

INTERBULL MEETING, NEUSTIFT, AUSTRIA, JUNE 7-8, 1992

Session I: Experiences from applications of Animal Models
in dairy cattle evaluations

The effect of cows with performance records but
unknown sire identification in an Animal Model

J. Claus, J. Jaitner, F. Reinhardt

1. Introduction

Under field conditions no milk recording scheme will
provide for all cows milked sire identification.

In Germany the proportion of such cows varies from 10 to
30 % depending on regional differences in the interest of
farmers for breeding.

Most Animal Models are solved by iterating on data. This
procedure gives a relation between computer resources
needed and number of animal in the data set.

As milk recorded cows without sire identification are not
relevant for breeding programs, exclusion of such cows
from genetic evaluations could be of benefit to
organizations which have to pay for evaluations.

The paper analyzes the effects of exclusion of milk
recorded cows without sire identification from milk trait
evaluation.

2. Model / Data sets

The German Multitrait Individual Animal Model (MIAM)
with traits defined as (part)lactation

- (1) 1st lactation, 1 - 100 days
- (2) 101 - 200 days
- (3) 201 - 305 days
- (4) 2nd lactation, 305 days
- (5) 3rd lactation, 305 days

has been used on two data sets

- i complete data sets with all cows milk recorded
for at least 45 days in the 1st lactation
- ii reduced data set with restriction

Cows with milk records must have

- a sire identification
- or
- descendants with sire identification

The restriction gave a reduction of 14,4 % animals
leading to a higher proportion of fully identified animals
in the reduced data set (Tabele 1).

Table 1: Pedigree completeness in the parental generation

		Data set	
		complete	reduced
Animals		105.792	90.605
Sire + dam	ident.	72,1 %	78,0 %
only sire	ident.	14,4 %	14,6 %
only dam	ident.	5,2 %	2,3 %
sire + dam not ident.		8,3 %	5,0 %

The loss of trait record in the reduced data set is highest in the beginning of 1st lactation (14 %) and lowest in the 3rd lactation (Table 2).

Table 2: No of cows with milk records

Records up to trait	Data set		
	complete	reduced	(%)
1st la, 1-100	9.014	7.797	-14
101-200	4.446	3.016	-12
201-305	21.725	19.281	-11
2nd la, 305	14.748	13.361	- 9
3rd la, 305	25.239	23.246	- 8

3. Results

3.1 Phenotypic yields

The reduced data set gives very similar phenotypic means and standard deviations compared to the complete data set (Table 3).

This means that missing sire identification of milk recorded cows is not connected to low management for milk or any other systematic reason.

Table 3: Phenotypic means and standard deviation
(Fat-kg)

Trait in the evaluation	Data set			
	complete		reduced	
	$\bar{x}$	s	$\bar{x}$	s
1st la, 1-100	80	16,7	81	16,6
101-200	70	14,3	71	14,2
201-305	68	18,4	68	18,4
2nd la, 305	265	52,3	266	52,1
3rd la, 305	285	55,4	286	55,3

3.2 Convergence

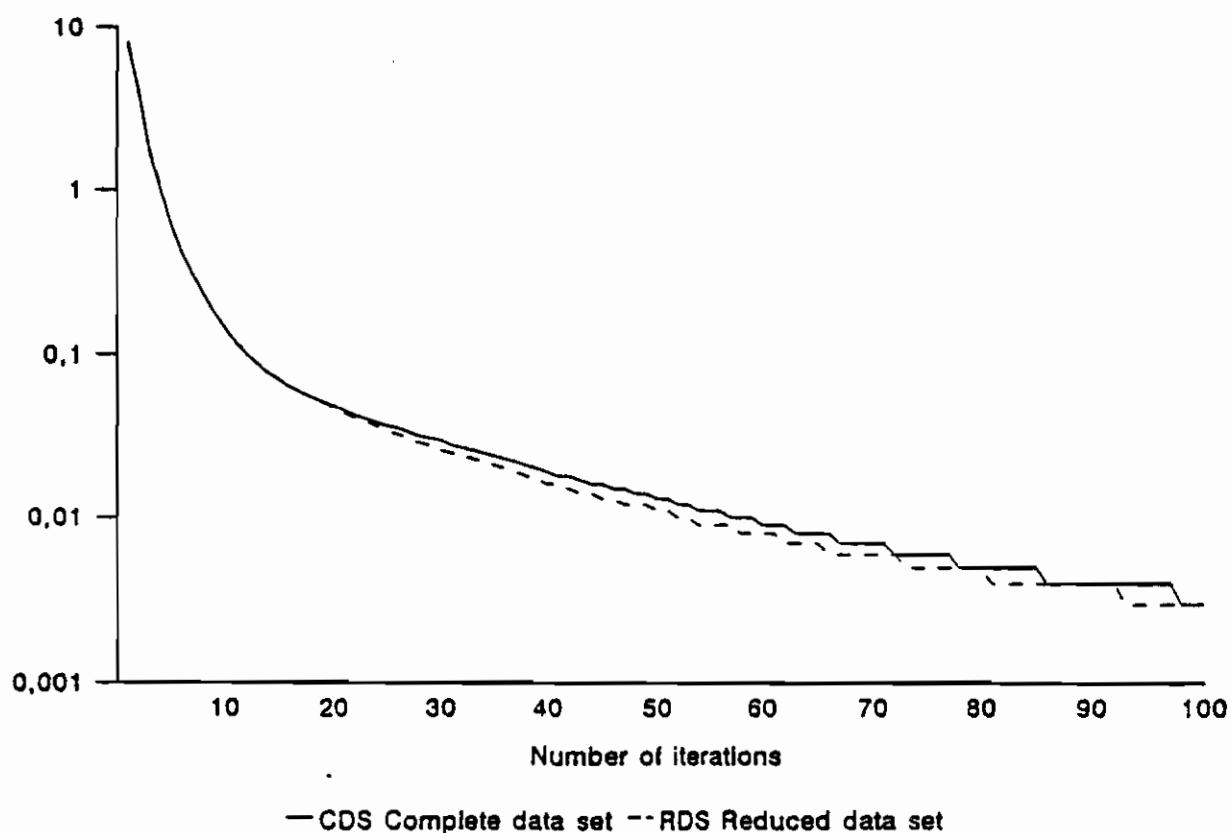
100 rounds of iteration were used on both data sets.

Convergence was defined as mean absolute change from round to round for the HYS effect, group effect and genetic animal effect.

A slower convergence could be expected at the reduced data set for the group effect, because in this case only few milk record informations are available to get group solutions.

However, only small differences in favour to the reduced data set could be found in the convergence. Combining all criteria, until rounds 10 to 15 convergence was essentially same at both data sets (Figure 1).

Figure 1: Trend in convergence at two data sets
(Fat_kg)



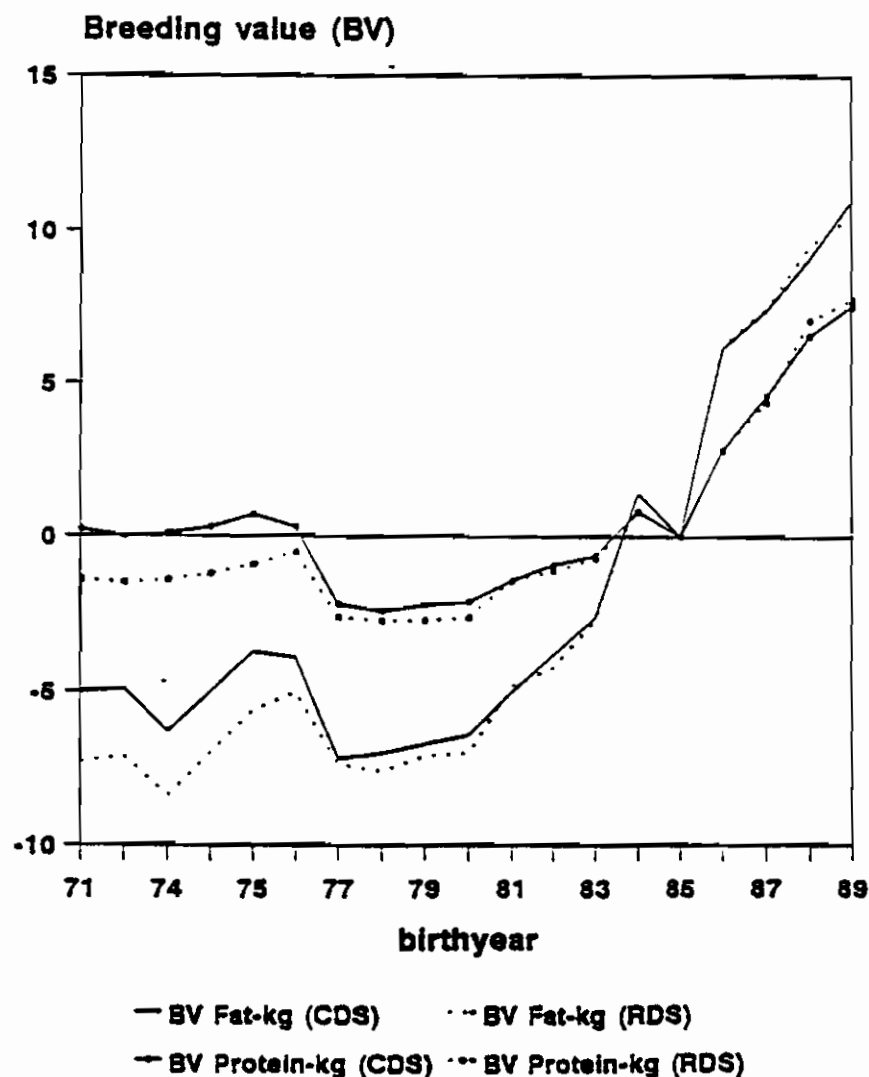
.N Verden 1992

3.3 Trend of breeding values

As long as breeding values are based - apart from relationship - on yields (records since 1979), trends in all kg_traits are in both sexes very similar (Figures 2 and 3).

Iteration was stopped after 100 rounds. It could be that both trends would even more adjust with further rounds of iteration.

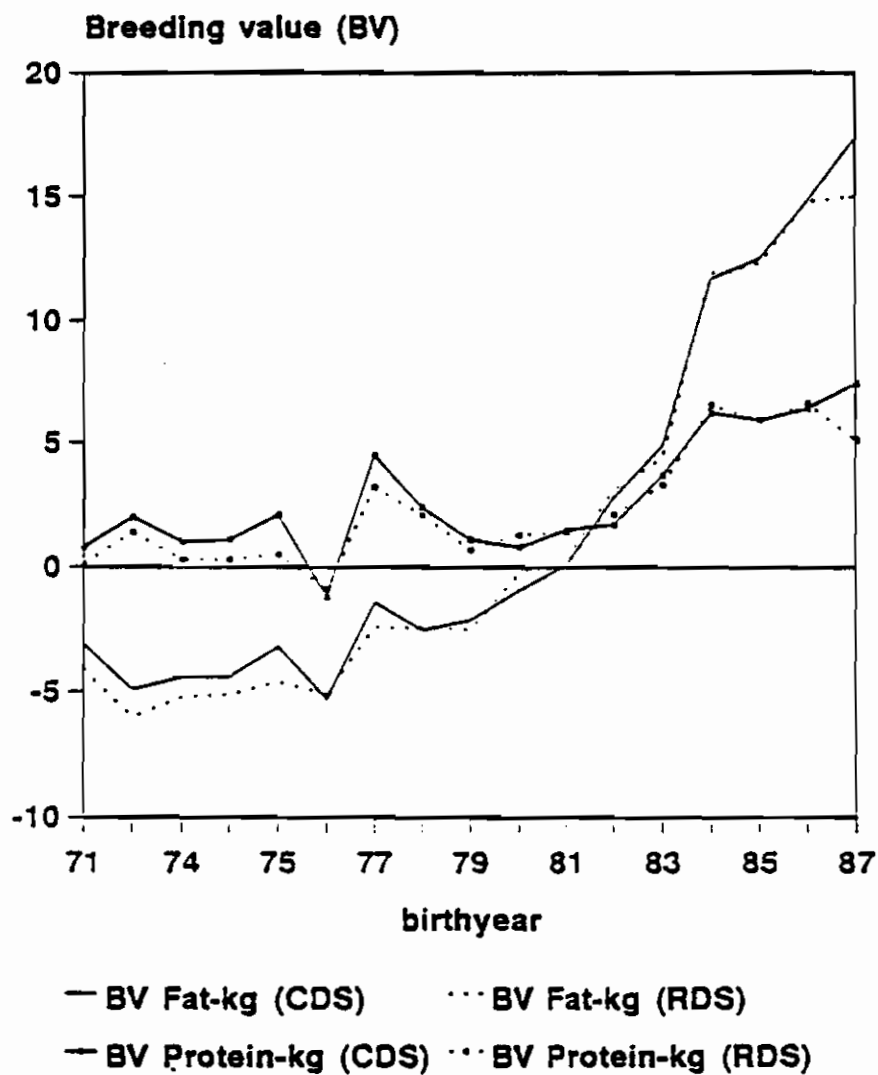
Figure 2: Trend of breeding values in cows derived from two data sets (Fat_ and Protein_Kg)



(cowbasis 1985)

RLN Yarden 1992

Figure 3: Trend of breeding values in bulls derived from two data sets (Fat_ and Protein_Kg)

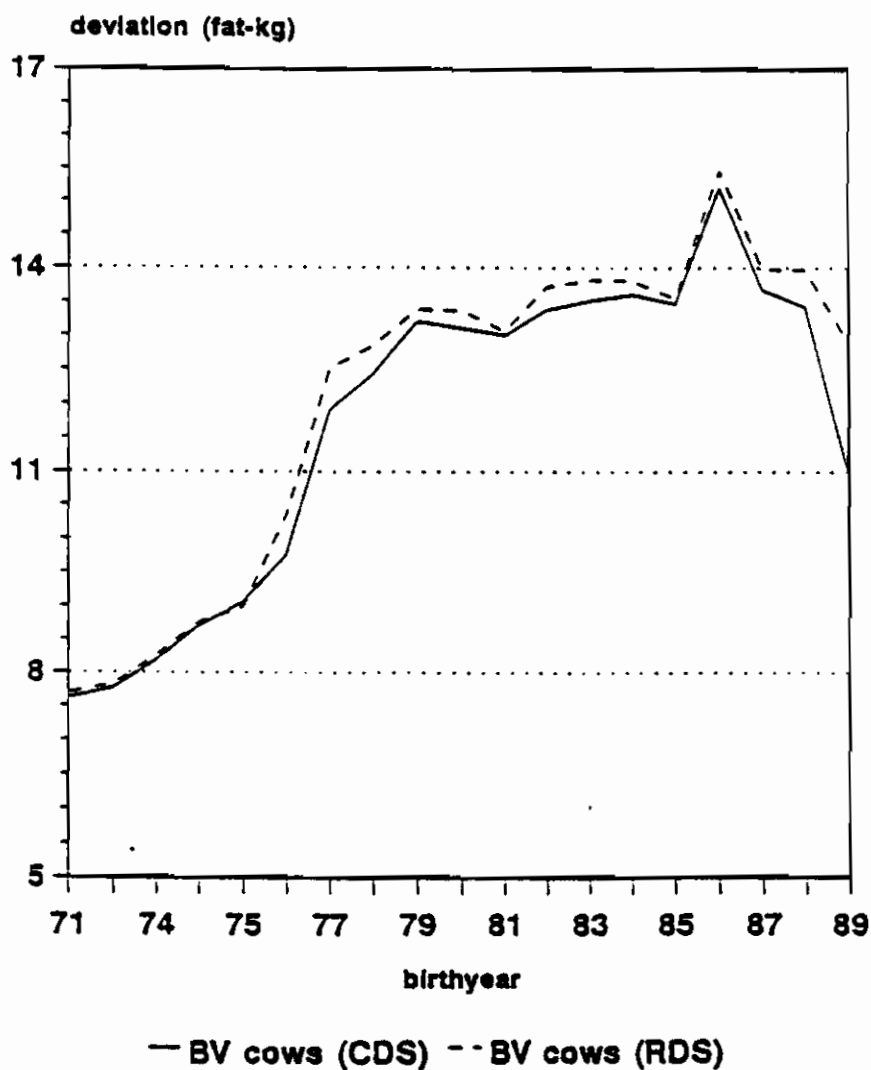


(cowbasis 1985)

RLN Verden 1992

Breeding values estimated from the reduced data set gave a slightly higher variance in all kg_traits. Differences to the results from the complete data set are of no practical order. Figure 4 shows the trend of standard deviation of fat-Kg. for cows as an example.

Figure 4: Trend of standard deviation of breeding values of cows derived from two data sets (Fat_ kg)



(cowbasis 1985)
RLN Verden 1992

3.4 Computer resources

The MIAM package has been run on a HITACHI DATA SYSTEMS EX 50 (22 MIPS / 128 MB main storage)

The whole equation could be kept in memory during iteration.

100 rounds of iteration needed on the complete data set 596 seconds and 521 seconds on the reduced data set.

Saved CPU time (-13,6 %) was as expected linear to the reduction of animals in the data sets.

4. Discussion

The inclusion of milk recorded cows without parental information in a genetic evaluation system could be justified, if

i such animals are needed to get better solutions for environmental effects within the model

or

ii such animals have any effect on estimated breeding values of animals relevant to selection schemes

In the study presented no effects of practical meaning on the results of the active breeding population could be found.

One reason could be the definition of the HYS effect in the model used. Small average herd size (app. 5 heifers / herd / year) made it necessary to define herd classes. The average no. of yield observations ranged from 72 (first trait in the model) to 33 (3rd lactation) in the complete data set. Corresponding figures were 66 and 31 res. in the reduced data set. In any case there were enough observations for stable estimates of the HYS.

Another reason could be the small proportion of cows (14 %) being eliminated by the restriction of milk recorded cows with sire identification. Similar results have been found however on a large data set with 6 mill. animals and with a higher proportion (25 %) of such cows.

5. Conclusion

If computer resources for genetic evaluations are limited and / or costs have to be considered, the rejection of milk recorded cows without sire identification seems to be justified.

This conclusion was derived from an Animal Model with herd classes and should be verified in other situations.