# **Prediction Of Rates of Genetic Gain and Inbreeding From Different Breeding Strategies In Pacific Oysters**

S. Dominik\*, P. Kube<sup>†</sup> and J. Henshall\*

# Introduction

Following the disease related collapse of the Sydney Rock oyster industry in 2006 (Nell, 2007) prevention of disease outbreak is one of the primary objectives of commercial oyster breeding programs in Australia. To reduce disease risk, breeding programs select individuals within population, and there is a need to design the breeding program so that high rates of genetic gain are achieved while maintaining acceptable rates of inbreeding. The effects of inbreeding manifest themselves in decreased genetic variation and inbreeding depression, resulting in decreased production, in particular in reproductive and fitness characteristics (Falconer and Mackay, 1996). Evans et al. (2004) reported on inbreeding effects in Pacific oysters even amongst crosses of distantly related parents in yield, individual growth rate and survival. The objective of the current study was to develop a breeding strategy for a commercial breeding program by stochastically simulating and comparing breeding strategies with different population sizes, different numbers of related individuals selected and breeding programs with discrete year classes versus those where a percentage of matings were used to link year classes.

# Material and methods

Computer simulation. Breeding program strategies were simulated using stochastic simulation software written in Fortran. A polygenic model was assumed with progeny genotypic merit simulated as the mean of the parents' genotypic merit plus a random Mendelian sampling term drawn from a normal distribution. An environmental effect was sampled from a normal distribution with mean zero and variance equal to the environmental variance. The simulation commenced with a number of founder animals, assumed to be unrelated. For all animals complete pedigree was maintained. Neither dominance effects or effects for inbreeding depression were simulated, all effects were additive.

**Breeding program structure**. Starting from an unrelated base population, parents were chosen at random over 10 years to produce a starting population for the breeding program simulation. Parents were selected at three years of age on a weighted mean of own phenotype and family mean phenotype. To limit inbreeding, pedigree information was used to control the distribution of the animals selected to be parents of the next generation across families. In the simulations the number of males and females selected from each family was capped by

<sup>\*</sup> CSIRO Livestock Industries and Food Futures Flagship, Armidale, NSW 2350, Australia

<sup>&</sup>lt;sup>†</sup> CSIRO Marine and Atmospheric Research and Food Futures Flagship, Hobart, TAS 7001, Australia

selecting a restricted number of full-sibs per family. The breeding program was simulated for 15 years of selection and various breeding strategies applied. Each strategy was simulated 50 times and the mean results were stored. A commercial Pacific oyster breeding program was modeled with a mating ratio of 1 male to 1 female, 800 progeny of each mating are measured for economically important traits. Animals are selected on a composite trait reflecting the breeding objective. In addition to the selection candidate's own phenotypic records, the family mean was included in estimating the merit of the individual for the composite trait. The heritability of the composite trait was assumed to be  $h^2 = 0.3$  and the coefficient of variation CV = 0.25.

**Breeding program strategies.** Seventeen breeding program strategies were tested. They investigated 1) the effect of varying population size as defined by the number of families, 2) the effect of the maximum numbers of full-sibs selected per family as a tool to control inbreeding and 3) breeding programs with discrete year classes were compared to breeding programs that link year classes genetically. Genetic linkage across years enables more accurate genetic evaluation. Of interest in this study was the effect of deliberately using an increased proportion of related animals on inbreeding. Each simulated breeding strategy was identified by a code (Table 1), which is a concatenation of numbers of families, numbers of full-sibs selected per family and, for some, the percentage of matings used to link year classes (genetic linkage (GL) with 10% or 15% of matings). Strategy 24-4GL10 with 24 families, a maximum of four full-sibs selected and genetic linkage of year classes with 10% of the matings characterized the an early commercial breeding program.

Table 1: Simulated breeding program strategies with varying numbers of families (PopSize), varying maximum number of fullsibs per family selected (Max FS) and varying percentage of genetic links (GL)

Strategy	PopSize	Max FS	GL (%)
24-4	24	4	0
30-4	30	4	0
30-6	30	6	0
30-8	30	8	0
30-10	30	10	0
40-4	40	4	0
40-6	40	6	0
40-8	40	8	0
40-10	40	10	0
50-4	50	4	0
50-6	50	6	0
50-8	50	8	0
50-10	50	10	0
24-4GL10	24	4	10
24-4GL15	24	4	15
50-8GL10	50	6	10
50-8GL15	50	6	15

#### **Results and discussion**

Genetic gains. The genetic gain ( $\Delta G$ ) in the index over 15 years of selection was high for all breeding strategies, ranging from 58% to 67% (Table 2). This was due to high selection intensities applied in all breeding strategies. As described in the breeding program structure each family produces 800 progeny which are available for selection and only 48 to 100 parents are required to create 24 to 50 families. The high selection intensities allowed selection of the very best candidates. If selection of individuals from the best performing families was restricted (lower numbers of full-sibs selected per family), selection intensities and consequently  $\Delta G$  dropped slightly, but remained high (Table 2). Even though differences were small,  $\Delta G$  increased slightly with increasing size of the breeding population (Table 2).

Table 2: Rate of genetic gain ( $\Delta G$ ) for the index over 15 years of selection and average rate of inbreeding per generation ( $\Delta F$ )

<b>Breeding strategy</b>	$\Delta G$ (in $\sigma_G$ )	ΔF (in %)
24-4	0.51	1.30
30-4	0.52	1.08
30-6	0.55	1.66
30-8	0.56	1.98
30-10	0.57	2.38
40-4	0.52	0.82
40-6	0.55	1.28
40-8	0.58	1.64
40-10	0.58	1.78
50-4	0.52	0.66
50-6	0.56	1.05
50-8	0.59	1.44
50-10	0.59	1.55
24-4GL10	0.52	0.88
24-4GL15	0.52	0.94
50-8GL10	0.59	0.96
50-8GL15	0.58	0.96

Rate of inbreeding. The different breeding strategies resulted in important differences in the rate of inbreeding ( $\Delta F$ ). As a general rule 1% per generation is the upper threshold of an acceptable  $\Delta F$ , if the aim is to create a long-term sustainable breeding population. Table 2 shows that  $\Delta F$  was influenced by the population size as well as the numbers of related animals that are selected.  $\Delta F$  decreased with increasing population size because the scope to select superior unrelated individuals between families was higher.  $\Delta F$  increased with increasing numbers of full-sibs selected, but this trend was less pronounced with more families in the population because of the increased flexibility to select unrelated animals. This means more full-sibs can be selected with increasing population size to achieve the same  $\Delta F$ .

The lowest  $\Delta F$  of 0.66% resulted from the breeding strategy 50-4 with the largest number of families and least number of full-sibs selected. Inbreeding rates well below 1% suggest that the breeding strategy is conservative and more related animals could be selected to increase genetic gains if  $\Delta F$  remains below 1%. Therefore 50-6 is considered the best balanced strategy with  $\Delta F$  around 1% and slightly higher  $\Delta G$  than 50-4. Breeding strategy 40-4 is another scenario that kept inbreeding at an acceptable level and is a cheaper and easier to manage strategy to implement in the hatchery. All other breeding strategies resulted in  $\Delta F$  higher than 1% with one breeding strategy even yielding more than twice the 1% threshold. In the strategy with 24 families and selection of a maximum of four full-sibs per family,  $\Delta F$  was 1.3% per generation. Even though in that strategy the numbers of full-sibs selected were conservative in relation to inbreeding, the population size was too small to keep  $\Delta F$  below the recommended threshold.

Discrete vs genetically linked year classes. Two breeding program strategies were simulated with discrete year classes and with genetically linked year classes (24-4GL10/GL15 and 50-8GL10/GL15). The simulations showed that breeding strategies with genetically linked year classes produce lower  $\Delta F$  compared to strategies with discrete classes (Table 2). This result may seem surprising, but can be explained by the two year generation interval, which literally creates two separate unrelated populations if year classes are not genetically linked. The use of siblings of previous year's broodstock in matings to genetically link years introduces unrelated individuals and as a consequence reduces  $\Delta F$ . The effect on  $\Delta F$  was initially pronounced, but decreased with time. Genetically linking year classes can potentially reduce  $\Delta F$  in the medium term to an acceptable level. However, linking year classes by more than 10% of matings has little benefit (Table 2).

# Conclusion

Stochastic computer simulation showed that if year classes have been unlinked, the use of related individuals that provide genetic links between years can reduce the rate of inbreeding to an acceptable level that is sustainable in the short to medium term. High genetic gains can be achieved, irrespective of the numbers of families and numbers of full-sibs selected, through the high selection intensities that can be applied in oysters and aquaculture species in general. However, larger population sizes provide more flexibility in selecting superior animals within or across families without increasing the rate of inbreeding. Therefore, to achieve long term sustainability in a commercial oyster breeding program a population size of 40 to 50 families is recommended.

#### References

- F. Evans, S. Matson, J. Brake and C. Landon (2004). Aquaculture 230 (1-4): 89 98.
- D.S. Falconer and T.F.C. Mackay (1996). In *Introduction to quantitative genetics*, Longman, England, pages 247 262.
- J. Nell (2007). Primefacts 589, July 2007, NSW DPI, Australia.