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**Crossing barriers:  
Genetic consequences of translocating  
wild cleaner fish for aquaculture**

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## Abstract

Several species of fish show a symbiotic cleaning behaviour, where they assist other species by feeding and removing dead skin or ectoparasites. Some of these cleaner fish species are used as a low-cost parasite control in salmon aquaculture, often considered to be more environmentally friendly than other delousing methods. Approximately 54 million cleaner fish are annually used in Norwegian salmon farms. This has resulted in an increasing fishing pressure on wild cleaner fish populations. Together with long-distance translocation, this raises concerns of potential overfishing, anthropogenic introductions, and hybridisation.

Recently, increasing numbers of corksiding wrasse (*Symphodus melops*), have been reported in mid Norway, north of its described distribution range. This is an area heavily relying on the import and translocation of cleaner fish from Skagerrak-Kattegat, more than 1000 km away. Using genetic markers, I show that the new population is both a result of a northward range expansion, as well as a translocation of individuals from southern populations. Further investigation revealed that escapees and hybrids may constitute up to 20 % of the populations at the northern edge of the species distribution. In contrast, escapees and hybrids are rare in other parts along the Norwegian west coast, where salmon farming is also common. The set of genetic markers has a high power to detect escapees and hybrids, and can be applied to monitoring of wild populations.

Investigations of corksiding wrasse in Skagerrak-Kattegat revealed reduced genetic diversity, a weak pattern of isolation by distance, and surprisingly little population structure. This suggests a very recent colonisation and high connectivity among sites in this region. Along the Swedish west coast, I evaluate the potential effects of the newly established wrasse fishery on local ecosystems and populations, and provide a baseline to support ecosystem-based management for wrasse fisheries in Sweden. I also investigate the genetic population structure of lumpfish (*Cyclopterus lumpus*) across the Atlantic, which is the most commonly used cleaner fish species. I show that there is a lot more structure than previously known, and identify eight genetically divergent regions. Hierarchical analysis of these regions demonstrates additional local and cryptic substructure. The genetic markers used here can also be applied for management of wild lumpfish populations and the identification of population origin.

Overall, these findings provide important information both for aquaculture management and conservation of wild populations, and have implications for the increasing use and translocation of cleaner fish for parasite control in aquaculture. Moving genetic material between isolated populations could drastically alter the genetic composition and erode population structure, potentially resulting in loss of local adaptation and hampering natural range expansion. Although the ecological and evolutionary significance of escapees warrants further investigation, these results should be taken into consideration in the use of translocated cleaner fish.