Effect of Number of Days between Semen Sampling on Variance Heterogeneity of Semen Concentration of Young Simmental Bulls

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SUMMARY

The objective of this study was to estimate heterogeneity of genetic and environmental variances and heritabilities for semen concentration of young Simmental bulls due to different number of days between semen collections. Data utilized in this study consisted of 1132 young Simmental bulls born from 1974 to 2001 with total number of 6994 records, and 3000 animals in pedigree. The data were provided by the Performance Test Station – Varaždin. In order to analyze heterogeneity of variance, four data sets with two days periods (i.e. two and three; three and four; four and five; and five and six days) between semen samplings were derived. Similarly, three data sets with three days periods between semen samplings were derived. Variance and covariance components and associated heritabilities for such defined data sets were estimated by Restricted Maximum Likelihood from a set of single-trait animal models. Fixed effects were defined as birth year x season and number of days between collections, and animal effect was defined as a random effect. The heritability estimates ranged between 0.01 to 0.08. Days between collections influenced variance heterogeneity. An increase of days between collections increased additive and permanent environment variance, decreased error variance, thus the estimation of heritability was improved.

KEY WORDS

semen, cattle, heterogeneity of variance, heritability

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INTRODUCTION

When repeatability model is used in estimating genetic parameters of semen concentration, the assumption of variance homogeneity must hold. In practice this assumption has often been violated. The estimates of genetic and residual variances can differ not only among but also within a cattle population. Heterogeneity of variances across the herds has been reported in many studies (Short et al. 1990, Wiggans and van Raden, 1991, Gengler and Wiggans, 2001. Further, the problem in finding objective estimates can be due to small amount of data available, because the number of sires needed for a breeding program is relatively small. This is especially true for traits that can be measured only on male animals such as semen traits. Utilization of pedigree information in an animal model (or similar models) can partly account for selection (Sorensen and Kennedy, 1983). Different methods have been studied to account for heterogeneity in Animal Model (Hill, 1984; Gianola, 1986; Garrick and Van Vleck, 1987; Weigel and Gianola 1992) and some of them were applied in the genetic evaluation of animals. The objective of this study was determine variance heterogeneity and to estimate genetic and environmental variances and associate heritabilities of semen concentration for different days between semen collections of young Simmental bulls.

MATERIAL AND METHODS

Data utilized for this study were provided by the Performance Test Station - Varaždin and consisted of semen concentration of 1132 young Simmental bulls born from 1974 to 2001. Animals entered Station at the age of 60 days with average weight of 130 kg (Mikulić and Nazansky, 1995). Actual test began at 120 days of age. Animals were housed individually in 8 m^2 pens and were given about 12 m^2 of paddock.

The bulls were fed a diet of hay and concentrate. During the whole period bulls were offered hay ad libitum. Concentrate was given twice a day as follows. When animals entered the Station small amount of concentrate PII was given. Concentrate was gradually increased so bulls received 4 kg daily at 120 d of age and 6 kg at the age of 300 d. At 300 d of age concentrate PII was replaced with concentrate PIII This concentrate was gradually increased up to maximum 8 kg daily. During the whole test period bulls were fed individually. The concentrate PII consisted of 30% corn, 30% oats, 15% wheat bran, 22% soybean meal, 1% dicalcium phosphate, 1% bone meal and 1% vitamin-mineral supplement, with 16,1% digestible protein and 11 MJ ME. The concentrate PIII consisted of 35% corn, 40% oats, 7% wheat bran, 15% soybean meal, 1% hostafos, 1% bone meal and 1% vitamin-mineral supplement, with 13.4% digestible protein and 11 MJ ME.

Semen collections started at approximately 11 months of age. Number of semen collections per bull varied. The maximum number of collected ejaculates was up to 15. Descriptive statistics were calculated using the Univariate procedure (SAS, 1990), pedigree and data structure of semen concentration of bulls are presented in Table 1.

Table 1. Pedigree and data structure of semen concentration

Mean (10^9/ml)	911,1
Standard deviation	176,8
No. of animals	3000
Total no.of records	6994
No.of base animals	1279
No.of animals with records	1132
No.of sires with progeny records	154
No.of dams with progeny records	437
No.of grand-sires w. progeny records	200
No.of grand-dams w. progeny records	267

In order to analyze heterogeneity of variance, four data sets with two and three; three and four; four and five; and five and six days between semen collections were derived. Similarly, three data sets with two, three and four days; three, four and five days; and four, five and six days between semen collections were derived. Variance and covariance components and associated heritabilities for such defined data sets were estimated by Restricted Maximum Likelihood (REML) from a set of single-trait animal models:

$$\mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_c\mathbf{c} + \mathbf{e}$$

where y is a vector of observed traits, β is a vector of fixed effects, a is a random vector of additive genetic effects, c is a random vector of permanent environment due to repeated measurements per bull, X, Z_a and Z_c are incidence matrices relating β, a to y, and e is a random vector of error effects. The model has the following distributional assumptions:

$$\mathbf{E}[\mathbf{y}] = \mathbf{X}\beta$$

and

$$Var\begin{bmatrix}\mathbf{a}\\ \mathbf{pe}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{A}\sigma^2_a & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{I}\sigma^2_{pe} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma^2_e\end{bmatrix}$$

where σ^2_a is the additive genetic variance and σ^2_{pe} is the permanent environmental variance due to repeated measurements on the same bull, and σ^2_e is the error (temporary environmental) variance. Vectors **pe**, **a** and **e** are assumed to be uncorrelated. Also, **A** is the additive genetic relationship matrix and **I** is the identity matrix.

Fixed effects were defined as birth year x season and number of days between collections. The seasons are defined as follows: winter = December, January and

February, spring = March, April and May, summer = Jun, July and August, and fall = September, October and November. Animal effect was defined as random effect.

Calculations were carried out using the module DFUNI of the DFREML software (Meyer, 1998). This program performs univariate analysis using a derivative-free algorithm to locate the maximum of the log likelihood (*logL*). Convergence was considered to have been reached when the difference between estimated parameters in two consecutive iterations was less than 10^{-8}. To insure convergence of *logL* to a global maximum the single trait models were run several times restarting the program with initial values from the previous run.

RESULTS AND DISCUSSION

In the present study the heritability estimate for semen concentration was 0,07 (table 2). Estimates of heritability for semen traits reported in the literature are very diverse. For example, Schlote and Munks (1980), Makulska et al. (1993) and Kapš et al. (2000) reported low estimates for semen concentration. On the other hand Ducrocq and Humboldt, (1995) reported moderate to high heritabilities for semen production traits. They argued that if various environmental and management factor, such as frequency of collection, season, duration of sexual preparation, were taken into account, moderate to high heritability estimates could be expected. Unfortunately, in the present study a sexual preparation was not recorded.

Figure 1 shows changes in additive genetic, permanent environment variance and error variance due to different days between semen collections. Generally, more days between semen collections depicts increasing of additive and permanent environment variance and decreasing of error variance.

Figure 2 shows changes in the estimates of heritability and permanent environment variance expressed as a proportion of the phenotypic variance. Following changes in variance estimates the estimates of heritability were increased when number of days

Table 2. Estimates of genetic parameters of semen concentration.

Additive genetic variance	1983,1
Variance due to permanent environment	11231,6
Error variance	14284,8
Phenotypic variance	27499,5
Phenotypic standard deviation	165,8
Phenotypic coefficient of variation (%)	18,2
Heritability	0,07 ± 0,04
Permanent environment variance as a proportion of phenotypic variance	0,41 ± 0,04

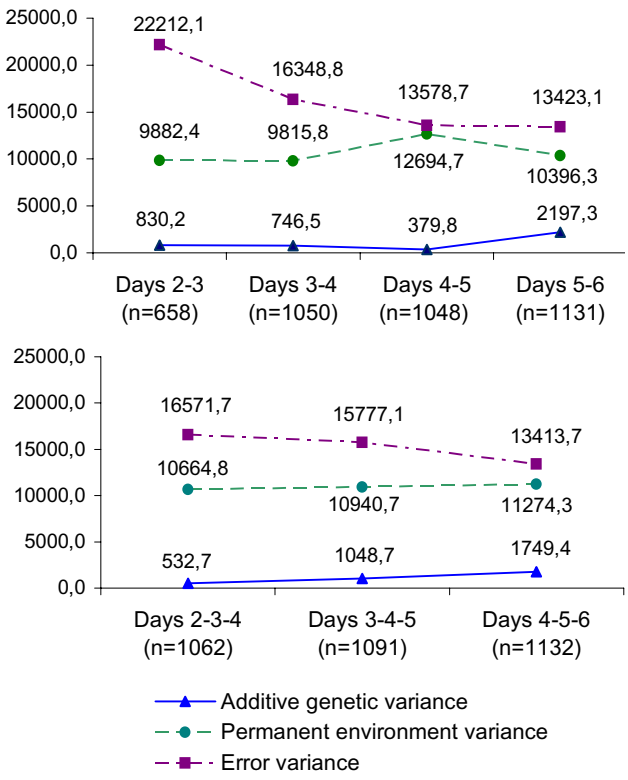

Figure 1. Changes in additive genetic, permanent environment and error variances due to different number of days between semen samplings (n is the number of bulls with records)

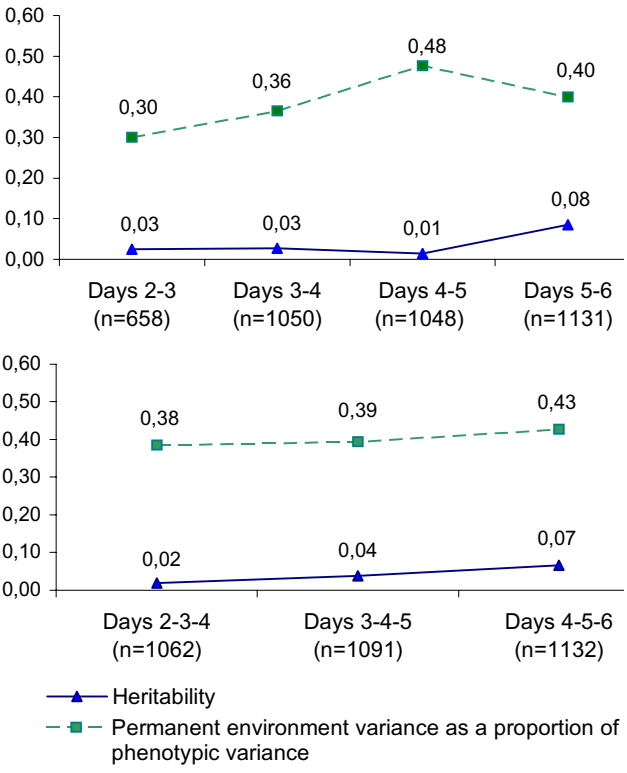

Figure 2. Changes in heritabilities and permanent environment variance as a proportion of phenotypic variance due to different number of days between semen samplings (n is the number of bulls with records)

between semen collections was increased. Similar trend was observed for the proportion of permanent environment variance.

It follows that some animals could differ in semen concentration only because they need more time for new semen production, although they are genetically similar for semen concentration. In that case, the number of days between semen collection and genetic effects are partially confounded and the genetic differences between animals in different groups are underestimated. Therefore, if heterogeneity is not taken into account it might result in biased breeding value predictions. Besides the proper definition of factors determining heterogeneity the proper adjustment procedure should be applied.

CONCLUSION

Number of days between semen sampling influences variance heterogeneity. In this study, an increase in number of days between collections increased additive and permanent environment variance, and decreased error variance. Consequently, the heritability estimates were increased. The heterogeneity of variance of semen concentration may be considered in improving routinely breeding value estimation in the national breeding program.

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