Minimizing Genotyping In Breeding Programs With Natural Mating

R.J.W. Blonk[*], J. Komen[*] and J.A.M. van Arendonk[*]

Introduction

In many aquaculture populations highly skewed parental contributions are observed when natural mating in groups is used to obtain offspring (Bekkevold 2006; Fessehaye, El-Bialy, Rezk *et al.*, 2006; Blonk, Komen, Kamstra *et al.*, 2009). In such situations, pedigree information is missing and mass selection will result in high rates of inbreeding (Blonk, Komen, Kamstra *et al.*, 2009). Relationships can be reconstructed using DNA markers such as microsatellites or SNP's. However, with large numbers of selection candidates, this can be very expensive. Sonesson (2005) showed that for populations with a controlled mating design and contribution of parents, the number of genotyped selection candidates can be restricted by using a two stage selection scheme with optimal contribution selection on a phenotypically pre-selected fraction of the population. However, in situations where natural mating in groups is used to obtain offspring, rates of inbreeding and response to selection are difficult to predict and can be highly fluctuating depending on superiority of the highest contributing families. In this paper, we use stochastic simulation to determine the relation between nucleus size, genotyped fraction and achieved response and rate of inbreeding in two stage selection schemes with natural mating and skewed contributions of parents.

Materials and methods

Two single trait selection schemes were simulated: 1) mass selection, 2) mass selection followed by genotyping and optimal contribution selection (2-Stage selection). A population of $N = 8000$ selection candidates with nucleus size n = 200 or n = 300 ($n_{sires} = n_{dams} = ½ n$) was simulated. Heritability for the trait was 0.2 (simulations with heritability 0.5 were also performed but not included in the paper). In all simulations, the nucleus was divided in four groups and the number of parents was kept constant over all generations. In 2-Stage selection, different fractions (comprising 3, 4, 5, 6, 8,10, 12 or 15% of the population) with the best phenotypes were selected using mass selection. Assuming that these animals were pedigreed by genotyping, ASReml (Gilmour, Gogel, Cullis *et al.*, 2006) was used to obtain BLUP of breeding values. A fixed number of parents (n) was then selected under a restriction of ΔF of 1% per generation using optimal contribution selection with GENCONT software (Meuwissen 1997). Offspring of all full sib families were pooled for each generation and response and rate of inbreeding per generation were calculated.

Parental contributions. To construct skewed parental contributions (c), n_{sires} and n_{dams} random numbers were drawn from a gamma distribution ($x \sim \Gamma(0.75, 1/3)$) and transformed to relative contributions. Only sires and dams with $c > 0$ (n_{csires} and n_{cdams}) were used to contribute to the next generation. Parental contributions were not correlated to selected trait. Using the relative contributions, a full factorial mating design with dimensions n_{csires} by n_{cdams} was set up with the size of full sib families (c_{FS}) as the kronecker product of the parental

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[*] Animal Breeding and Genomics Centre, Wageningen University, PO Box 338, 6700 AH Wageningen, the Netherlands.

contributions. To reflect that some full fib families are not contributing, a maximum number of possible families ($n_{maxfam} = n_{csires} + n_{cdams}$) was randomly drawn from the full factorial mating design. Sire and dam breeding values in the founder population were simulated as $z\sqrt{\left(h^2 \cdot \sigma_p^2\right)}$ with z as a normal deviate generated from a simulated normal distribution (N~(0,1)) and phenotypic variance σ_p^2 set to 1. For each full sib family, phenotypes of $N \cdot c_{FS}$ offspring were calculated using the parental breeding values, a Mendelian sampling term including inbreeding coefficients of the parents and a residual.

Results and Discussion

For each selection scheme and $h^2 = 0.2$, results of ten generations selection (averaged over 50 replicates) are presented in figure 1. With only mass selection (see figure 1) and nucleus size n = 200, ΔF after 10 generations was estimated on 1.52% per generation while ΔG was 35% per generation. For n = 300, ΔF and ΔG were respectively 1.01% and 33.7%. This is considerably higher than in populations with random mating and equal contributions. Prediction of ΔF and ΔG using Selaction software (Bijma, Van Arendonk and Woolliams 2001) for the same selection scheme yields a ΔF of 0.56% and ΔG of 41% for *n* = 200. For *n* = 300, a ΔF of 0.35% and a ΔG of 38% are predicted. These results show that normal mass selection will lead to excessive rates of inbreeding in populations where natural mating in groups is used to obtain offspring.

In a 2-stage breeding program, ΔF is restricted while ΔG is maximized. As expected, an overall lower ΔF and ΔG is obtained in a 2-stage breeding program when compared to mass selection. In a 2-stage breeding program, ΔF has a U-shaped trend for increasing genotyped fractions (figure 1). For fractions 3% to 5% (for *n* = 200) and fractions 4% to 5% (for *n* = 300), ΔF decreases. This is probably due to fixed nucleus sizes and limited availability of families in the relatively small genotyped fractions. In such cases, optimal contribution routines can not hold the set restriction and are expected to yield relatively high ΔF. As the genotyped fractions increase, more families become available, yielding lower ΔF.

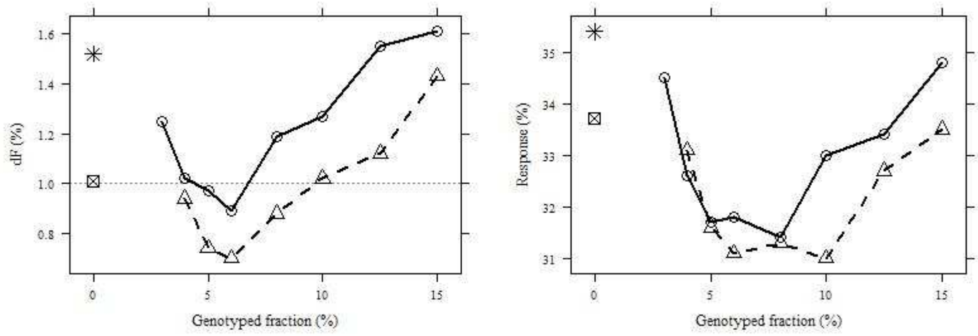

Figure 1: Mean ΔF (%) and response (%) for a two stage breeding program including optimal genetic contribution selection on different genotyped fractions. Results are shown for nucleus size 200 (circles) and 300 (triangles). Population size = 8000. Restriction for ΔF = 1% (dotted line). ΔF and Response for mass selection on a natural mating population are depicted for nucleus size 200 (star) and 300 (square).

With genotyped fractions higher than 5%, ΔF increases to 1.4 - 1.6% per generation. At these fractions, short term 1% ΔF restrictions are met at an early stage. Consequently, there is little room left to lower ΔF when unexpected high ΔF is reached due to natural mating with skewed contributions. Again, optimal contribution selection can not hold the set restriction of ΔF, resulting in higher values.

In many schemes, ΔF was above the restriction of 1%. This is probably due to the fixed number of selected parents (nucleus size). Optimal contribution selection can suppress ΔF once the number of parents to select is free. However. in practical circumstances, nucleus sizes are generally fixed for economic reasons. Also, nucleus size often has a constrained minimum set by the required reproductive output of fertilized eggs.

Implications ΔG of a 2-stage breeding program with natural mating is relatively stable across increasing mass selected and genotyped fractions, i.e. genotyping more animals does not considerably increase ΔG. For example, with a genotyped fraction of 5% (400 animals), response is approximately 32%. This increases to approximately 35% with a genotyped fraction of 15% (1200 animals). It will depend on the economic importance of the trait whether this increase in response outweighs the increasing genotyping costs. However, with respect to ΔF, there is an optimum size of mass selected and genotyped fractions; rates of inbreeding exceed acceptable levels once too few or too many candidates are genotyped. Moreover, when mass selected and genotyped fractions comprise less than 10% of a population of 8000 animals, ΔF remains below values of mass selection.

In conclusion, using mass selection to genetically improve stocks which are dependent on natural mating in groups, is likely to yield excessive rates of inbreeding, unless a large nucleus is maintained. However, when genotyping 5 to 10% of the selection candidates and applying optimal contribution selection, levels of inbreeding can be kept at or close to the generally accepted level of 1%. This means that there are good prospects for genetic improvement of aquaculture industry when natural mating in groups is used to obtain offspring.

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