Development of efficient genetic markers to trace fish fraud and IUU fishing

Hillen Jasmien, Ilaria Coscia and Filip Volckaert

Laboratory of Biodiversity and Evolutionary Genomics, KU Leuven,
Ch. Deberiotstraat 32, 3000 Leuven, Belgium
E-mail: jasmien.hillen@bio.kuleuven.be

Due to the increasing demand for fish, in combination with chronic overfishing and IUU (illegal, unreported and unregulated fishing), fish stocks are declining worldwide and food security is likely to be hampered in the future. It is estimated that globally a quarter of the catches are through IUU fishing. This leads to major economic losses, undermines sustainable fisheries and causes unfair competition. Nowadays the deficiencies in wild fish are largely compensated through aquaculture production. However, the aquaculture industry raises concerns about its environmental compatibility. One of the most pressing issues is the amount of escapees into the wild and their subsequent mixing with natural populations. Escapes not only impose large economic costs, they also form a threat to local biodiversity through competition and genetic pollution. In addition, despite the strict national and European regulations, there are increasing problems with mislabeling of fish (products). In this project, we will use state-of-the-art Next Generation Sequencing (RAD-seq) to develop SNP markers to unravel the fine scale population structure of European sea bass (*Dicentrarchus labrax*) across its full distribution range - but with special attention for the North East Atlantic Ocean - and to distinguish wild fish from (escaped) aquaculture fish. Previous studies have shown that this approach guarantees the statistical power needed to successfully trace catches back to their farm (or population) of origin. After intensive validation and standardization procedures, a diagnostic tool based on a selected set of highly discriminatory SNP makers will be developed. This tool will be precise enough for forensic applications but at the same time cheap and efficient to be used as a routine control by fisheries authorities and in the food industry. The generic methods developed here for sea bass will facilitate similar future investigations on other economic important marine fish.