

Fishing for genes that affect efficiency of gynogenesis in rainbow trout (*Oncorhynchus mykiss*)

Sexual reproduction is the most common type of reproduction mode among animals. It is based on males and females producing respective haploid gametes which fuse and become a diploid zygote. Gynogenesis is a reproductive mode with offspring that inherit only maternal chromosomes. Gynogenesis has been reported in small number of invertebrates, fish and amphibians.

Gynogenetic development can be induced artificially under controlled conditions. In fish, such processes require activation of eggs with UV-irradiated spermatozoa. Haploid set of maternal chromosomes is doubled by interruption of the first cleavage of the zygote. For this purpose, haploid embryos are exposed to environmental shock (e.g. high hydrostatic pressure or sublethal temperatures) after DNA replication but before karyokinesis. Environmental shock results in the spindle depolymerisation, prevents chromosome segregation and leads to duplication of the maternal set of chromosomes. Provided specimens are fully homozygous gynogenetic Doubled Haploids (DHs). Such embryos are useful in research regarding phenotypic consequences of recessive alleles, functions of particular genes and tumorigenesis. Doubled Haploids are especially useful in research in the field of gene mapping and genome sequencing. Gynogenesis has been applied in selective breeding programs in order to produce all-female stocks of fish and specimens with the desired breeding traits. Unfortunately, high mortality of the gynogenetic fish limits their use in practice. Only a small number of gynogenetic specimens hatch and survive till the swim-up stage (less than 15%), and only few of such individual reach sexual maturity. Increased mortality of the gynogenetic DH fish results mostly from expression of the recessive alleles.

However, results of our recent research exhibited that eggs from some females of rainbow trout show increased potential for efficient gynogenesis. Transcriptome analysis of maternal RNA in eggs with different ability for gynogenetic development displayed significant differences in expression of some genes related to cell migration, development, metabolism of triglycerides, biosynthesis of polyunsaturated fatty acids and senescence and aging. Thus the main goal of the present research is identification of genes which expression increase gynogenetic developmental capacity of rainbow trout eggs. The research will include application of RNA-seq analysis followed by q-PCR verification of obtained results. We already know that eggs show inter-clutch differences in ability for gynogenetic development, now we need to find genetic differences between such eggs. Knowledge about genes that expression affect efficiency of gynogenesis will enable to provide genetic markers that application let for choosing females that eggs have increased ability to develop after gynogenetic activation. Due to this discovery we will increase efficiency of the process and make it applicable in studies from varied fields including developmental biology and production of homozygous and clonal lines of rainbow trout. Moreover, results provided within this project will help to better understand molecular basics of different modes of vertebrate reproduction.