Genetic risk of stocking on fishes having environmentally influenced sex-determination

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Sex determination of many fish species is influenced by environmental variables. For example, Japanese flounder has male heterogametic sex determination (XX female - XY male) but XX juveniles can develop to become functional males depending upon environmental conditions. Environmental variables such as temperature, salinity and/or pH reverse a genetically determined sex against genetic sex as sex-reversal. If such a species is involved in a stocking operation, the sex-reversal ratio between wild and hatchery reared juveniles may be different, and there is a risk that the gene for sex determination may be eliminated. We have evaluated conditions for the elimination of the sex determination gene for Japanese flounder and discussed how we can reduce such a risk (Kanaiwa & Harada 2002). In this paper, we extend the analysis to more general situations with both one locus-two allele and environmental sex determination.

We construct the one locus-two allele, *A* and *B*, population genetics model. We consider the scenario for which environmental variables make only a one way sex change from genetic sex: i.e., either genetic female or male alone changes to reversed sex by environmental variables. First, we evaluate the condition for the elimination of one of two genes for sex determination when there is no stocking operation. Then, we evaluate the condition for the elimination of one gene for sex determination in the presence of a stocking operation.

When there is no stocking enhancement, we need to consider four cases (Table 1). For case 1, A allele will be eliminated if " $\gamma < 0.5$ & $\beta < \gamma$ " or " $\gamma > 0.5$ & $\beta > \gamma$ " and B allele will never be eliminated. For case 2, A allele will be eliminated if $\gamma < 0.5$ and B allele will be eliminated if $\alpha < 0.5$. For cases 3 and 4, elimination is impossible. These results show that there is a risk that the environmental change may eliminate genes for sex determination.

	AA	AB	BB
Case 1	1	β	γ
Case 2	α	0	γ
Case 3	α	0	0
Case 4	1	β	1

Table 1

Probability of having each genotype for one sex (female or male) in the absence of stocking operation. In the presence of a stocking operation, we need to consider four cases, of which two can lead to the elimination of genetic sex determination (Table 2). We consider three scenarios on how the hatchery broodstock is prepared. For scenario 1, broodstock is the hatchery produced fish in successive generation. For scenario 2, broodstock is the fish randomly collected from a wild population without discriminating hatchery released fish. Scenario 3 considers using only individuals born in the wild for broodstock.

		AA	AB	BB
Case 5	Wild	1	β	γ
	Hatchery	1	β '	γ'
Case 6	Wild	α	0	γ
	Hatchery	α'	0	γ'

Table 2
Probability of having each genotype for one sex (female or male) in the presence of a stocking operation.

Due to the limited space, we can only show the results for the cases where there is no sex reversal in the wild (i.e. β and γ of case 5 are 0 and α and γ of case 6 are 1). For case 5, B allele can never be eliminated in any scenario but A allele can be eliminated in scenario 1 when " $\gamma' < 0.5$ & $\beta' < \gamma'$ " or " $\gamma' > 0.5$ & $\beta' > \gamma'$ " and for scenario 2, it can be eliminated when " $\gamma' < \beta'$ & $r > \frac{1}{2\gamma'}$ ". Here r shows the relative contribution rate of hatchery fish to recruitment. For case 6, in scenario 1, A allele can be eliminated when " $r > \frac{1}{3-2\gamma'}$ & $\gamma' < \frac{1}{2}$ " and β allele can be eliminated when " $\gamma' > \frac{1}{3-2\alpha'}$ & $\gamma' < \frac{1}{2}$ ". In this scenario, if one allele is eliminated accidentally in hatchery (e.g. by genetic drift), the condition " $\gamma' < \frac{1}{2}$ or $\gamma' < \frac{1}{2}$ " becomes unnecessary. For scenario 2, $\gamma' < \frac{1}{2}$ allele can be eliminated when $\gamma' > \frac{1}{2(1-\gamma')}$ and $\gamma' < \frac{1}{2}$ and $\gamma' < \frac{1}{2}$ becomes unnecessary. For scenario 2, $\gamma' < \frac{1}{2}$ allele can be eliminated when $\gamma' > \frac{1}{2(1-\gamma')}$ and $\gamma' < \frac{1}{2}$ becomes unnecessary. For scenario 2, $\gamma' < \frac{1}{2}$ and $\gamma' < \frac{1}{2}$ becomes unnecessary. For scenario 2, $\gamma' < \frac{1}{2}$ and $\gamma' < \frac{1}{2}$ becomes unnecessary. For scenario 2, $\gamma' < \frac{1}{2}$ and $\gamma' < \frac{1}{2}$ becomes unnecessary. For scenario 2, $\gamma' < \frac{1}{2}$ and $\gamma' < \frac{1}{2}$ becomes unnecessary. For scenario 2, $\gamma' < \frac{1}{2}$ and $\gamma' < \frac{1}{2}$ becomes unnecessary. For scenario 3.

From these results, we can argue that there are some genetic risks to the sex-determining system by releasing sex-reversed individuals, considering that environmentally influenced sex determination may be rather common in fishes. We can also argue that such a risk increases in scenario 1 with a stocking operation. To reduce these risks, it is useful to use individuals born in the wild as parents for hatchery production. If we cannot employ scenario 3, we need to have a better understanding of the sex determination system for each target species of the stock enhancement program.

Kanaiwa, Minoru and Yasushi Harada. 2002. Genetic risk involved in mass release of fishes having environmental sex determination. Population Ecology 44: 7-15.