Populations of sea trout *Salmo trutta* m. *trutta*, cod *Gadus morhua* L. and mussels *Mytilus* spp. from the Baltic Sea were studied using SNPs (single nucleotide polymorphisms) genotyping methods, next generations sequencing, gene expression using HRM (RT-PCR) and 44K-oligo microarray.

### SEA TROUT

#### Genotyping of nine Baltic populations of sea trout

South East Baltic populations (from Poland, Lithuania, Denmark: Bornholm, Estonia and Russia) were genotyped with iPLEX Gold Sequenom method using a diagnostic panel of 23 SNPs. The highest level of genetic differentiation was observed between eastern populations from East Gulf of Finland and Polish populations from the Baltic Main Basin and the lowest differences were between the both Polish, and Polish and Lithuanian populations.

**Genetic differentiation**


**Genetic structure analysis**

The NJ tree constructed using the Nei’s distances among the nine sea trout populations.

**454 pyrosequencing**

Selected transcripts putatively involved in immune response, by using 454 pyrosequencing technology were studied in Vistula river specimens. A total of 1,440,373 reads were obtained with the average read length 334 nucleotides. At present, 3 groups of genes were identified: *Mx*, *C7* and MHC.

**44K-oligo microarray**

Differences in gene expression in hatchery *Salmo trutta* m. *trutta* and *Oncorhynchus mykiss* under stress caused by infection with a bacterial pathogen *Aeromonas salmonicida* spp *salmonicida* and non-infected were observed. Some genes were up-regulated (chaperones, mainly HSPs, *Mx*, interleukin IL17A and proinflammatory cytokine) and down-regulated (acute phase proteins, chemokines, cytokines, COX, lectins, lectin receptors and inflammation related proteases, TNF-related and apoptotic proteins and other) as found by the application of transcriptome hybridisations to 44K, oligo-microarray.

### COD

Populations of Baltic cod were studied using 5 SNPs. According to the obtained HRM (high resolution melting) results populations of the cod were characterized by clinal variation of alleles at loci known to be linked with salinity gradient. The obtained results confirm that eastern population of cod is a separate one.

Exposure of cod from western (Kiel) and southern (Gdansk) Baltic to different salinity ranging from 3 to 33ppt. revealed its high tolerance to different environmental conditions. This tolerance is being studied at the level of gene expression and high number of SNPs.

### MYTILUS SPP.

Baltic populations of *Mytilus* spp. are locally adapted, with a unique composition of loci derived from *M. trossulus* and *M. edulis* genomes. To identify markers and genes associated with the hybrid zone in Danish Straits and to determine the uniqueness of Baltic populations, 60 polymorphic SNPs were used to genotype individual mussels from the Baltic, North Sea and Canada. In total 35 SNPs turned out to be significant in FST outlier analysis and therefore were clearly related to the interactions with environment. The majority of new SNPs show greater participation of *M. trossulus* than *M. edulis* genes in the nuclear DNA of Baltic *Mytilus*.

#### Correspondence analysis (CA) of Mytilus populations from Baltic Sea region and Canada.

The locations and acronyms of 23 European *Mytilus* sampling sites. Structure results for the populations for K = 3 are presented in pie diagrams. These proportions are Q values.