

GENETIC RESOURCES OF FISH AND SHELLFISH POPULATIONS IN THE SOUTHERN BALTIC SEA

Roman Wenne¹, Anita Poćwierz-Kotus¹, Agnieszka Kijewska¹, Magdalena Warzecha¹, Aleksei Krasnov², Małgorzata Zbawicka¹, Matthew Peter Kent³ and Sigbjørn Lien³

¹ Institute of Oceanology, Polish Academy of Sciences, Powstancow Warszawy 55, 81-712 Sopot, Poland

E-mail: rwenne@iopan.gda.pl

² Nofima Marin, PO Box 5010, Ås 1430, Norway

³ Centre for Integrative Genetics, Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, N-1432 Ås, Norway

Populations of sea trout *Salmo trutta* m. *trutta* L., cod *Gadus morhua* L. and mussels *Mytilus* spp. from the Baltic Sea were studied using SNPs (single nucleotide polymorphisms) genotyping methods in order to characterize their genetic differentiation. Sea trout, a migratory form of brown trout is represented by numerous populations in the Baltic Sea. Many populations are enhanced by releases of artificially reared alevins and smolts (supportive breeding). South East Baltic populations of migratory (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 pairwise Fst differences was observed between Russian population 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 differences were found between 2 closely related *Salmo trutta* m. *trutta* populations in Poland by genotyping using an Atlantic salmon derived custom design Illumina iSelect SNP-array (Drywa *et al.*, 2013). 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. 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 IL17D a 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 (Agilent).

Populations of cod were studied using 5 SNPs. According to the obtained HRM (high resolution melting) results populations of the Baltic 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 population of Atlantic cod. 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.

Baltic populations of *Mytilus* spp. are locally adapted, with a unique composition of loci derived from *M. trossulus* and *M. edulis* genome. 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*.

References

Drywa A., A. Poćwierz-Kotus, A. Wąs, S. Dobosz, M.P. Kent, S. Lien, R. Bernaś and R. Wenne. 2013. Genotyping of two populations of Southern Baltic Sea trout *Salmo trutta* m. *trutta* using an Atlantic salmon derived SNP-array. Marine Genomics 9:25-32.