



**UNIVERSITÀ DEGLI STUDI DI NAPOLI  
“FEDERICO II”**



**Tesi di Dottorato**

**“Frauds and fish species authentication: study of  
the complete mitochondrial genome of some  
*Sparidae* species to provide specific barcode  
markers”**

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## Abstract

The growing global diffusion of seafood for human consumption requires always more accurate sanitary and quality controls. Among the globally marketed fish, the species belonging to the family *Sparidae* are excellent food-fishes of high economic value.

The *Sparidae* family comprises about 38 genera and 159 species, some of which are highly appreciated as seafood. In Italy, the fish species of commercial interest are defined by the law (DM n. 19105 del 22 Settembre 2017). Among them, 41 species belong to the *Sparidae* family. The identification of these species is difficult even when external characters are preserved due to their morphological similarity.

Species identification becomes even harder to achieve after industry processing, when distinctive external traits are removed. Nevertheless, despite their similarity, sparid species have different organoleptic quality that corresponds to variable prices in fish markets. Consequently, substitution of commercially important *Sparidae* species is common. The sparid specie with highest commercial value, *Dentex dentex*, is often replaced with less expensive species or lower quality alternatives. All this premised, *Sparidae* species identification requires immediate resolutions. Research on fish mitochondrial *DNA* (*mtDNA*, mitogenome) has led to substantial advances in the fields of species authentication and population biology.

The main species' specific *DNA* sequences used as markers for fish species identification belong to the mitochondrial genes encoding ribosomal **16S** and **12S** subunits, cytochrome b (**Cytb**), and cytochrome c oxidase I (**COI**). However, current research shows that mitochondrial *DNA* markers perform well for certain species but may be less discriminating for others. Therefore, they cannot be used indiscriminately for the identification of all fish species. This situation has led to the formulation of the proposal to study and analyze the complete *mtDNA* sequence with the aim to identify mitochondrial markers or multiple marker approaches with higher and more specific discrimination capacity. At present, *mtDNA* genomes of *Sparidae* fishes are not conspicuously represented in the scientific literature, which makes difficult to understand if currently used genetic markers are the most effective for sparid species identification.

This thesis project had the aim to study and analyze Sparids' complete *mtDNA* sequence to identify mitochondrial markers or a multiple marker

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approach to achieve a higher and more specific discrimination capacity. We focused on the genera *Dentex*, *Pagellus* and *Pagrus*, listed in the Ministerial Decree.