

Assemblage of pairs of spawners based on their individual genetic profiles as a tool in managing genetic variation in salmonid fish stocks

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Project addresses relationship between the level of genetic variation and the growth rate and survival of fish in a specific stock under aquaculture conditions.

Examination of a number of microsatellite DNA (msatDNA) loci in a mature fish (spawners) results in individual genetic profile of each fish. By assembling the appropriate pairs of spawners one

can obtain groups of their progeny differing in heterozygosity and allele richness. Revealing correlation between the level of genetic variation and the viability of fish stock was the goal of this project.

The experiment is conducted on rainbow trout (*Oncorhynchus mykiss*), an important species in freshwater aquaculture, well adapted to breeding and rearing under the aquaculture conditions.

OBJECTIVES

1. To assemble pairs of spawners based on their individual genetic profiles in order to reach a desired change (increase or decrease) in the genetic variation in their offspring (as compared to the genetic variation in the stock of spawners' origin).
2. To assess the influence of increased and decreased genetic variation of the stock on the viability of the fish, measured as their survival and growth rate, which are features critically important in aquaculture.

EXPERIMENT

Aquaculture activity is performed in the salmonid breeding and rearing centre in Rutki near Gdansk, Poland, and genetic examinations are performed in the Department of Environmental Biotechnology, University of Warmia and Mazury in Olsztyn (UWM), Poland.

Spawners of rainbow trout, 31 females and 31 males, were tagged and the sample of fin tissue was taken from each fish. Nuclear DNA was extracted from each sample, polymorphism of 12 microsatellite loci was measured and the heterozygosity and allelic richness of the broodstock was evaluated. Then individual genetic profile of each spawner was determined as the list of msatDNA alleles detected in each investigated fish. Genetic profiles were applied in calculating expected heterozygosity and allelic richness in the progeny of each potential pair of spawners.

Four pairs of spawners were chosen which secured highest heterozygosity and allelic richness of their progeny, and three pairs of spawners were assembled in order to secure lowest heterozygosity and allelic richness of their progeny. Each experimental group was divided into two equal subgroups, which were incubated and reared under the same aquaculture conditions.

Rearing of fish lasted 6 months, and during this time the fish growth rate and survival were monitored. When the fish reached 60-80g body weight the fragments of their fins were taken for the msatDNA analysis (altogether 350 samples).

The results of this project will provide knowledge on how to make correct decisions concerning assembling pairs of fish spawners in order to optimize genetic variation in their offspring and how to implement this technique in the conservation programs of hatchery depended fish species.

The practical output of this project will be expanded by developing the software applicable in estimation of expected heterozygosity and allelic richness in the groups of progeny obtained from various combination of individual female and male spawners. This in turn will secure best use of genetic properties of spawners available from a given broodstock. The software will be available free of charge from the server of UWM in Olsztyn, Poland.

Educational impact of this study is achieved by carrying genetic experimental work by Engineer and Master of Science students.

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