The Use of Test Day Models in Genetic Evaluation

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Abstract

Genetic evaluation with test day models seems to be of increasing importance. An attempt was made to characterize the main features of test day models although it is not possible to describe 'the' test day model because too many different approaches can be taken to make better use of test day information. Currently the two main applications of test day models for improvement of functional traits in cattle are for estimation of persistency proofs and for improvement of mastitis resistance through the indicator trait somatic cell counts. Computational aspects might hinder application to very large national datasets, especially when test day records in dairy records processing centres are stored only for a short period of time. However, application for Somatic Cell Score (SCS) evaluation on a large dataset from Germany showed that several years of test day data can be handled with modern computers using specifically designed programs. Using this example some features and problems for application to large datasets were discussed.

Introduction

Traits in genetic evaluation for dairy cattle may be differentiated into two groups. First production traits which are measured on a regular basis (e.g. every 4 weeks) from milk recording agencies. For use in genetic evaluation test day records (TD) are usually aggregated to a lactation measure like 305-day yield. Second traits which are measured only once in a lactation (or even once in the life) of a cow like type traits, calving performance, stayability, etc.. Non-production traits, or so-called 'secondary' traits do belong usually to the second group, however attempts have been made to exploit information from test day records, which are originally recorded for management purposes or genetic evaluation for production traits. An example is the calculation of persistency proofs from standard deviation of test day yields or ratios of production in late lactation to production in early lactation (Sölkner and Fuchs, 1987). Another example is the use of somatic cell counts as an indicator trait for selection against mastitis (Shook, 1989, Schutz, 1994, Philipsson et al., 1995).

Also evaluation for production itself, which is traditionally based on lactation measures like 305-day yield or parts thereof may be enhanced by the use of test day records instead of the aggregated information in a 305-day observation. There are several problems associated with the use of 305-day yields in genetic evaluation: Terminated lactations have to be extended to prevent bias due to selection for production in early lactation. Records in progress also have to be extended to allow for early evaluations of young animals to reduce generation interval. Different recording schemes lead to different number of test day records and therefore different amount of information included in a 305-day observation. Effects of the individual herd-test-day cannot be considered by the model of evaluation although numerous studies showed that there is a considerable amount of environmental influences on individual test day results which are not accounted for by common herd-year-season classification of most genetic evaluation systems. Attempts have been made in Australia (Jones and Goddard, 1990) to consider an herd-test-day effect prior to aggregation to a lactation measure. Visscher and Goddard (1995) showed that a large amount of environmental variation could be removed from the aggregated lactation yield through this procedure. However, other problems like need for extension of incomplete records and different amount of information included in a 305-day yield cannot be solved in an optimal manner by this procedure. Another restriction of 305-day yield is, that 'normal' length of lactation is fixed to an arbitrary value of 305-days. This might not be justified for all breeds and all production systems. Especially for high producing cows their 305-day yield might represent a different part of their biological lactation compared to low producing cows, that might dry off naturally at around or even before 305-days in milk.

Aim of the present study is to characterize some of the applications of test day models for genetic evaluation. Because of the nature of this workshop it is not intended to give a comprehensive overview but to tackle some of the properties and features of test day models, which have been studied for production traits in detail and may be transferred to secondary traits as well. For a comprehensive review on application of test day models to dairy production traits see Swalve (1995). In the context of use of test day models in evaluation of secondary traits currently two applications can be mentioned. First genetic evaluation for persistency, which will be discussed by Dekkers et al. (1996) at this workshop and second evaluation for somatic cell counts, which will be discussed in this paper.

Application of test day models to dairy production traits

In the broad sense all common genetic evaluation systems for production make use of test day information, because lactation measures are usually computed by more or less sophisticated methods from several test day observations of the particular lactation. A **test day model** might be defined as a statistical procedure, which considers environmental effects directly on a test day basis. Given this definition one has to differentiate first between models which consider test day observations directly in the statistical model and second procedures, which do some kind of correction on a test day basis and combine these corrected values to a lactation measure which is later used for genetic evaluation. One application for the latter can be found in work from Australia (Jones and Goddard, 1990). Individual test day yields are adjusted for age and stage of lactation and then expressed as a deviation from test day average of the herd. In a second step these test day deviations are combined to one lactation measure, called index of overall lactation performance. Visscher and Goddard (1995) showed, that this lactation measure might be a much more heritable measure than conventional lactation yield. Visscher and Goddard reported an increase in heritability estimates of these mean test day deviations of about 40% compared to conventional lactation yield. A similar approach has been reported by researchers from the University of Cornell (VanTassell et al. 1992, Everett et al. 1994). Prior to aggregation to the so-called residual lactations (on a 305-day basis) test day records are adjusted for herd, season, age, month of calving, days carried calf, and days open. Everett et al. (1994) advocate to estimate these correction factors within herd, however herd size will be a crucial factor for this procedure and might restrict application on a national basis.

An interesting approach has been presented by Meyer et al. (1989). Based on a multi-trait analysis of test day records linear functions of several test day observations were aggregated into a canonical index that might be used as selection criterion. This procedure combines adjustment for environmental effects on a test day basis with different weighting of the individual test day results, thus putting more emphasis on test day results from more informative parts of the lactation in estimation of 305-day production. However, a practical application of this strategy in routine evaluation has not been brought to the attention of the author.

Beside these attempts to better correct for effects specific to a test day record before aggregation to a lactation measure, models are of interest that define all environmental and genetic effects on a test day basis and analyse test day records instead of lactation measures. In the context of use of such a test day model the work of Ptak and Schaeffer (1993) was one of the first applications. One of the models of this study was:

$$y_{ijkl} = HTD_i + A_j + P_j + b_{k1}(D/c) + b_{k2}(D/c)^2 + b_{k3}\ln(c/D) + b_{k4}[\ln(c/D)]^2 + e_{ijkl}$$

where y_{ijkl} is the l^{th} test day observation of the j^{th} cow; HTD_i is a fixed herd-test-date effect; A_j is an animal additive genetic effect (random); P_j is a within lactation permanent environmental effect to account for common environmental effects associated with all test-day records of the j^{th} cow (random); b_{k1} and b_{k2} are regression coefficients on the linear and quadratic effects of D/c, where D is days in milk and c=305; b_{k3} and b_{k4} are regression coefficients on the linear and quadratic effects of ln(c/D); e_{ijkl} is a random residual effect. Individual test day records were considered as repeated observations of the same trait. They demonstrated that a herd-test-date instead of a herd-year-season classification of the contemporary group removed a considerable amount of environmental variation. When analysing test day records with a repeatability model the adjustment for stage of lactation is an important issue. Based on work of Ali and Schaeffer (1987) Ptak and Schaeffer used a set of four covariates on days in milk (DIM), which account for the shape of the lactation curve. These multiple linear regressions were nested within age and season of calving classes, thus accounting for these effects as well. Repeated test day observations have a common permanent environmental effect, which accounts for residual correlations between test day observations. One main feature of this model is that it allows for heterogeneous residual variance in the course of the lactation.

Based upon the previously described model two other models were developed. First a model which treats lactation curve parameters as random effects in the model, thus allowing for individual deviation of animals' curve from the fixed curve of animals in the same age-season group. This model was first presented from Schaeffer and Dekkers (1994), several studies followed this work, i.e. Jamrozik and Schaeffer (1995) for estimation of variance components via Gibbs sampling for this model, Jamrozik et al. (1995) for genetic evaluation for production traits, and Dekkers et al. (1996) for genetic evaluation for persistency. However, all applications so far have been restricted to first lactation data.

The second refinement of the model of Ptak and Schaeffer (1993) was the extension to multiple lactations. Especially for Somatic Cell Count evaluation observations from second and later lactations might be an important trait for selection for mastitis resistance. Therefore Reents et al. (1995a,b) extended the model of Ptak and Schaeffer (1993) to a multiple trait model, in which test day records were considered as repeated observations within lactation and as different traits across lactations. The multiple-trait animal model included random animal additive genetic and permanent environmental effects by lactation. Application of this model has also be shown for production traits in Canada (Reents et al. 1995c) and in Germany (Reents, 1996, unpublished).

Computational aspects

Dramatic increase of computing capacity along with new solving strategies (i.e. iteration on data by Schaeffer and Kennedy (1986)) allowed the implementation of large scale animal models during the eighties (e.g. Wiggans et al., 1988). Application of test day models under an animal model however leads to a further increase in computational demand. First nearly ten times more records (with a four week interval between samples) have to be processed compared to one lactation measure and second models are more complicated because a proper adjustment for stage of lactation has to be defined in the statistical model. Also consideration of herd-test-day classes leads to much more levels compared to herd-year-season classification. Computational as well as genetic aspects will be demonstrated using a large national dataset of German Holsteins.

Application of a test day model to Somatic Cell Count data

Data

Data consisted of test day records for SCC from the database maintained at Vereinigte Informationssysteme Tierhaltung w.V. (VIT), Verden, Germany which contains about 75% of all Holstein cows in Germany. The time span was from 1990 to fall 1995. For each test day, SCC was transformed to linear Somatic Cell Score (SCS) to achieve normality and homogeneity of variances.

Table 1 shows numbers of records and numbers of herd-test-date levels and cows. Edits were on: age of calving in months (20 to 40, 30 to 56, and 44 to 75, for lactations 1 to 3, respectively), day in milk of the sample between 4 and 365, and interval between consecutive tests from 7 to 90 days. Following edits 39,874,942 records from lactation 1 to 3 on 2,771,627 cows remained. About 65% of all cows were from the western part of Germany, which is characterized by lower level of SCS compared to the eastern part. Pedigree was completed for cows with identification of dam and maternal grandsire from the national pedigree file. Pedigrees for bulls with daughter records or granddaughter records were completed for several generations. Unknown parents were assigned to phantom parent groups, grouped by birth year of offspring (5 years per interval). Total pedigree file comprised of 4,514,103 animals.

Model

For genetic evaluation of test-day observations, a multiple trait test day model with repeated observations within each lactation was used.

The statistical model for analysis of test-day records was:

$$y_{ijkmn} = HTD_{im} + A_{jm} + P_{jm} + RAS_{km} + b_{km1}(D/c) + b_{km2}(D/c)^2 + b_{km3}\ln(c/D) + b_{km4}[\ln(c/D)]^2 + e_{ijkmn}$$

where y_{ijkmn} is the nth test day observation of the jth cow in parity m; HTD_{im} is a fixed herd-test-date effect; A_{jm} is an animal additive genetic effect (random); P_{jm} is a within lactation permanent environmental effect to account for common environmental effects associated with all test-day records of the jth cow in parity m (random); RAS_{km} is a region-age-season subclass mean effect in parity m; b_{km1} and b_{km2} are regression coefficients on the linear and quadratic effects of D/c, where D is days in milk and c=381; b_{km3} and b_{km4} are regression coefficients on the linear and quadratic effects of ln(c/D); e_{ijkmn} is a random residual effect. Regression coefficients were estimated within 135 region-parity-age of calving-season groups. Contemporary groups for second and third lactation records from a specific herd-test-date were combined into a common herd-test-day class to increase the size of subcells. Higher level of SCS in 3rd lactation is then accounted for by regression coefficients, which are defined by parity.

Table 2 displays (co)variance matrices of additive genetic (G_0), permanent environmental (PE_0), and residual (R_0) effects, which were estimated using Gibbs sampling procedures on a subset of the analysed data set. Methods are described in a paper by Reents et al. (1995a) on Canadian data. Variance components were estimated applying the same methodology using a dataset of 26,216 German Holstein cows with 362,478 test day records from lactations 1 to 3. Table 3 contains genetic parameters calculated from variance components displayed in Table 2. Based on detailed examinations for definition of the proper model on Canadian data it was concluded, that covariances among the permanent environmental effects in the 3 considered lactations have to be fitted.

The multi-lactation test day model provides separate EBV for SCS in the first three lactations. The three EBVs were combined into an overall EBV for SCS by index weights of .26, .37, .37 for EBV for SCS in lactations 1, 2, and 3.

Computing strategies used for iterative solution of large scale test day animal models were described in detail by Reents et al. (1995b). The important key for processing a large number of test day records is the use of efficient input and output routines of C-HP (fread) in FORTRAN programs. Using 6 mio. records (5 variables, 4 byte each) time for unformatted FORTRAN read was 112 CPU seconds on a HP-9000 891 workstation, binary read using *fread* reduced time to 16 CPU seconds, thus increasing time for processing by a factor of 7. This allowed solving for each effect in the model by iteration on data (Schaeffer and Kennedy, 1986). Considerable amount of random access memory was saved by using an implicit representation of the mixed model equations for a multiple trait animal model, as described by Tier and Graser (1991). In this method unique diagonal blocks of random effects are stored in memory only once and addressed by pointers when processing the permanent environment or animal effect. Animal effects were solved via Second Order Jacobi iteration with a relaxation factor of .7. All other effects were solved by the Gauss-Seidel method. The relative difference between consecutive solutions prior to relaxation was used to monitor convergence.

Results and discussion

Memory requirements were found to be no limitation for application of a multiple lactation test-day model to the national dataset of Germany. Although the multi lactation test day model for the data set from Table 1 consisted of 25,721,896 equations less than 350 MBytes of memory were required. Due to the implicit representation of the mixed model equations the multi lactation test-day model required only slightly more memory than a lactation average model would have needed. Nearly 40 mio test day records had to be processed three times in every round of iteration, therefore one round of iteration took about 28 minutes CPU time on a HP 9000-891 workstation. Processing time decreased by 25% if all test-day-records were stored in memory. Each record required 18 bytes of memory, thus overall demand of random access memory increased by about 720 MB. In this data set, 2588 different diagonal blocks for permanent environment effects on 2.8 mio cows were found. Consideration of inbreeding for construction of the A-1 increased number of different elements in A-1, but still only a total of 90408 different diagonal blocks of the MME for animals were found, although the complete dataset comprised of nearly 4.6 mio animals.

From a detailed study on Canadian Holstein data (Reents et al. 1995b) it was concluded that the use of solutions from previous evaluations as starting values reduces numbers of iteration to reach a defined criterion of convergence. The same level of convergence, which was reached after 300 rounds without starting values, was now reached after about 120 to 150 rounds. Benefits from the use of starting values will likely be larger when more than two evaluations per year are computed (and therefore less new observations are present).

Records from different lactations on the same sample day were fitted in different herd-test-date groups. For third lactation herd-test-date levels, subcell size can become small in small herds and, therefore, the effective contribution of these records to genetic evaluation is small when herd-test-date effects are considered as fixed. Assigning records from second and third lactation to the same herd-test-date group resolved this problem, giving only 2.3% of second and third lactation records in herd-test-date levels of size 1 or 2.

Common genetic evaluation for nearly all Holstein cattle in Germany was complicated by the fact, that SCS level is quite different across regions. This is especially evident for regions in the eastern part compared to regions in the western part. Average SCS level for first lactation cows is about 2.73 in western states compared to 3.13 in eastern states. Most of this effect should be removed through definition of herd-test-date in the model, which is naturally nested within regions, but also lactation curves (i.e. multiple regression coefficients) were nested within regions to allow also for different shape of lactation. Figure 1 shows solutions for lactation curves for two out of 135 different lactation curves. Upper curve is from cows in eastern Germany (average HTD solutions of the specific regions, which contain also the mean for the respective region, were added) and lower curve was from cows in western part. In the period from about 50 DIM to 300 DIM there seems to be only a parallel shift in lactation curve between east and west. In the beginning of lactation and at the end shape seems to be slightly different, so definition of lactation curves by regions might be necessary.

Expression of SCS proofs

Scale of SCS proofs is an important issue for proper use of this information in selection programs. Concern has been expressed that too much emphasis is placed on the SCS proofs. Two main problems of presenting SCS proofs have been mentioned: 1) mean of SCS might be an independent culling level, especially when SCS proofs are standardized to a mean of 0 and a standard deviation of one and 2) on the original SCS scale larger numbers are undesirable. If farmers are used to the phenotypic scale of SCS the approach of the US and Canada of adding the phenotypic mean to the SCS proof might solve the problems mentioned before. In Europe most farmers are not used to presentation of somatic cell count results as SCS, therefore the North American approach might not be suitable for all European countries.

In many EU countries, and especially in Germany, expression of EBVs as relative breeding values has been proved to be a successful tool, i.e. in Germany the production index RZM, type traits, fertility traits etc. are all expressed as Relative Breeding Values (mean of 100, SD of 12). For SCS, focus would be mostly on avoiding bulls with high EBV for SCS, which would be undesirable. Use of a scale with relative breeding values should be reversed to indicate undesirable bulls with values below 100. This index is called **RZS**, which stands for **R**elative EBV (EBV=**Z**uchtwert) **S**omatic Cell Score. Like all relative breeding values in Germany this figure is standardized to a mean of 100 and a standard deviation of 12 points (for bulls with 100%reliability). Figure 2a displays distribution of SCS proofs (combined index from lactations 1 to 3) for bulls with at least 20 daughters. Figure 2b displays proofs of the same bulls on the RZS scale. Table 4 shows some statistics for EBV, expressed either on the original SCS scale or on the RZS scale.

It is known that there is a genetic association between EBVs for RZS and some production and type traits. Correlations of EBV for RZS with the German production index RZM (weight on milk : fat : protein = 0 : 1 : 4) and some type traits are in Table 5. Although these correlations should not be interpreted as genetic correlations they indicate that there is a genetically undesirable association of SCS with production. Selection for udder health could be enhanced by the use of RZS proofs along with some udder conformation traits.

Conclusion

Test day models, even with a multi trait model, can be applied for genetic evaluation to national datasets as has been proven for Germany and Canada. So far the described methodology has been used in national genetic evaluation for SCS in Canada and Germany. In Germany unofficial production proofs for use as additional information between official runs were estimated with the same multi-lactation test day model, results will not be presented here because of the nature of the workshop. Further possibilities of application to production traits and persistency were already mentioned.

If more frequent evaluations are required to reduce generation interval, test day evaluations based on individual test day yields would be the method of choice. Evaluation without extension of records is already possible with at least one test day yield. In subsequent evaluations all available information up to the cut off point in the data will be used.

Another field of application of TD models might be for management purposes of dairy producers. Many milk recording agencies measure and store also additional information like lactosis content and urea content on a test day basis. Along with somatic cell counts, fat, and protein content test-day-models might be exploited also for description of the stability of the physiological system of a cow. Additional traits like conductivity and temperature of the milk might be worth to collect already from the milking equipment and to be stored along with the established traits belonging to a test day record. Probably this will be a management tool but a genetic background might also exist for some of these traits as has been shown for somatic cell counts.

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Tables

TABLE 1. Number of test-day records, cows, and levels of herd-test-date effects.

	Lactation			
	1	2	3	Total
Number of test day records	17,286,599	13,088,063	9,500,280	39,874,942
Number of herd-test-date levels*	1,916,678	1,947,353	1947353	
Cows with records**	2,771,627	1,624,580	1,198,607	

* Same no. of levels for lactation 3 as lactation 2 because herd-test-date classes were combined for lactation 2 and 3

** Number of cows for lactation 2 and 3 are subsets of cows in lactation 1

TABLE 2. Variance components used for genetic evaluation of SCS.

	Variances by lactation			Covariances between pairs of lactations		
Random effect	1	2	3	1 : 2	1 : 3	2 : 3
Animal additive genetic	.154	.270	.323	.183	.189	.286
Permanent environment	.737	.695	.764	.248	.209	.327
Residual	1.053	1.098	1.159	0	0	0

TABLE 3: Genetic parameters for SCS of lactations 1 to 3 (calculated from variance components of Table 2)

	Heritability	Repeatability	Genetic correlation		Corr. between PE-effects	
			Lact. 2	Lact. 3	Lact. 2	Lact. 3
Lactation 1	0.08	0.46	0.9	0.85	0.35	0.28
Lactation 2	0.13	0.47		0.97		0.45
Lactation 3	0.14	0.48				

TABLE 4. Means and standard deviations (SD) of estimated breeding values for AI bulls (combined EBV for lactations 1, 2, and 3)

	Number of bulls	Scale of EBV			
		SCS		RZS	
		Mean	SD	Mean	SD
No. of daughters					
5 -25	3204	0.0	0,343	102,0	8,39
26 - 50	2576	0.0	0,385	101,6	9,40
51 - 100	1358	0.0	0,409	101,3	9,99
> 100	2901	0.1	0,432	100,5	10,55

Table 5: Correlations of EBV for RZS with production index RZM and some type traits (1348 bulls with a reliability of the RZS proof of > 0,6)

Trait	Correlation to RZS	interpretation
RZM	-0,1	undesirable
EBV-Udder	0,2	desirable
Fore-Udder-Attachment	0,3	desirable
Rear-Udder-Height	0,1	desirable
Suspensory Ligament	0,1	desirable
Udder Depth	0,3	desirable
Teat Placement	0,1	desirable

Figures

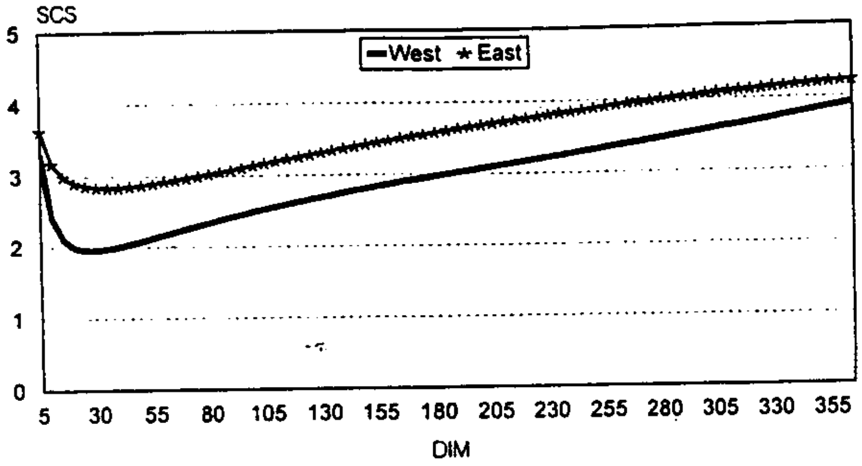

Figure 1: Lactation curves for first lactation Holstein cows, calving between Sep. and Dec., with an age of 29 to 31 months from two regions in Germany.

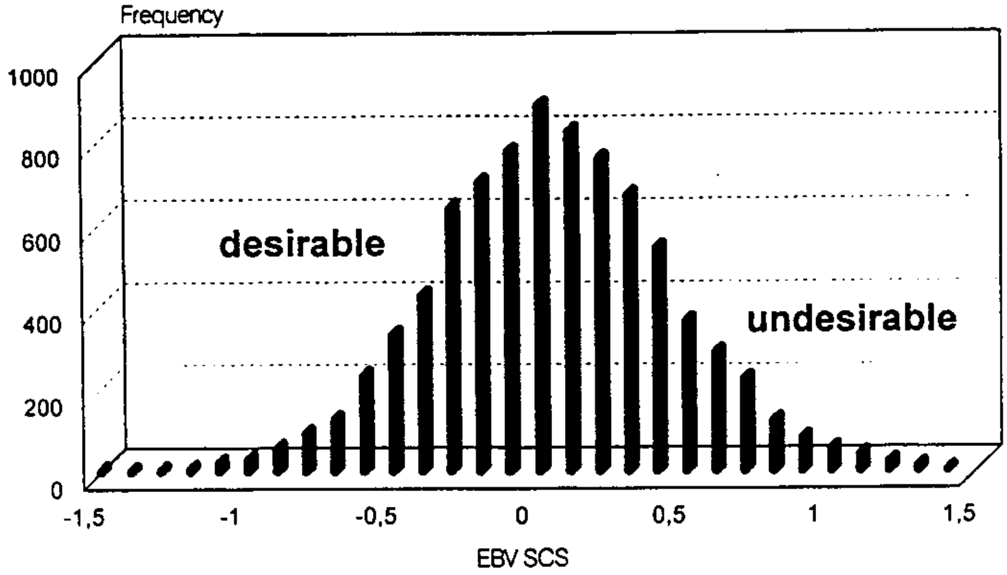

Figure 2a: Distribution of SCS proofs for bulls with more than 20 daughters

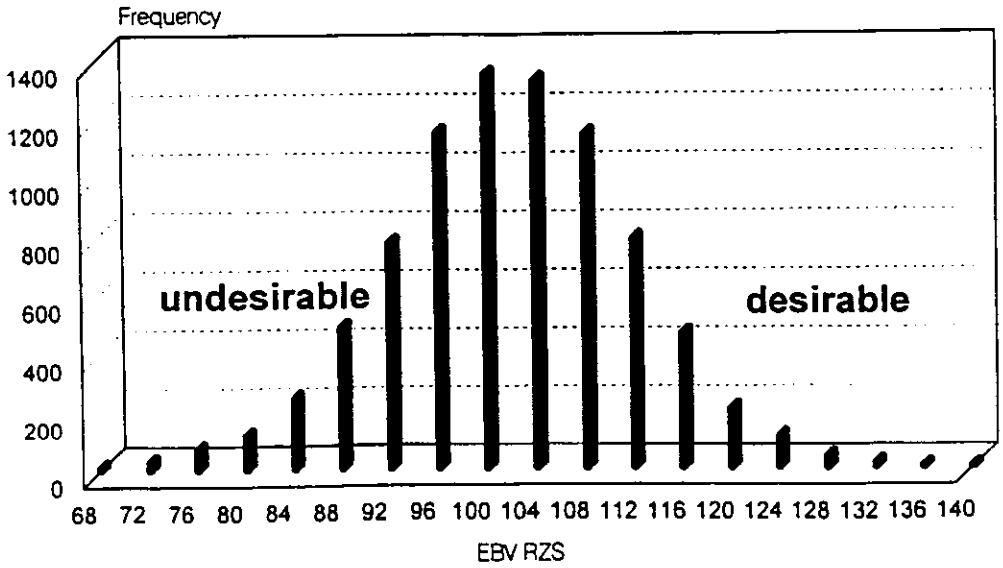

Figure 2b: Distribution of RZS proofs for bulls with more than 20 daughters