The philopatric Baltic Sea pike shows weak genetic substructuring with patterns of long distance gene flow

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Summary
We have investigated population genetic patterns (population structure, isolation by distance, and gene flow) of northern pike (Esox lucius) collected from different parts of the brackish water Baltic Sea. We sampled over 650 individuals covering large parts of the Baltic coastline. The results showed weak population structure with an average Fst of 0.033 among areas. Genetic isolation by distance was significant when geographic distance was measured as shortest waterway distance, but not when it was measured along the coast. Estimated migration was asymmetric and the highest migration rates were not estimated among neighboring populations. These results suggest that long distance gene flow occurs in Baltic Sea pike and that migration is not restricted by deep water areas as has been suggested for other coastal fish species.

Introduction
Understanding patterns of genetic structure and gene flow is a prerequisite for effective management and conservation of species. In the Baltic Sea large variations in basic population genetic patterns among species have been documented, and species-specific studies are thus warranted (Laikre et al. 2005a; Wennerström et al. 2013).

The northern pike (Esox lucius) is an important predator in coastal areas of the Baltic Sea (Larsen et al. 2005). Studies of anadromous populations of Baltic Sea pike have shown strong homing behavior to freshwater spawning grounds, and subsequent pronounced genetic differentiation among populations (Bekkevold et al. 2015; Larsson et al. 2015). Adult pike sampled in the Baltic Sea primarily along the Swedish coastline has shown lower genetic divergence (Laikre et al. 2005b). One reason for lower divergence could be that sampling was not restricted to spawning populations and thus might reflect mixing of populations. In this study we focus on brackish water populations of Baltic Sea pike, sampled during the spawning period, in order to investigate the distribution of genetic variation among areas.

Material and methods
We sampled a total of 662 georeferenced individuals from 16 areas, covering major parts of the Baltic Sea and genotyped them for 11 microsatellite loci. The main part of the sampling was conducted around spawning time (April – June) 2010. We estimated population structure by Bayesian clustering techniques. We also calculated F-statistics, and isolation by distance among samples, and estimated migration rates.

Results and Discussion
Genetic structuring in the in Baltic Sea pike was weak, although statistically significant, with an average Fst = 0.033 among areas. The most likely number of genetic clusters according to the STRUCTURE software was two. These clusters were not geographically separated and individual assignment probabilities to each cluster were generally low. A higher number of genetic clusters and use of location as additional priors gave a better geographic grouping of genetic clusters, but admixture rates were consistently high and few individuals were strongly assigned to any cluster.
There was a clear pattern of isolation by distance when geographic distance was measured as shortest waterway distance ($P = 0.0029$, $r = 0.42$). However, when geographic distance was measured along the coast there was no relationship between genetic and geographic distance ($P = 0.78$, $r = -0.13$).

Estimated migration rates were high among several populations. Migration was asymmetric, and the highest migration rates were not found among neighboring populations. Rather, central populations (e.g. from Stockholm and Turku) seemed to act as sources, whereas other populations acted as sinks.

Our results indicate that there is potential for long distance dispersal in the Baltic Sea Northern pike and that deep water areas do not seem to act as barriers to gene flow as has been shown for other coastal species (Olsson et al. 2011). Levels of genetic differentiation were in the same magnitude as has previously been shown for brackish water populations collected outside spawning time (Laikre et al. 2005b), but lower than what has been shown for freshwater spawning populations (Bekkevold et al. 2015; Larsson et al. 2015). These results show that non-anadromous Baltic Sea pike might represent a more interconnected system than has previously been presumed. Local management measures such as stocking might potentially affect genetic composition in areas far from the site of release.

References

Bekkevold, D., Jacobsen, L., Hemmer-Hansen, J., Berg, S, and Skov, C. 2015. From regionally predictable to locally complex population structure in a freshwater top predator: river systems are not always the unit of connectivity in Northern Pike Esox lucius. Ecology of Freshwater Fish, 24: 305-316.


