Comparsion of Mating Designs in Breeding Schemes with Genomic Selection

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Introduction

In selective breeding, selection and mating are important components to be optimized by the breeder. Many authors have compared the effect of mating criteria on rates of inbreeding and/or genetic gain. With the aim of increasing genetic gain and/or decreasing rates of inbreeding, mating criteria comparsions have been done on simulated breeding schemes with truncation selection on phenotypes (Caballero (1996)); truncation selection on BLUP estimated breeding value (Caballero (1996); Henryon *et al*. (2009)) and selection based on optimum contribution-BLUP estimated breeding value (Sonesson and Meuwissen (2000)). Sonesson and Meuwissen reported 22% more genetic improvement over random mating when factorial mating (Woolliams (1989)) was combined with minimum coancestry mating and optimum contribution selection. The benefit of Minimum Covariance of Ancestral Contributions (MCAC) over random mating was up to 28% less inbreeding and 3% more genetic gain (Henryon *et al*. (2009)). A comparison by Caballero (1996) shows also up to 40% reductions in rates of inbreeding can be achived when a combination of compensatory and minimum coancestry mating is used in comparison with random. However, none of the mating criteria were compared when using genomic selection, which is increasingly used in practice (Hayes *et al*. (2009)). Genome wide breeding value estimation gives a different emphasis among information sources which may have an effect on the optimum mating design. Therefore it is worthwhile to investigate the effect of each mating criteria in genomic selection schemes.

This simulation study is aimed to compare a wide variety of mating criteria for their genetic gain and inbreeding in a typical aquaculture breeding scheme using genomic selection. The mating designs compared are Random, MC (minimum coancestory), Factorial, Hierarchal and MCAC (minimizing covariance of ancestral contributions).

Material and methods

Simulation: Stochastic simulations were carried out for 4000 founder generations with an effective population size of 1000 to create a base population as in (Nielsen *et al*. (2009), Sonesson and Meuwissen, (2009)), which will be called G0**.** A total of 5000 SNPs with 1000

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QTL were distributed over 10 chromosomes each of length 1 Morgan. SNPs were generated at a rate of 10^{-8} per base pair per meiosis, and the 1000 causative SNPs were chosen randomly amongst the SNP with minor allele frequency (MAF) > 0.05. The 5000 SNP markers were selected as the SNPs with the highest MAF. Sonesson and Meuwissen (2009) give details on how to create the True Breeding Value (TBV) for individuals and their genome-wide estimated breeding value (GWEBV; Meuwissen *et al.* (2001)) using BLUP and marker data.

A sib-test breeding design was simulated as it is commonly used in aquaculture where the trait under selection is recorded on sibs of the selection candidates. In each generation, parents obtained two sib groups as offspring, one group became selection candidates (size $\geq$ 1) and the other group became test-sibs. In total there were 200 selection candidates per generation, which were genotyped for the 5000 SNPs, and there were 1000 test-sibs, which were genotyped and phenotyped. In each generation, 10 males and 10 females were selected out of the selection candidates based on truncation selection for GWEBV, except in generation G0 from which sires and dams were randomly selected. The latter is because G0 animals did not have a known pedigree and thus did not have known (test) sibs. The selected breeding sires and dams were mated according to the following criteria: (i) hierarchical mating which in this case creates 10 full-sib families of size 20, a standard mating design for aquacultural species; (ii) factorial mating (Woolliams (1989)) which makes that every sire is mated to every dam and vice versa; (iii) minimum coancestry mating (MC), where matings are arranged such that the coancestry of the mating pairs is minimized and thus the inbreeding of the offspring is minimized; (iv) minimum covariance of ancestral contributions (MCAC; Henryon *et al.* (2009)) and (v) random mating as a control.

In each of the breeding schemes, we calculated genetic gain and level of inbreeding over all generations of selection at heritabilities of 0.01, 0.1, 0.4 and 0.9. The genetic gain and level of inbreeding calculated were average results over 100 replicates. Inbreeding was calculated based on the pedigree of the animals, where G0 animals were assumed to be unrelated.

Results and discussion

Levels of inbreeding and total genetic gain for a trait with heritability 0.4 are shown in Figure 1(A) and 1(B) respectively for all of the five breeding schemes. Results at 0.01, 0.1 and 0.9 heritabilities had the same pattern as in Figure 1(A) and 1(B) (results not shown). Inbreeding levels were substantially larger for the traditional hierarchical mating design (Figure 1(A)). Substantially less inbreeding was obtained by MCAC, random and factorial mating. Again smaller levels of inbreeding were obtained by MC mating. MC seemed to delay the inbreeding by about 1 generation. At generation 12 (G12), the approximate s.e. for accumulated gain was 0.74 and for accumulated level of inbreeding was 0.0038 (Table 1).

In this study the genetic gain per generation was highest with factorial mating. This could be probably due to effect of mating one sire with all dams, and vice versa, which decouples the contributions of sires and dams as much as possible. Initial genetic gain was also high for hierarchal mating, but this was reduced when the inbreeding started to accumulate.

Generally the alternative mating designs resulted in only minor differences in genetic gain and inbreeding although hierarchical mating increased inbreeding and MC mating delayed the inbreeding. A possible explanation is that GWEBV yield better predictions of the within family component of the EBV than traditional EBV, which reduces the relative importance of the between family component. As a result, these family structure based mating designs have a lesser impact than when genomic selection is used.

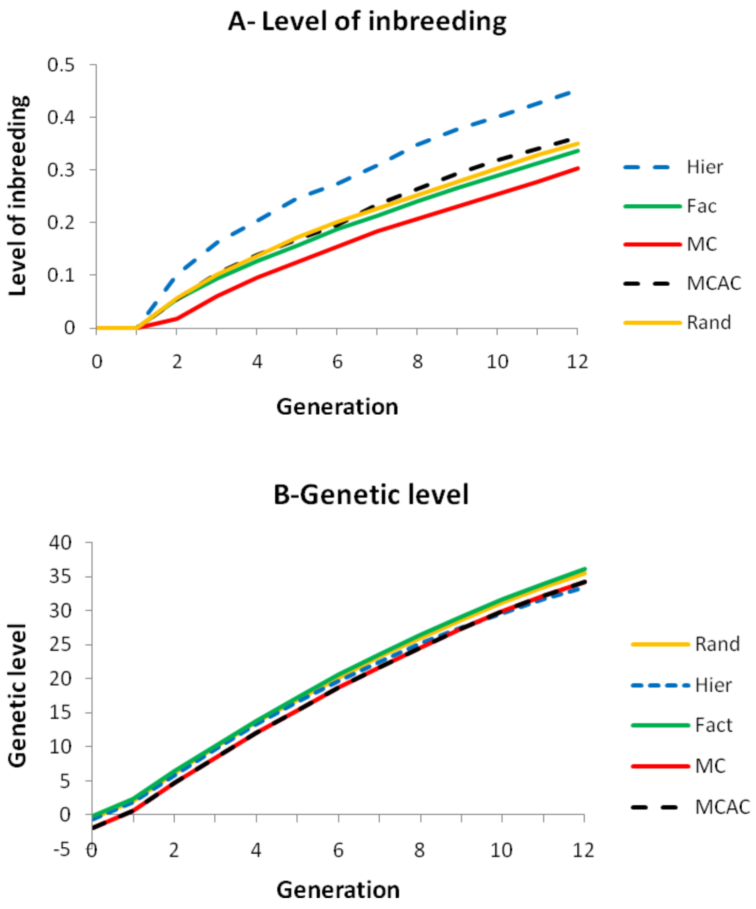

Figure 1. Level of inbreeding (A) and Genetic level (B) for simulated breeding schemes with trait heritability 0.4, Trunction GWEBV selection, and parent mating based on MC, Hierarchical, Factorial, Random and MCAC mating criteria.

Table 1. Standard error for Level of inbreeding and Genetic gain at generation 12, Trait heritability 0.4, Trunction GWEBV selection, and parent mating based on MC, Hierarchical, Factorial, Random and MCAC mating criteria.

Parameters	Random	Hierarchal	Factorial	MC	MCAC
Genetic Level (S.e)	0.776308	0.786183	0.765765	0.729034	0.640228
Level of inbreeding (S.e)	0.003634	0.007149	0.002998	0.002372	0.003062

Conclusion

Results show that the reduction in level of inbreeding was larger for breeding schemes with MC mating criteria than for the other mating methods, although the rate of inbreeding for factorial mating after the initial generation was similar. On the other hand, genetic gain was higher with factorial mating although the difference was small. Overall, non-random mating designs had smaller effects with genomic selection than has been reported for traditional breeding schemes. Novel mating schemes may need to be designed for genomic selection, that are less concerned with controlling the built-up of family structure, since family structure may play a less important role in the GWEBV than it was for traditional EBV.

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