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DEVELOPMENT OF A SYSTEM FOR GENETIC TRACEABILITY OF FISH SPECIES AND DERIVING FOODS BY THE IMPLEMENTATION OF A MICROARRAY PLATFORM

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Recent emergencies regarding animal derived foods have underlined the necessity of the development and adoption of a suitable system for controlling every single step of food production from animal breeding to the final product. Moreover, the identification of species is important to fight against food swindle and to guarantee meats origin. For what concern fish food industry, few genetic methods have been developed and applied, although the rising economical importance of fish foods. This is also more important as European Community in the last decade has approved many norms on food traceability in order to guarantee food safeness.

The use of molecular techniques based on specie specific DNA sequences allows an absolutely reliable identification of species even in final transformed products which are impossible to analyze with conventional methods based on phenotypic approaches. In 2003, Paul D. Hebert demonstrated that the nucleotidic sequence of a single gene is sufficient to differentiate and to identify the majority of animal species. This approach, based on the analysis of the mitocondrial gene *cox1* coding the Cythochrome oxydase subunit I, is called DNA barcoding as the polymorphisms of the nucleotidic sequence of a specific region of this gene can be assimilated to a bar code by which every specie is idendified by an highly conserved sequence or by a group of sequences.

Usually DNA barcoding approach is implemented by sequencing the fragment of interest (as cox1) and by comparing the sequences with DNA bar codes available. But this require the use of a sequencer and allows the analysis of a single fragment per time, while for discriminating phylogenetically very close individuals would be more suitable to analyze different sequences corresponding to more genes. For these reasons we implemented an oligo microarray platform to detect specie specific sequences based on solid-phase APEX. The technology use immobilized probes of 20-30 nucletides length designed on species specific sequences. Most of the species of economical interest in Italy will be barcoded and the sequences will be collected in a specific database. These data will then be used to construct a microarray for fish species identification and food traceability.