Summary

The Puck Bay is an ecosystem inhabited by several migratory and brackish water fish species, including those of high economic value. Starting from 1970s, the environmental conditions of the Puck Bay ecosystem have gradually deteriorated, causing major changes in the composition of its fauna and flora. The two most important predatory fish species, the northern pike (*Esox lucius*) and pike perch (*Sander vitreus*), have been replaced by the ‘weed’ fish species, gasterosteiformes (*Gasterosteiformes*) and gobies (*Gobiidae*). The northern pike population ceased to exist, while the pike perch population was strongly reduced in size. At the same time, the devastation of underwater meadows, the main spawning and nursery ground for fish, was observed. This devastation was caused by collection of water plants for agar production. The key component of the underwater meadows in the Puck Bay is an eelgrass (*Zostera marina*), the population which has declined over the years.

The deterioration of the natural environment of the Puck Bay ecosystem has alarmed local ecologists and fishermen communities. The complex restoration project ‘ZOSTERA: Restoration of ecosystem key elements in the inner Puck Bay’ was initiated in 2010. The main objective of this project was to restore the populations of the northern pike and the pike perch. Parallel restoration of eelgrass meadows was also envisaged.

The crucial step in projects of this type, is to obtain the results of genetic analyses performed to determine the level of genetic polymorphism of populations under restoration. In this thesis the results of genetic analyses of natural populations of pike and pikeperch are presented, together with analyses of aquaculture stocks and the produced fry. The Puck Bay eelgrass population was also studied and compared with two other Baltic Sea populations from Greifswalder Bodden and Cudema Bay.

For each of the three species under study, two multiplex PCR assays for screening the microsatellite loci (msDNA) were developed. The genetic polymorphism of the northern pike, pike perch and eelgrass populations was determined. Additionally, the genetic diversity of the northern pike populations was estimated through the analysis of the mtDNA CR fragment sequences. In case of the eelgrass populations, their genetic diversity was estimated by the AFLP markers.

Dry scales collected in years 1960s - 1970s served as a material for DNA isolation and analysis of the genetic polymorphism of the original northern pike population in the Puck Bay. The genetic polymorphism of 15 contemporary northern pike populations was studied in parallel to indicate the population most suitable for stocking the Puck Bay. It was found that
most populations exhibit an average level of polymorphism. The original Puck Bay population (1960 - 1970) exhibited the highest level of genetic diversity. The genetic differentiation analysis ($F_{ST}$) indicated that this population is genetically closest to that from the Motława river estuary. Additionally, the Motława population exhibited the relatively high polymorphism. Genetic analyses of spawners from the aquaculture stocks, the produced fry and the Puck Bay population after restocking, have shown that the polymorphism of this population is even higher than observed in years 1960s - 1970s.

The analysis of genetic structure of contemporary northern pike populations has shown that there is rather small genetic differentiation between them. This conclusion, based on the analysis of 12 msDNA loci has been strengthen by results of analysis of the mtDNA control region sequences of individuals from Polish and European populations. Small genetic differentiation and the lack of the phylogeographic structure could be the result of uncontrolled stocking with the homogenized material across Europe.

16 natural populations, including the remnant one from the Puck Bay, were chosen to characterize the genetic polymorphism of the pikeperch populations in Poland and to indicate those, which could serve as a source of breeding material for the Puck Bay. 12 msDNA loci were analyzed. The results of this analysis has shown that those populations exhibit rather low levels of genetic polymorphism, with the highest value obtained for the Puck Bay population. The genetic differentiation between populations was found moderate. There was no pronounced genetic differentiation between the groups of fresh and brackish water populations. This might suggest that similarly to the pike populations, the loss of the genetic diversity of the natural pike perch populations in Poland, is an effect of a long - term, uncontrolled stocking practices. Populations inhabiting brackish lakes Resko Przymorskie and Jamno as well as the Eastern part of the Vistula Lagoon are genetically closest to the population remaining in the Puck Bay. Those populations can serve as a source of material for stocking. The results indicate that stocking should not be based on originally selected populations from the Vistula Śmiała and Martwa, because they are genetically more distant to the Puck Bay population.

The success of the northern pike and pike perch restoration depends on the revitalization and the conservation of spawning grounds for fish, mainly the eelgrass (Zostera marina) beds. To find the most suitable planting material for eelgrass population, genetic analyses of the Puck Bay population were run together with analyses of the two Baltic populations, located in the Greifswalder Bodden and the Cudema Bay.

Eelgrass reproduces both vegetatively (clonally) and sexually. It is known that the prevalence of vegetative reproduction, decreases the population’s genetic polymorphism. To
make the proper estimations of the level of genetic diversity, it is necessary to determine the population’s clonal structure. It was found that the Cudema Bay population is composed of individuals each of a different genotype, while among 23 individuals representing the Greifswalder Bodden and 23 representing the Puck Bay populations, respectively eight and 20 genotypes were distinguished. For analyzes of the genetic polymorphism both msDNA loci and AFLP markers were used. The highest level of polymorphism was observed in the Cudema Bay population and the lowest in the one from the Greifswalder Bodden. Puck Bay population shows an average level of genetic diversity. Taking all together, for rebuilding of the Puck Bay eelgrass population, the use of local material should be recommended.

The results presented in this PhD dissertation were handed over to institutions responsible for the restoration of the Puck Bay ecosystem and should help in planning the restitution of the northern pike, the pike perch and the eelgrass populations.