

# Single Nucleotide Polymorphisms in Polish Wild and Hatchery Populations of Sea Trout (*Salmo trutta m. trutta*): Differentiation in Space and Time

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Salmonid fish family is ecologically and economically important with significant commercial fisheries, recreational angling in both Baltic Sea and rivers in Poland and frequent hatcheries populations. Representatives of this family are Atlantic salmon – *Salmo salar*, sea trout – *Salmo trutta m. trutta* and introduced to Poland in the 60s of the XX<sup>th</sup> century rainbow trout – *Oncorhynchus mykiss*. Difficulties in species identification due to their morphological similarity may result in overfishing of restituted Atlantic salmon leading to imbalances in the Baltic Sea ecosystem. Therefore it is vital to create a genetic tool differentiating these species. Another issue is a past rivers stocking method of sea trout specimens from artificial spawning leading to the population mixing. Presently, since the early 1990s of the XX century, most sea trout rivers are enhanced in controlled conditions. This thesis presents:

- The use of SNP microarray in a cross-species study for non-ambiguous species identifications. In total 566 SNPs loci have been identified as highly polymorphic ( $F_{ST}=0,999$ ) across the three salmonid species enabling the molecular basement for various monitoring applications in aquaculture and food industries.
- The methodology and assessment use of the same microarray to identification of genetic diversity between Vistula and Pomeranian sea trout populations. As a result two panels of highly polymorphic markers have been selected (108 SNPs ( $F_{ST}=0,0407$ ) and 39 SNPs ( $F_{ST}=0,1298$ )). All data have been clustered in two groups corresponding to their origins.
- Diversity and changes in the genetic structure in Vistula and Pomeranian sea trout populations sampled in 1996 and 2009. Samples have been genotyped with the use of Sequenom MassARRAY iPLEX technology. The analysis of 22 polymorphic SNPs markers, selected from 62 SNPs form microarray, has shown differences in genetic structure in the Vistula populations in the selected period of time, while the Pomeranian populations were stable.

The obtained results indicated that observable changes in the genetic composition of populations may be induced in time by the implementation of a stocking strategy for the restitution and protection of Vistula sea trout genotypes in the Vistula River and its tributaries.