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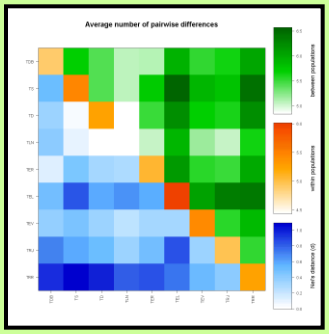
Genotyping of nine Baltic populations of sea trout

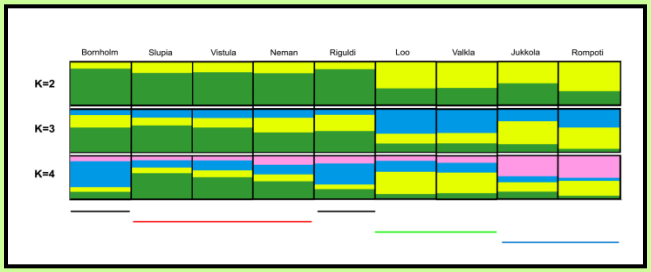
South East Baltic populations of sea trout *Salmo trutta* (from Poland, Lithuania, Denmark: Bornholm, Estonia and Russia) were genotyped with iPLEX Gold Sequenom method using panel of 23 SNPs. The highest level of pairwise Fst differences was observed between Russian population from East Gulf of Finland and Polish populations from the Baltic Main Basin and the lowest differences were between the both Polish, and Polish and Lithuanian populations.

Genetic differentiation



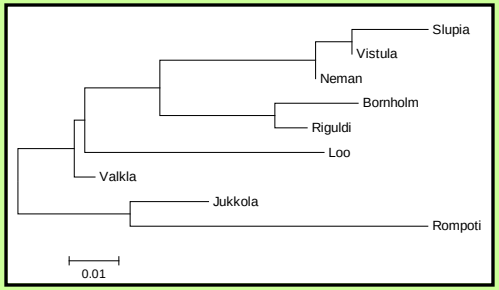
Comparison between and within populations.
Above diagonal: pairwise Fst for all pairs of populations
Diagonal: an average number of pairwise differences
as a measurement of the within-population diversity
Below diagonal: Nei's average number pairwise differrences

Genetic structure analysis



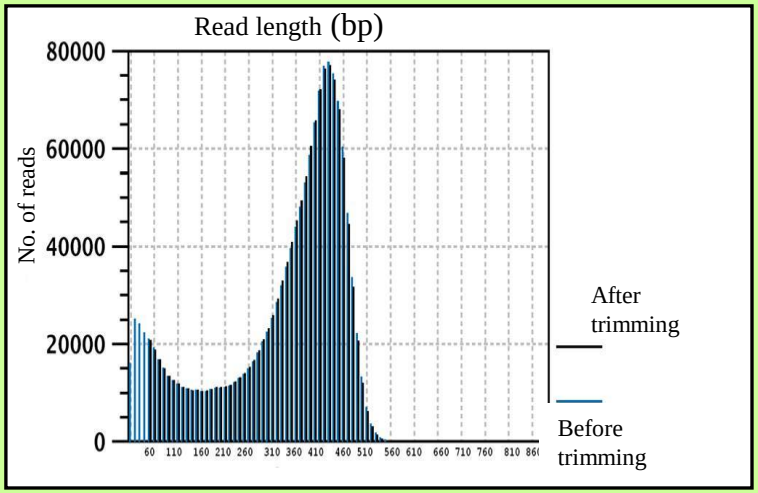
Results of genetic structure analysis indicate that individuals from 9 populations were grouped into four clusters.

The NJ tree constructed using the Nei's distances among the nine sea trouts populations.

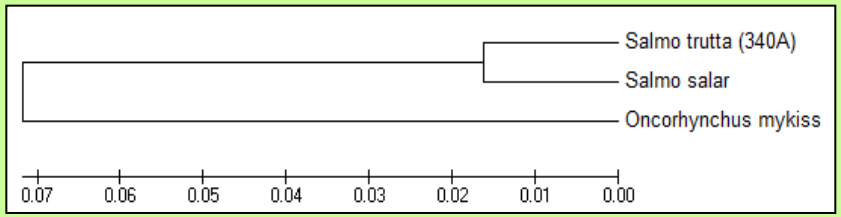


454 pyrosequencing

Selected transcripts putatively involved in immune response in sea trout *Salmo trutta* from Vistula river, Poland were studied using 454 pyrosequencing. 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.



Read length distribution of 1,440,373 reads produced from the transcriptome of *S. trutta* generated by CLC GenomicWorkbench.



Identification of myxovirus resistance gene (Mx2) sequence in *S. trutta*. Phylogenetic tree for sea trout, salmon and rainbow trout.

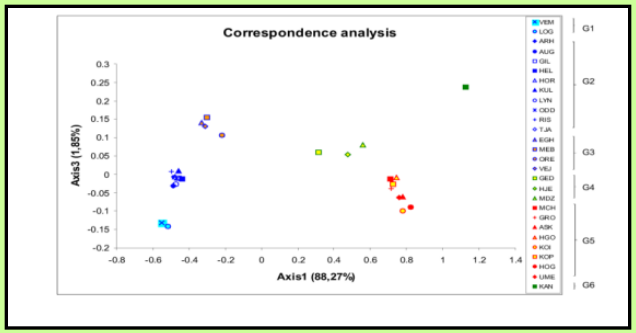
44K-oligo microarray

Name	PLFUR1.txt>1157.diff	PLFUR2.txt>1158.diff	PLFUR3.txt>1159.diff	PLFUR4.txt>1160.diff	PLFUR5.txt>1161.diff	PLFUR6.txt>1162.diff	PLFUR7.txt>1163.diff	PLFUR8.txt>1164.diff	mean
Immune system genes									
acute phase serum amyloid A (SAA)	-3,1	-3	-3,6	-3,4	-2,8	-0,8	-2,5	-2,6	-2,73
Interleukin-1 beta; Flags: Precursor	-4,7	-2,9	-7,1	-6,4	-3,9	-0,5	-4,8	-1,5	-3,99
interleukin 17 isoform D	2,55	1,09	2,07	2,07	1,69	1,15	0,21	0,97	1,48
Small inducible cytokine A13	3,34	1,21	4,51	2,94	1,49	1,91	2,79	0,6	2,35
Hepcidin-1 precursor	-4,7	-4	-4,5	-4,8	-4,7	0,74	-3,8		-3,67
cathelicidin antimicrobial peptide	-5,6	-4,3	-5,2	-5,1	-4,3	0,1	-4,1	-0,2	-3,58
cyclooxygenase-2	-2,9	-1	-4,2	-3,5	-2,1	1,39	-2,7	0,11	-1,86
Mx1 protein	1,65	1,87	1,51	1,83	2,98	-1,5	1,98	-0	1,29
C type lectin receptor B	-7	-3,7	-6,5	-6,8	-6,2	0,31	-3,9	-3,6	-4,66
Collagenase 3 precursor	-4	-4,1	-5,1	-4,2	-2,7	-0,7	-4,6	-1,3	-3,34
matrix metalloproteinase 9	-4,9	-4,3	-4,2	-4,2	-2,8	0,44	-4,4	-1,4	-3,22
Metalloreductase STEAP4	-4,1	-2,4	-3,8	-4,5	-3,1	1,27	-2,9	-2,7	-2,77

Name	PLFUR1.txt>1157.diff	PLFUR2.txt>1158.diff	PLFUR3.txt>1159.diff	PLFUR4.txt>1160.diff	PLFUR5.txt>1161.diff	PLFUR6.txt>1162.diff	PLFUR7.txt>1163.diff	PLFUR8.txt>1164.diff	mean
Other genes									
DNA replication licensing factor mcm5	1,2	3,58	2,43	1,85	2,76	-0,2	2,92		2,07
heat shock 70kDa protein 8 isoform b	1,92	2,64	-1,4	2,19	3	0,44	2,7		1,64
heat shock protein hsp90	6,13	5,92	3,48	2,32	-0,5	2,74	1,41	-1,1	2,55
Cathepsin L1	4,15	1,44	-1,8	4,22	3,65	4,03	3,66	-0,2	2,39
procathepsin B	5,86	0,92	-1,5	5,65	5,54	5,32	4,89	-0,1	3,32

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) 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).

Mytilus spp.



Correspondence analysis (CA) of *Mytilus* populations from Baltic Sea region and Canada. Each dot is a population. Populations from the North Sea (G1), North Danish Straits (G2), South Danish Straits (G3 and G4), inner Baltic Sea (G5), Canada (G6).

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*.