

International Sire Evaluations and Conversions in Upgrading Populations with Changing Means and Variances

K. A. Weigel¹, G. Banos², and A. Sigurdsson²

¹ Department of Dairy Science, University of Wisconsin, 1675 Observatory Drive, Madison, WI 53706 USA

² INTERBULL Centre, Box 7023, S-750 07, Uppsala, Sweden

Introduction

International dairy sire evaluations are sensitive to genetic standard deviation (SD) parameters, particularly with regard to rankings of outlier bulls (Schaeffer, 1995; Banos, 1995). Underestimation of genetic SD for a particular country can result in overrepresentation of this country at the top of international ranking lists, and overestimation of genetic SD can disadvantage a member country in a similar manner. Within-country genetic SD are influenced by genetic selection, importation of different breeds or strains, heterogeneous variance adjustments, improvements in herd management practices, and other factors.

Estimated genetic SD for INTERBULL member countries clearly differ and depend on the time period of data chosen:

Estimated Sire SD Protein (kg): Holsteins (2/96)

Country	All Data	Since 1980	Change
CAN	12.21	12.31	+0.8%
DEU	6.80	7.10	+4.2%
DNK	7.23	7.28	+0.8%
FIN	6.10	6.04	-0.8%
FRA	6.74	6.48	+8.5%
ITA	6.46	6.46	0.0%
NLD	7.23	7.53	+3.9%
SWE	7.20	6.12	+11.3%
USA	6.66	6.44	-2.3%
CHE	5.24	5.66	+8.1%
GBR	6.08	6.16	+1.3%
NZL	4.59	4.61	+0.4%

Because differences in estimated SD due to data selection can have a large effect on breeding value estimates, it is important to

determine the optimum strategy for data selection in estimation of within-country genetic SD. The objective of this study was to examine the effects of data selection on genetic SD estimation when genetic mean and variance parameters differed among populations.

Materials and Methods

Data were simulated for two populations, three mean and variance structures, and three levels of genetic exchange. True genetic SD for each animal was a function of the genetic SD within each population in the current generation and the proportion of genes inherited from each population. Eight generations were simulated, with 36,000 cows, 300 progeny test bulls and 30 proven bulls per generation in each population. Ten sires and 150 dams were chosen as parents of test bulls for the next generation in each population. Each test bull had 80 progeny in the current generation, and selected proven bulls had 400 additional progeny in the next generation. Selection occurred within populations during generations 1 through 4, and genetic exchange occurred between populations in generations 5 through 8. High, low, and one-way exchange of sires of sons, dams of sons, and sires of cows (proven bulls) was considered.

Genetic SD for each country were estimated using the REML procedure of Sigurdsson (1995). Data selection effects were examined using data from generations 0-8, 1-8, 2-8, ..., 7-8, and generation 8 only in genetic SD estimation.

Results and Discussion

When genetic mean and variance parameters were the same in both populations, estimated genetic SD tended to decrease as data from early generations were discarded. Presumably this was due to the effects of selection on genetic variances.

Importation of animals from a strain with higher genetic mean and variance gave a blended estimate of genetic SD when all data were included. Usage of more recent data gave estimates which were closer to true and estimated SD in the exporting population. Estimated SD were largest when data beginning with the first generation of importation were used. Differences in estimated genetic SD between populations were larger when genetic exchange was limited, and estimates for the importing population were often larger in this case. When true genetic SD were increasing over time, estimated SD were larger using more recent data.

Apparent decreases in genetic variances over time due to selection in closed populations were large in the current study, but it is likely that selection effects are smaller in real life, because actual national populations are much larger than the simulated populations, and inbreeding avoidance is practiced by most breeders. In addition, the effects of herd variance adjustment procedures should be examined.

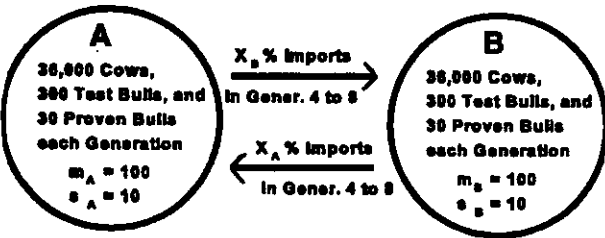
Conclusions

It is clear that factors such as genetic selection and importation can cause true and estimated within-country genetic SD to depend heavily on the time period of data chosen. Estimation of genetic SD parameters using data from more recent generations only will give estimates which more closely reflect the breed composition and production level of the current population, but one must be willing to overlook possible decreases in variance due to selection.

METHODS: SIMULATION SCENARIOS

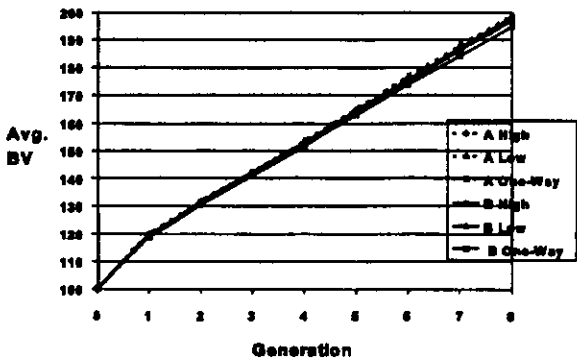
RESULTS: GENETIC TRENDS

Equal Means; Equal Variances

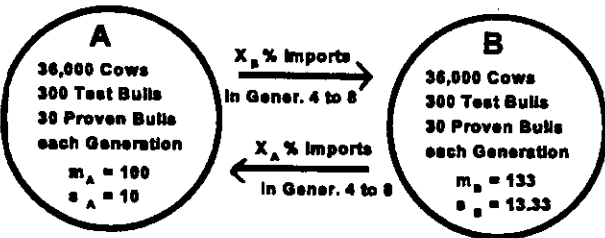


X_A % = 70%, 30%, or 70% (High, Low, or One-Way Exchange)
 X_B % = 20%, 10%, or 0% (High, Low, or One-Way Exchange)

Average True Sire Breeding Value by Generation;
Equal Means, Equal Variances

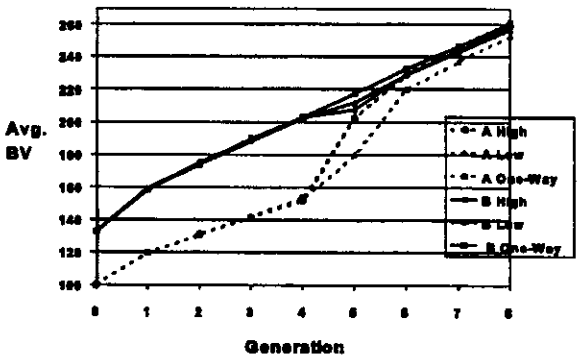


Different Means; Different Variances

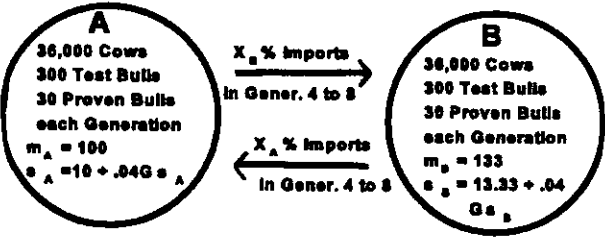


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Average True Sire Breeding Value by Generation;
Different Means, Different Variances

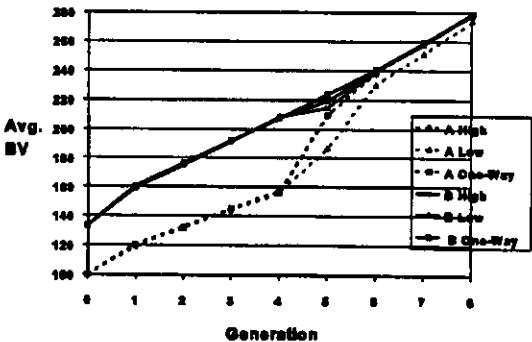


Different Means; Different Variances;
Variances Increasing over time



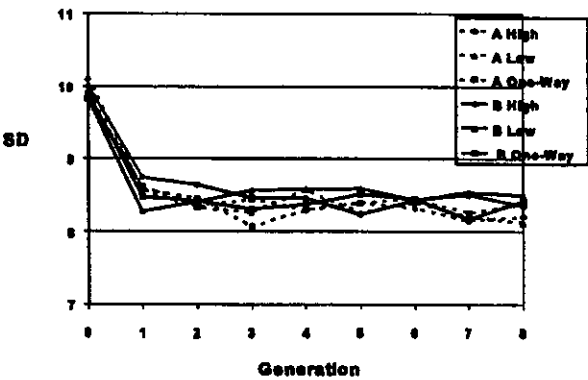
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 X_B % = 20%, 10%, or 0% (High, Low, or One-Way Exchange)

Average True Sire Breeding Value by Generation;
Different Means and Variances; Increasing Variances



RESULTS: SD OF TRUE BV

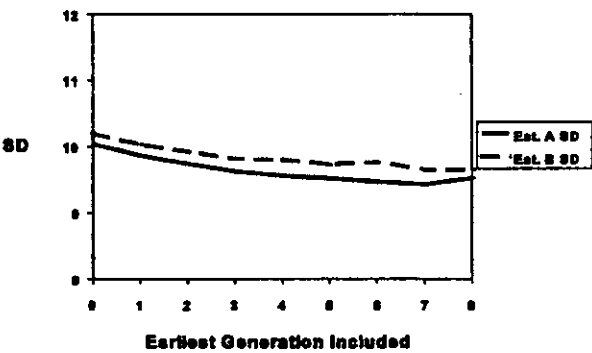
SD of True Sire Breeding Value by Generation;
Equal Means, Equal Variances



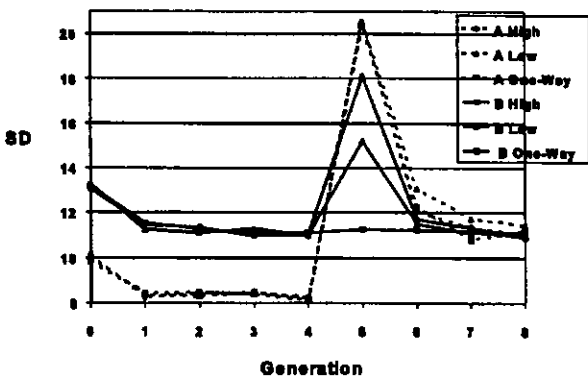
RESULTS: GENETIC SD ESTIMATION

EQUAL MEANS AND VARIANCES

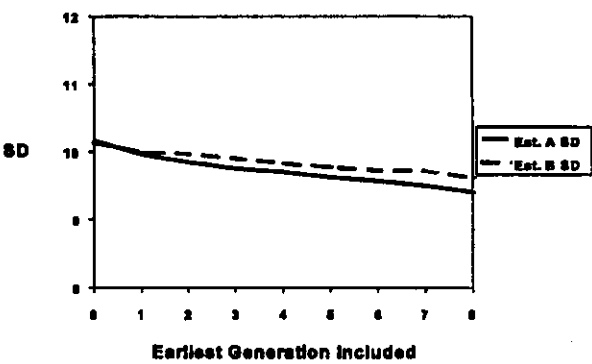
Estimated Genetic SD with Equal Means
and Variances and High Genetic Exchange



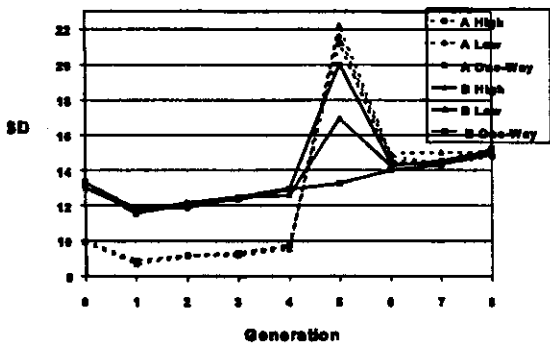
SD of True Sire Breeding Value by Generation;
Different Means, Different Variances



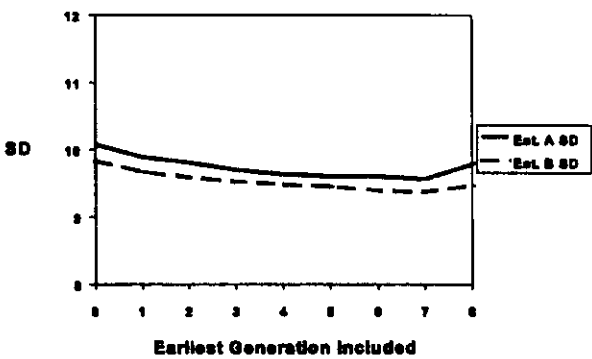
Estimated Genetic SD with Equal Means
and Variances and Low Genetic Exchange



SD of True Sire Breeding Value by Generation;
Different Means and Variances; Increasing Variances

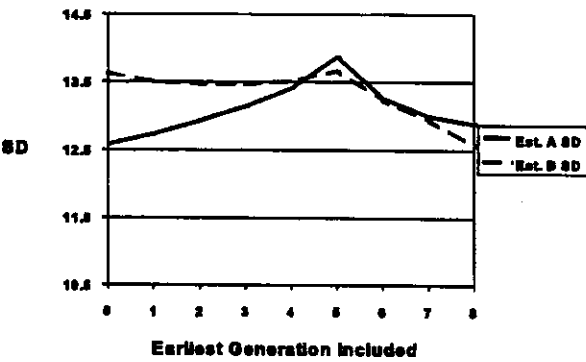


Estimated Genetic SD with Equal Means
and Variances and One-Way Genetic Exchange



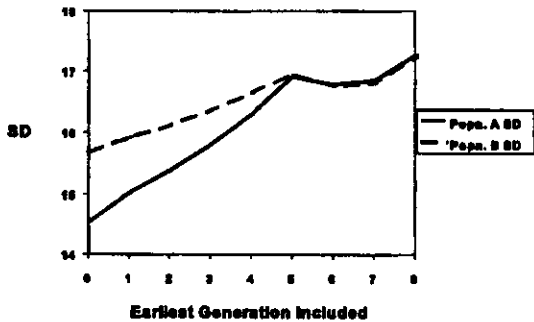
DIFFERENT MEANS AND VARIANCES

Estimated Genetic SD with Different Means, Different Variances and High Genetic Exchange

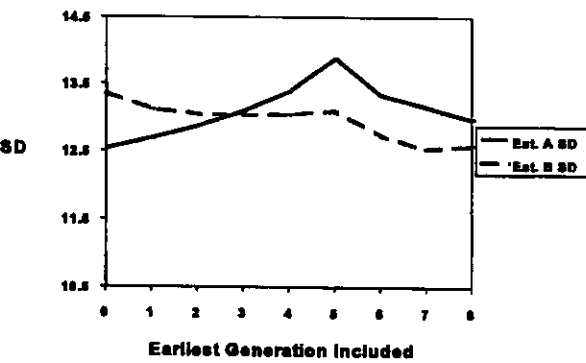


DIFFERENT MEANS AND VARIANCES
INCREASING VARIANCES

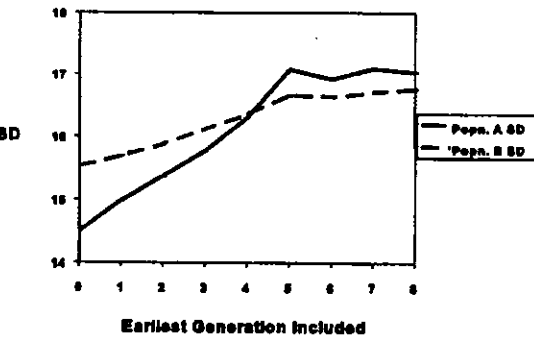
Estimated Genetic SD with Different Means and Variances, Increasing Variances and High Genetic Exchange



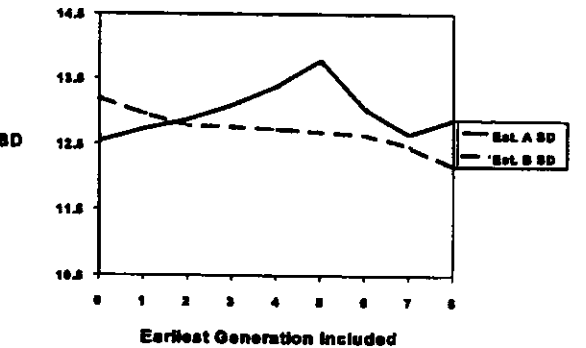
Estimated Genetic SD with Different Means, Different Variances and Low Genetic Exchange



Estimated Genetic SD with Different Means and Variances, Increasing Variances and Low Genetic Exchange



Estimated Genetic SD with Different Means, Different Variances and One-Way Genetic Exchange



Estimated Genetic SD with Different Means and Variances, Increasing Variances and One-Way Genetic Exchange

