Persistence of estimates of effects of genome-wide markers over generations when including a polygenic effect

T. R. Solberg[1], A.K. Sonesson[2], J. A. Woolliams[1,3], J. Ødegård[2] T. H. E. Meuwissen[1]

[1]Norwegian University of Life Sciences, Dept. of Animal and Aquacultural Sciences,
P.O. Box 5003, N-1430 As, Norway.
[2]NOFIMA Marin, P.O. Box 5010, N-1432 As, Norway.
[3]Roslin Institute (Edinburgh), Roslin, Midlothian EH25 9PS, UK.

Introduction

- Some markers will be more frequent in some families than others, and therefore may act as markers for family effects

- By including a polygenic effect in the BayesB model (Meuwissen *et al*, 2001), the expectation is that the marker effect will be more reliably estimated and more persistent over time

- Main objective to investigate the effect of including a polygenic effect and study their persistence over time

Population structure and genome size

- Population with Ne = 100 simulated over 1000 generations (Solberg *et al*., 2008)
- Descending generations (t = 1002 to t = 1006) produced by random sampling with replacement among the parents from the previous generation (1000 animals in each generation)
- Genome consisted of 10 chromosomes of 100 cM each, and Mendelian inheritance and the Haldane mapping function assumed for all loci (Solberg *et al*., 2008)

Estimation model including polygenic effect

$$\mathrm{y_i} = \mu + \mathrm{a_i} + \sum_{\mathrm{j=1}}^{\mathrm{Nloc}} \mathrm{X_{ij} g_{ij}} + \mathrm{e}$$

$$Var(\mathbf{a}) = \mathbf{A}\sigma^2{}_a$$

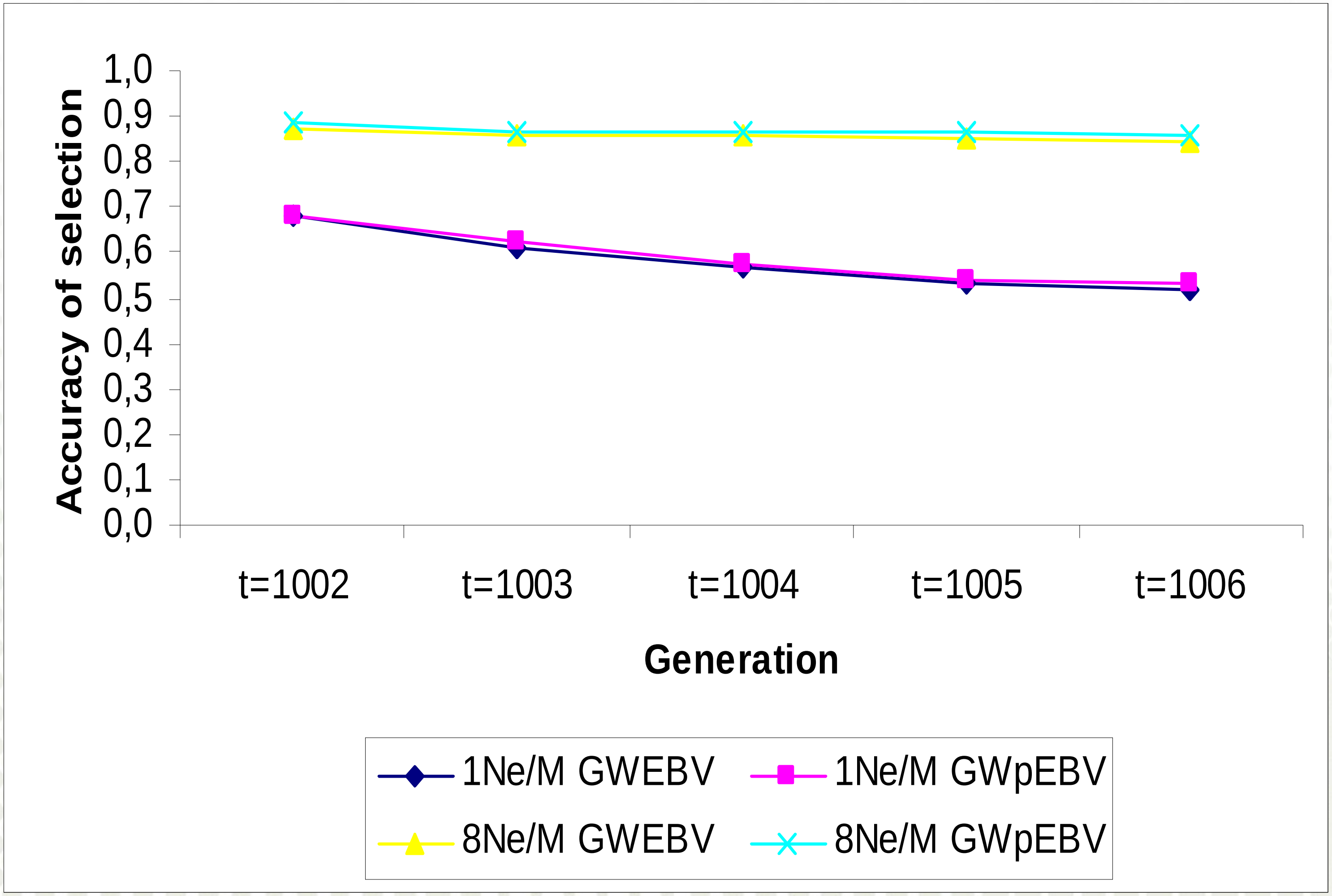
$$p(\sigma^2{}_{gj}) = \left\{ \begin{array}{ll} 0 & \text{with probability } \pi \\ \chi^{-2}(v, S) & \text{with probability } (1\text{-}\pi) \end{array} \right\}$$

Prediction of genome-wide breeding values

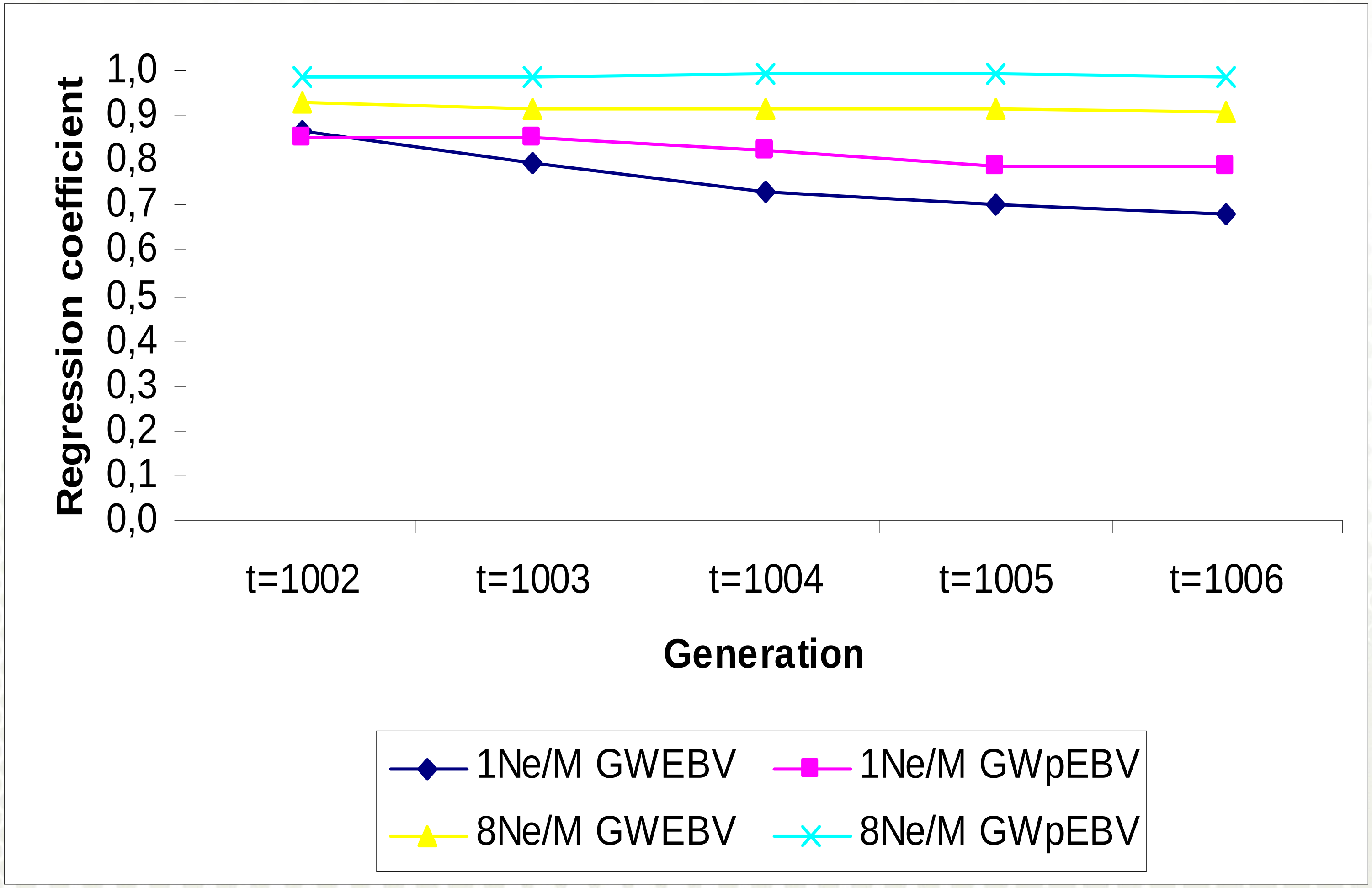
$$\mathrm{GWEBV}_i = \sum_{j=1}^{\mathrm{Nloc}} X_{ij}\hat{g}_j$$

$$\mathrm{GWpEBV}_i = \sum_{j=1}^{\mathrm{Nloc}} X_{ij}\hat{g}_j + a_{i(t)}$$

Accuracy of selection



Regression coefficient



Conclusions

- Including a polygenic effect did not increase the accuracy of selection significantly
- However, reduced bias significantly!
- Result dependent on the genetic architecture and parameters used in the study, but including a polygenic effect were especially beneficial when estimated marker effects were used to predict GWEBV over multiple generations
- A marker density of 8Ne/M seemed sufficient for the estimated marker effects to persist over 5 generations of selection with small bias and a minimal reduction in accuracy

Conclusions

- Phenotypic records may be expensive to record for all generations, may reduce animal welfare, or sometimes not be possible for live selection candidates
- Significantly reduced costs may be achieved if the estimated marker effects could be used over multiple generations