still between 0.10 and 0.20. Theoretically these values should have been close to zero, as functional survival is (phenotypically) corrected for yields on a within herd basis. Correlations with milk persistency, female fertility, and maternal calving ease traits were all above 0.20, which was a very consistent pattern across samples. This finding showed that these traits can be valuable indicator traits for survival. The most correlated trait seemed to be maternal fertility with a value over 0.30. Miesenberger et al. (16) stressed already that in the Simmental breed, more cows are culled for fertility disorders than for low milk yield. Also interesting was the correlation of 0.23 with milk persistency, as better persistency means lower metabolic load, therefore less stress during lactation. Correlations with calving ease traits were as expected, as difficult calvings lowered the chances of survival. A recent study (5) using less reliable samples with fewer bulls for Austrian breeds, notably Holstein and Brown Swiss, showed that correlations between functional survival and maternal fertility, milk persistency, and somatic cell count ranged from 0.09 to 0.49 and that correlations between survival and milk yield traits were variable. This trend had already been noticed by Ducrocq (6) and Vollema and Groen (28), who found nearly null correlations for Brown Swiss and negative ones for Holstein (the phenotypic adjustment for yields were done in the same way in the Simmental breed). Somatic cell count had a positive relationship with functional survival with the strongest correlation being in Holsteins. This finding has been confirmed by Rogers et al. (18), who estimated correlations of 0.06 and 0.30 between somatic cell count and herd life, and by Jairath et al. (13), who estimated a correlation of 0.17 among the same traits.

As residual covariances were forced to be zero, estimates of genetic covariances could have been biased. Fortunately, comparisons of the genetic correlations with results in the literature showed no great differences. But traits measured for the same cows share a common environment and have an impact on each other. For instance, female performances for fertility and calving ease are taken into account by the farmer in his culling decisions. When this phenotypic relationship between these traits and functional survival is not included in the model, estimated genetic correlations will be influenced. The same can be concluded for female fertility and maternal calving, as a difficult calving can result in fertility problems. The assumption that residual covariances are zero can also explain variability of correlations for yield traits (5). Genetic correlations between milk yield and functional survival were lower or even negative when cows were phenotypically producing more. More environmental stress existed for these cows because of the yield level of the cow. This difference of results could also be interpreted as breed differences or perhaps as a problem of efficiency in the phenotypic adjustment for culling decisions related to yields.

TABLE 4. Genetic correlations (empirical SE below) among yield and functional traits in Austrian Simmental cattle.

Fat	Protein	Survival	Persistency	Somatic cell count ¹	NRR90 (s) ²	NRR90 (f) ³	Calving ease (d) 4	Calving ease (m) 5
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Milk	0.78 0.00	0.91 0.00	0.11 0.02	0.06 0.02	-0.07 0.03	- 0.07 0.04	- 0.22 0.03	- 0.03 0.07	-0.02 0.02
Fat		0.83 0.00	0.14 0.03	0.08 0.02	-0.01 0.01	- 0.03 0.06	- 0.16 0.04	- 0.08 0.06	0.01 0.05
Protein			0.14 0.03	0.11 0.02	-0.04 0.02	- 0.06 0.05	- 0.18 0.04	- 0.05 0.06	0.00 0.01
Survival				0.23 0.03	0.11 0.02	- 0.08 0.05	- 0.34 0.02	0.21 0.01	0.22 0.03
Persistency					0.17 0.01	0.05 0.04	0.13 0.05	0.14 0.03	0.12 0.03
Somatic cell count ¹							- 0.01 0.02 0.05	0.05 0.02	-0.01 0.03
NRR90 (s) ²								- 0.11 0.16 0.02	-0.01 0.01
NRR90 (f) ³								0.00 0.04	0.19 0.03
Calving ease (d) ⁴									-0.05 0.03

¹ For this trait greater values were desirable.

² NRR90 (s) = male (service bull) component of nonreturn rate at 90 d.

³ NRR90 (f) = female (cow) component of nonreturn rate at 90 d.

⁴ Calving ease (d) = direct component of calving ease score.

⁵ Calving ease (m) = maternal component of calving ease score.

Prediction of Survival

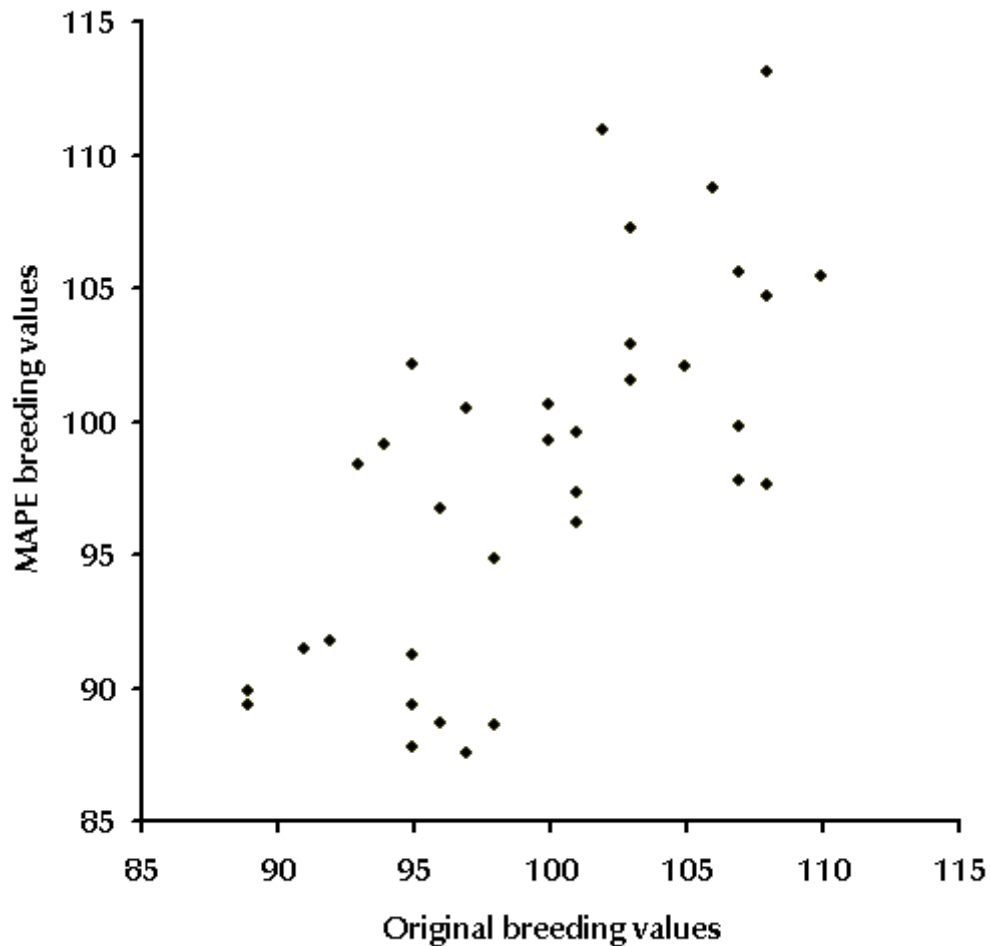


Figure 1. Comparison of estimated breeding values for survival from multitrait, a posteriori evaluation (MAPE) and original breeding values for bulls born in 1992.

Rank correlations between direct and combined (MAPE) estimated breeding values for survival are in [Table 5](#). Mean correlation between official breeding values and the new estimates using MAPE were 0.85. This result was close to that obtained by Jairath et al. (13), who estimated a correlation of 0.80 between direct herd life and combined herd life including type information. The rank correlations showed a greater influence of MAPE procedures on the ranking for young bulls. Rank correlation was 0.88 for bulls born in 1987 and was only 0.67 for bulls born in 1992. For these last bulls, [Figure 1](#) shows the official breeding values and the estimated breeding values (MAPE solutions). These 34 bulls were clearly reordered and, therefore, using MAPE solutions would have had some influence on selection decisions.

TABLE 5. Rank correlations between direct and combined breeding values by birth year, and direct, indirect, and combined reliabilities by birth year.

Year of birth	Number of bulls	Rank correlation	Reliability		
			Direct	Indirect	Combined
before 1985	1552	0.868	0.64	0.33	0.68
1985	458	0.839	0.42	0.23	0.49
1986	370	0.838	0.40	0.21	0.47
1987	385	0.877	0.39	0.21	0.46
1988	313	0.863	0.38	0.22	0.46
1989	276	0.813	0.38	0.22	0.46
1990	210	0.701	0.38	0.24	0.47
1991	117	0.696	0.38	0.26	0.49
1992	34	0.674	0.26	0.23	0.39
All bulls	3715	0.854	0.50	0.27	0.56

Direct, Indirect, and Combined Reliabilities

Reliabilities from different models are given in [Table 5](#). Direct reliabilities were those reported officially; combined reliabilities were computed using [Equation \[7\]](#). Indirect reliabilities, combining all indirect information, were also computed using [Equation \[7\]](#) but assumed a direct contribution of zero for survival. When computing these new multitrait reliabilities, a bias was introduced by assuming that residual covariances were equal to zero so that the gain could be overestimated. To compare young and older bulls, results were given by birth year. Results confirmed the expectations that reliability improvements were rather important for younger animals. For bulls born in 1992, estimated breeding values were very inaccurate, basically parent averages, but indirect reliability was nearly as high as direct; therefore, combined reliability was 0.13 reliability points (or 50 %) greater than direct reliability.

[Table 6](#) shows the improvement of reliabilities as a function of direct and indirect achieved reliabilities. The most affected animals were those for which direct reliability values were low and indirect information was high. The improvement could be up to 0.24 reliability points or nearly 100 % for such animals. For all the animals, mean gain of reliability was 0.06 which represents still 12% of their original mean reliability.

TABLE 6. Reliability improvement (difference between combined and direct) through the multitrait, a posteriori evaluation for direct and indirect reliability classes (in parentheses are the number of bulls for each class).

Direct reliability	Indirect reliability					
	0.07 - 0.15	0.16 - 0.19	0.20 - 0.23	0.24 - 0.32	0.33 - 0.43	0.44 - 0.74

0.20 - 0.29	0.08 (428)	0.11 (382)	0.13 (65)	0.16 (14)	0.24 (2)	
0.30 - 0.39	0.06 (83)	0.08 (183)	0.09 (95)	0.12 (18)	0.17 (4)	
0.40 - 0.49	0.04 (11)	0.06 (62)	0.08 (116)	0.09 (93)	0.12 (12)	0.18 (2)
0.50 - 0.59	0.04 (1)	0.05 (13)	0.05 (57)	0.07 (149)	0.09 (31)	0.16 (3)
0.60 - 0.69			0.04 (1)	0.04 (85)	0.06 (86)	0.10 (7)
0.70 - 0.79				0.03 (3)	0.04 (46)	0.06 (29)
0.80 - 0.89						0.03 (37)
0.90 - 0.99						0.01 (26)

CONCLUSIONS

The MAPE procedures offered the possibility to improve early prediction of survival breeding values by using information on correlated traits. Some functional traits were indicated to improve accuracy of survival values. The most important traits in this study were female fertility, milk persistency, somatic cell count, and calving ease traits. Yield traits also had to be included in such a model. However, current MAPE procedures are only approximate assuming that nongenetic correlations among DYD or deregressed breeding values are zero. Future MAPE procedures need to include residual covariances, which can be done by approximating covariance among DYD based on daughters in common across evaluations for different traits. Also deregression procedures showed some limits for traits with poor heritability and animals with poor reliabilities. A possible improvement would be to avoid deregression by using DYD rather than deregressed breeding values.

The impact of genetic correlations on indirect and combined reliability must be considered. As these correlations become greater, the influence of the correlated traits will increase. Unfortunately, correlations are only estimations, and we need to acknowledge that different correlations might change results. If correlations that are too high are chosen, the influence of other traits will be overestimated, leading to some bias. If genetic correlations are underestimated, some information on correlated traits will be lost. Therefore, results from the estimation of covariances must be considered carefully with special attention to methods, number of animals, and sampling errors. There are indications that correlations have to be estimated for each breed in each country and at a particular moment. Especially with current MAPE procedures for which residual covariances are assumed to be zero, estimated genetic correlations have to be checked carefully. Despite these points, our results showed that if the genetic correlations were estimated precisely, the use of MAPE could be useful to improve early prediction of sire survival breeding values.

The proposed MAPE method is, as MACE, only able to improve early prediction of survival breeding values for bulls. Essentially two possibilities exist to extend the improved evaluation to cows. First, if survival breeding values are computed for cows, both the deregression step and the MAPE step could be modified to include all animals, not only sires. If breeding values are not known for cows, cow breeding values could be approximated as half of the MAPE breeding value of her sire plus a quarter of the MAPE breeding value of her maternal grandsire.

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