



## GENOPOPTAILLE

### USING GENETIC IDENTIFICATION TO ASSESS THE ABSOLUTE SIZE OF ENDANGERED MARINE POPULATIONS

From an ecosystem perspective, the sustainability of fish stocks, and therefore of their exploitation, depends not only on populations of the main target species but also on those species taken as bycatch. Indeed, some bycatch species are more sensitive to exploitation than target species are. These include rays and sharks, numbers of which have declined sharply during the 20th century.

A new method has recently been developed to estimate the absolute size of small populations. It is based on genetically identifying parent-offspring pairs. This method is based on the tried and tested principle of capture-mark-recapture (CMR), using genetic marking of adults and recapture of this genetic material via their offspring.

The rapid rise of genomic techniques in the past decade means it is now possible to use sequencing or high-throughput genotyping for a large number of samples across several hundred or thousand genetic markers.

The GenoPopTaille project intends to develop an innovative application for these new genomic tools in relation to the thornback ray *Raja clavata*. This will estimate the absolute number of individuals in the Bay of Biscay based on genetic identification of parent-offspring pairs.

The project includes a cost-benefit analysis to determine how applicable this method would be to other fish populations, especially those species which it is difficult to evaluate by other means.

#### Partners

##### Research centers

Ifremer, unité Écologie et Modèle pour l'Halieutique (EMH), Département Ressources Biologiques et Environnement (RBE), Nantes [\[Project Developer\]](#)  
Ifremer, HGS, Unité Halieutique Gascogne Sud, Département RBE, L'Houmeau  
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