Proc. Assoc. Advmt. Anim. Breed. Genet. 22:449-452

COMPARISON OF DIFFERENT BREEDING DESIGN OPTIONS FOR LONG TERM GENETIC GAIN AND DIVERSITY IN AQUACULTURE SPECIES

M.S. Khatkar[1,2], G.J. Coman[1,4], P.C. Thomson[1,3] and H.W. Raadsma[1,2]

[1]ARC Research Hub for Advanced Prawn Breeding
[2]Sydney School of Veterinary Science, Faculty of Science, The University of Sydney, Camden, NSW, Australia
[3]School of Life and Environmental Sciences, Faculty of Science, The University of Sydney, Camden, NSW, Australia
[4]Aquaculture Program, CSIRO Agriculture and Food, Queensland Bioscience Precinct, St. Lucia, QLD, 4067 Australia

SUMMARY

Using simulation, we compared the effect of different numbers of families and skewed distribution of family size on long-term genetic gain and inbreeding in aquaculture species. In particular we focused on *P. monodon* specific input parameters and communal rearing of families, and showed that large number of families in a communal breeding scheme are required for increased genetic gain and diversity in addition to mitigating the effect of unequal family contributions. We present a two-stage cost effective scenario implementing combining truncation selection and genomic selection, and showed that 1,000-2,000 animals in the first stage are required for long-term genetic improvement.

INTRODUCTION

The application of genetic markers and genomic selection (GS) in aquaculture is becoming attractive in particular for selection of 'difficult to measure traits' and traits which cannot be directly measured on candidates under selection, and to capture within- and between-family genetic variation. With decreasing cost of sequencing and genotyping the development of SNP panels and application of genomic resources can be rapidly deployed for almost any species, yet limited information is available on the results of practical implementation of GS and have mainly been restricted to the use of simulated data. Such studies demonstrated that GS in aquaculture breeding programmes can increase the accuracy of selection and genetic gains, both in production (continuous) and diseases (dichotomous) traits (Sonesson and Meuwissen, 2009; Nielsen *et al.*, 2011; Lillehammer *et al.,* 2013).

The number of families reared in aquaculture breeding programs is generally limited by the resources especially if the families are produced and reared separately, and this can have a profound impact on inbreeding and long-term genetic gains. More families can be managed if bred and reared communally. However, because of mass spawning the contribution of different families is unequal (Harris *et al*., 2016), and this can distort selection efficiency and hence genetic gain and inbreeding.

Using simulation, we explored the effect of number of families and unequal distribution of family size on the overall inbreeding and genetic gain on a growth-like trait and examined a cost effective scenario implementing a two-stage selection scheme by combining truncation selection and genomic selection.

MATERIALS AND METHODS

Simulated datasets were generated by QMSim simulation software (Sargolzaei & Schenkel, 2009) by specifying the following input parameters. The initial founder generation was the last of

1,000 historic generations, containing 400 random mating individuals each, equal to the effective population size of wild *P. monodon.* From this founder population, 1, 5, 50,100 or 200 males and 1, 5, 50, 100 or 200 females were used for breeding, with one male mated to one female, each mating producing 200 offspring in each generation. The genetic map of 40 chromosomes each 50 cM long was specified. For each chromosome, 120 biallelic markers and 30 biallelic QTLs were simulated. Mutation rate for both markers and QTLs were set to 2.5E-5 per generation. All the scenarios were simulated with heritability = 0.30 such that heritability due to QTLs = 0.2 and the remaining one third due to polygenic effects. The heritability used was comparable to that of body weight at harvest in shrimp (Sui *et al.,* 2016). The phenotypic variance was set to 1 with mean equal to 0 in the base population. Ten replications for each of the following scenarios were explored:

Scenario A: Single family of 200 progeny produced from the mating of one male with one female in each generation.

Scenarios B-E: Scenario B was generated with five families of 200 progeny each produced from the mating of one male with one female in each generation. Similarly, scenarios C, D and E were generated with 50, 100 and 200 families, respectively.

Scenario F: 100 families with each family producing different numbers of progeny. The numbers of progeny per family were simulated with a discrete probability distribution of 0.3 (n = 1) + 0.3 (n = 5) + 0.2 (n = 50) + 0.1 (n = 700) + 0.1 (n = 900) = 1, where n is the number of progeny. In addition a two-stage selection scheme was implemented. In the first stage different numbers of animals (200, 300, 600, 1000, 2000 or all) were selected randomly from the top 25% of all the animals in the pond, tagged and genotyped. In the stage 2, 100 males and 100 females were selected from the tagged animals based on genomic EBV assuming a selection accuracy of 0.6. For this scenario the phenotypic variance was set to 36 with a mean of 30 in the base population.

Selection Method: The selection of parents to produce specific number of families for the next generation was based on the EBVs, which as noted above had an accuracy of 0.6. Rate of genetic progress was calculated as the change in mean breeding values across generations. Estimates of inbreeding coefficient and mean breeding values were computed for each generation using pedigree information, and compared across ten generations for the scenarios described above.

RESULTS AND DISCUSSION

A comparison of mean inbreeding coefficient and mean phenotypic value after ten generations of selection is presented in Figure 1 which shows that a smaller number of families under selection resulted in increased inbreeding, in particular for single family selection inbreeding was approaching 90% after 10 generations of selection. Inbreeding coefficients based on 50 or more families were generally low (< 10%), and the difference in inbreeding between scenarios with 100 and 200 families was negligible. Rates of genetic gain were highest for using 100 families or more, whereas using single families or low number of families (< 5) resulted in the lowest rate of genetic gain.

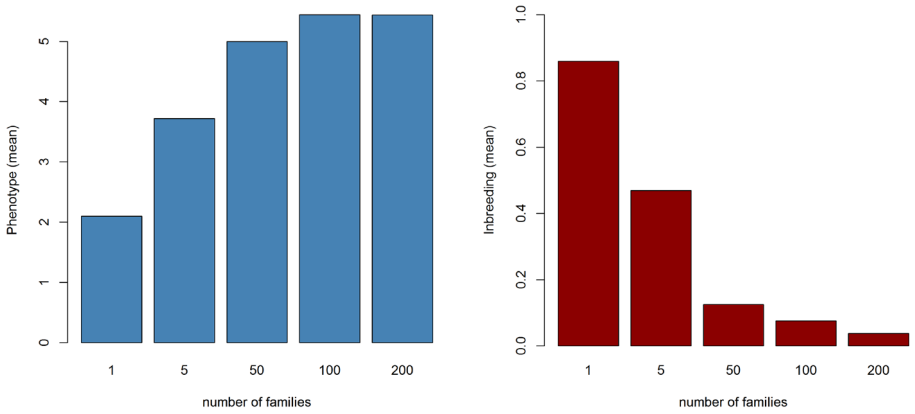

Figure 1. The effect of number of families on mean phenotypic values (A) and inbreeding coefficient (B) after 10 generations of selection (pooled across 10 replicates). Each family contributed an equal number of progeny (n = 200). (Scenario A-E)

Estimates of inbreeding coefficient and mean breeding values across ten generation and ten replicates for scenario D are presented in Figure 2. The replicates show a consistent increase in mean inbreeding and breeding value over generations. The differences between replicates were larger for scenarios with smaller numbers of families (results not shown).

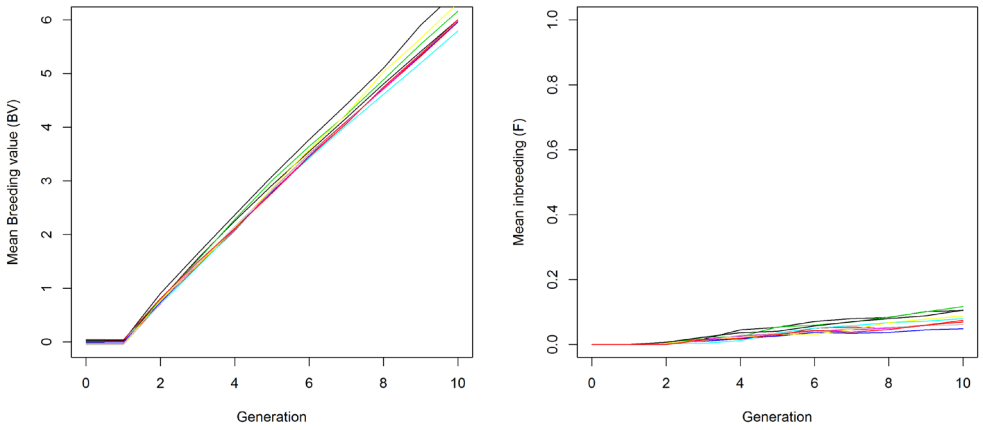

Figure 2. Mean breeding values (A) and inbreeding coefficient (B) over 10 generations of selection for scenario D. Ten replicates are shown by lines with different colours

Stage-wise selection: Scenario F presents a more practical situation where, due to mass spawning and differential survival, the contribution of different females (families) are unequal in communal breeding and rearing, with some families contributing a large proportion of the progeny *(Harris et*

al., 2016). In addition, to reduce the cost of genotyping, we implemented a two-stage selection by combining truncation selection based on phenotype (selecting randomly from the top 25%) in the first stage and selection based on EBV with moderate accuracy of 0.6 in the second stage. Figure 3 shows that selecting 1000-2000 animals in stage one with truncation selection provides most of the genetic gain possible with genotyping all the animals. Inbreeding increased only slightly with larger number of animals selected in the stage 1.

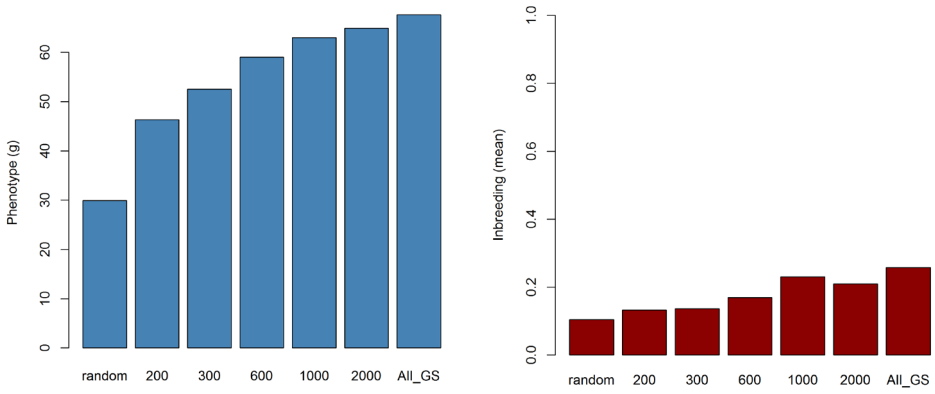

Figure 3. The effect of different number of animals (*x*-axis) in the first stage of two-stage selection scheme (Scenario F). "random" means selecting 200 randomly, "All_GS" selecting all in stage one

Compared to the scenarios with equal family contribution (presented in Figure 1), the effect of unequal family contribution was more pronounced when the smaller number of families were simulated (results not shown). There was a pronounced increase in inbreeding when the families' contributions are unequal. This is largely due to loss or low representation of families in the subsequent generations.

REFERENCES

Harris, L., Sellars, M., & Perez, F. (2016). Aquaculture International, 24(1), 273-279.
Lillehammer, M., Meuwissen, T. H., & Sonesson, A. K. (2013). Genet Sel Evol, 45, 39.
Nielsen, H. M., Sonesson, A. K., & Meuwissen, T. H. (2011). J Anim Sci, 89(3), 630-638
Sargolzaei, M., & Schenkel, F. S. (2009). Bioinformatics, 25(5), 680-681.
Sonesson, A. K., & Meuwissen, T. H. E. (2009). Genetics Selection Evolution, 41.
Sui, J., S. Luan, K. Luo, X. Meng, X. Lu, B. Cao, W. Li, Z. Chai, N. Liu, S. Xu and J. Kong (2016). Aquaculture Research, 47(9), 2795-2803.