SELECTIVE BREEDING FOR IMPROVED SURVIVAL TO JUVENILE PEARL OYSTER MORTALITY SYNDROME IN SILVER LIPPED PEARL OYSTER, *PINCTADA MAXIMA*

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SUMMARY

Juvenile pearl oyster mortality syndrome (JPOMS) causes mass-mortality of young pearl oysters impacting the production and financial revenue of farms. The use of selective breeding to improve survival is an effective solution to reduce impact, especially in the case of a poorly understood disease such as JPOMS. Here, we investigate the potential of implementing a selective breeding program for increased survival to JPOMS in the silver lipped pearl oyster, *Pinctada maxima*. Simulation results show that significant increases in survival could be achieved if selective breeding was applied (8% increase in survival per generation). Attention should be paid to balance genetic gain (increase of survival) and diversity to limit inbreeding where individuals are selected on their family mean.

INTRODUCTION

The revenue from Australian pearl production has dramatically reduced from AU$ 144 million in 2010, to AU$ 70 million in 2017 (ABARES, 2018). Part of the decline can be explained by the recurrence of mass-mortality of juvenile stocks, which severely reduces the number of oysters that are cultured to pearl seeding sizes. Repeated observations of mass-mortality have been reported over the last decade, but the actual pathogenic agent/s causing this juvenile pearl oyster mortality syndrome (JPOMS) is yet to be identified. Due to the limited knowledge on the actual causative agent, no treatment exists to this day. While the in-depth knowledge of the disease is extremely important for the Australian pearl industry, the process of unravelling the causative agent of JPOMS is non-trivial and time consuming.

Selective breeding for disease resistance (or survival) is increasingly becoming a primary selection trait in aquaculture (Gjedrem 2012; Houston 2017) and offers a practical alternative when little information about the causative agent of the disease is known. In the last few years, hatchery technology has been refined in pearl farms which permits broodstock selection and, to some degree, the control of family contribution to progeny cohorts. The advantage of the use of selective breeding to increase survival is that improvement can still be achieved even though understanding of the disease is limited.

To explore the potential of selective breeding focused on JPOMS survival, we simulated a breeding program under various parameters (family size, family number, selection methods) for 20 years. The mode of selection used for JPOMS survival is based on breeding value for survival per half-sib family and can potentially lead to high level of inbreeding. This study focus on the impact of restriction of selected individuals per half-sib family on the genetic merit and inbreeding generated by such breeding program.

MATERIALS AND METHODS

The simulated breeding program was run for 20 years which corresponded to 10 generations of the target species, the silver lip pearl oyster (*Pinctada maxima*) which becomes sexually mature around 2 years of age. The base scenario uses 100 males mated to 200 females. All individuals in the base generation are unrelated. Each female produced 100 offspring (which corresponds to 100 offspring per full-sib family and 200 offspring per half-sib family). Survival is recorded as an average per family. Under the current farm setting, it is not possible to obtain survival data per individual. The oysters, at this stage, are usually attached in panel nets on long-lines suspended in the ocean for the grow-out period and it is difficult to keep track of individual performance throughout the entire grow out phase. However, average of survival per half-sib family, after genotyping individuals before and after a JPOMS event, can be determined. Half-sib families were ranked according to their family mean survival and a maximum of 10 males and 20 females per half-sib family were taken as selection candidates from the best families until a total of 250 males and 500 females were selected. Families had unequal sizes due to mass mortality, in particular at the beginning of the breeding program. The best ranking families were also the largest families. Therefore, the number of families represented among the selection candidates was variable and decreased as the breeding program continued and the mortality decreased. From these selection candidates, 100 males and 200 females were selected and mated, half-sib and full-sib mating were not allowed.

Unfortunately, at this stage, actual estimates for heritability of PJOMS are currently in the process of being calculated and are not yet known. Heritability of survival is usually low and varies between 0.06 and 0.16 in aquaculture (Gjedrem and Olesen, 2005) and a review of selective breeding for disease resistance in oyster by Degremont *et al*. (2014) shows that heritability is scarcely reported (expect for summer mortality in Pacific oysters), therefore, we chose a conservative heritability of 0.1 at the start of the breeding program for the subsequent simulations. Breeding program simulations were run to explore the impact of the number and size of families and the maximum number of males and females selected per family (see Table 1). For all scenarios, the disease killed 90% of the reared progeny in the first generation and then occurred every subsequent generation. All scenarios were replicated 100 times.

Selective breeding scenarios were assessed using the cumulative genetic gain of survival of PJOMS (designated as the proportion of survival), the accuracy of breeding values (calculated from survival family mean) and rate of inbreeding per generation. The genetic gain of generation *t* was the difference of the average survival family mean between generation *t* and generation *t-1*. The rate of inbreeding was calculated as follow:

$$\Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}}$$

with F_t the average of inbreeding coefficient for a generation, *t* the current generation.

Table 1. Description of selection parameters used for the various simulated scenarios

Simulated scenario	# families	Half-sib families size	# sires / # dams selected / family
1	50	200	10 /20
2	150	200	10 /20
3	100	100	10 /20
4	100	300	10 /20
5	100	200	5/10
6	100	200	No restriction

RESULTS AND DISCUSSION

The cumulative genetic gain, accuray and rate of inbreeding in the base scenarios are shown in Figure 1 (black lines). After 10 generations of selection, survival had reached 75% and rate of inbreeding stayed under the acceptable limit of 1% per generation. This simulation showed that the South Sea pearl industry could benefit from implementing selective breeding for survival to JPOMS..

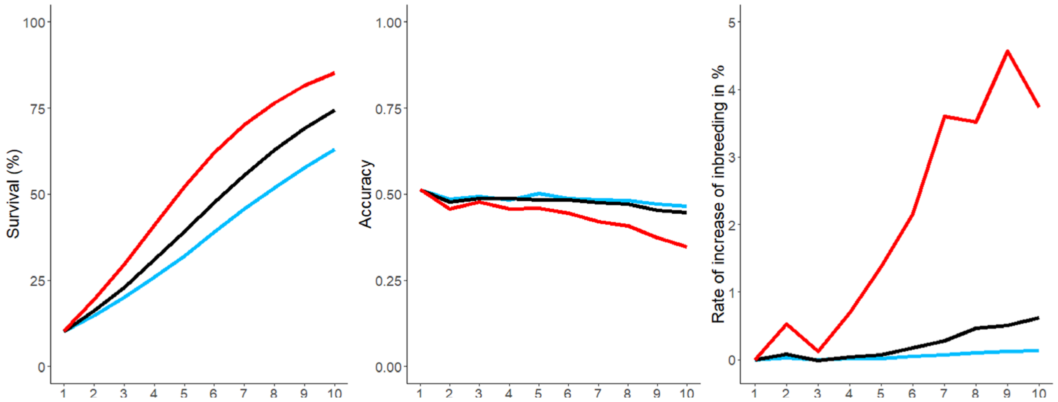

Figure 1. Proportion of survival (left), accuracy of breeding values (middle) and rate of increase of inbreeding (right) as a function of the number of sires and dams selected per families

There were no major differences in survival, accuracy of breeding program and rate of inbreeding when varying the number of families used or the family size. However, large impacts on genetic parameters were observed when varying the number of sires and dams selected per family (Figure 1). We observed an increase in survival as well as an increase in rate of inbreeding associated with an increased number of males and females selected per family. Both scenarios that included a restricted number of males and females per family as selection candidates had an acceptable rate of inbreeding (rate of inbreeding increase < 1%). However, decreasing the number of males and females selected per family as selection candidates also reduced the genetic gain with regard to survival (60% survival with 5 males and 10 females selected per family compared to 75% survival with 10 males and 20 females selected per family at generation 10). In the instance where there was no restriction on the maximum number of males and females selected per family (i.e. selecting whole families, red line in Figure 1), the survival rate reached 85% after 10 generations of selection, which is substantially higher than for the basic scenario (75%). However, this scenario also led to the highest rate of inbreeding (>4%), which will result in a higher number of matings between relatives at each generation and a likely increase in inbreeding depression in the long term.

The number of males and females per family that were used as selection candidates played a key role in the success of the simulated breeding program for pearl oysters. At the beginning of the breeding program, when survival was at 10%, families had few offspring survive. Therefore, to reach the goal of 250 male and 500 female selection candidates, a large number of families was required (around 20% of families under the base scenario with 5 males and 10 females maximum selected per family). With a maximum of 10 males and 20 females used per family, the average proportion of family selected was 10% (scenario 5), while with no restriction on the number of males and females used per family, selection candidates were coming from only 3% of the families (scenario 6). In the latest scenario, selection candidates were generated from only 3 families and therefore the number of related of individuals was very high and increase of inbreeding was therefore inevitable. Additionally, as selection on survival was performed, the proportion of survival increased and a larger number of offspring survived per family, which decreased the number of families selected per generation and increased the chances of mating among related individuals. This highlights the importance of balancing genetic gain and the maintenance of family-specific genetic diversity.

Survival to JPOMS under the base scenario would result in an increase of genetic gains of 7% per generation over 10 generations and by 6% at the first generation (from 10% at generation 1 to 16% at generation 2). These results are in line with those reviewed by Gjedrem (2012) for various species and diseases. Elston *et al*. (1987) reported a 73% survival increase between non-selected and selected individuals over a period of 4 to 10 generations of selection for resistance of *Bonamia ostrea* in European flat oyster (*Ostrea edulis)*, similar to the 64% increase in our simulation, over 10 generations.

The case of disease resistance to JOD in the eastern oyster *Crassostrea virginica* is of particular interest for this study as it demonstrated the benefit of selective breeding (increase of 85% survival in 2 generations) for a disease that primarily affects juveniles, like JPOMS, and that exhibits similar characteristics to it. Therefore, we can expect that the implementation selective breeding for survival to JPOMS will result in significant improvement of survival.

CONCLUSION

This study shows that implementing selective breeding for JPOMS in *P. maxima* could theoretically be very beneficial for the South Sea pearl industry and the predictions of genetic gain and rate of inbreeding for the basic scenario are in accordance to reported gains of selective breeding for disease resistance in other oyster species. However, attention should be paid to maintaining genetic diversity as well as improving survival, as the rate of genetic gain was also linked to higher inbreeding.

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