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Editorial Open Access

Current Trends on the Study of Microbiological Spoilage of Fresh Fish

Ioannis S. Boziaris*

Department of Ichthyology and Aquatic Environment, School of Agricultural Sciences, University of Thessaly, Greece

***Corresponding author**: Ioannis S. Boziaris, Assistant Professor (in Seafood Safety and Preservation), Department of Ichthyology and Aquatic Environment, School of Agricultural Sciences, University of Thessaly, Fitokou street, 38446, Nea Ionia, Volos, Greece, Tel: +302421093153; E-mail: boziaris@apae.uth.gr

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Editorial

Fresh fish is very perishable product and spoil due to microbiological activity, chemical oxidation of lipids and autolysis. However, microbial spoilage is the main mechanism affecting fresh fish quality. As the bacteria grow they utilize nutrients and produce by-products. It is well established that the accumulation of metabolic products is the primary cause of the organoleptic rejection of fresh fish. It is also known that spoilage is caused only by a fraction of the initial microbial population, known as specific spoilage organisms (SSOs), which produce metabolites (chemical spoilage indices-CSIs) responsible for off-flavours and cause the organoleptic rejection of the product. The fraction of the initial micro-biota that dominate and the metabolic products that are produced are determined mostly by the temperature and atmospheric conditions during storage [1].

Knowledge about the microbial biodiversity and the conditions under which bacteria are encountered as SSOs is crucial for understanding spoilage mechanisms, in order to apply effective strategies for fish preservation. The traditional identification of seafood spoilage microbiota by phenotypic tests (morphological, biochemical), after the isolation of microorganisms on various growth media lack the discriminatory power of molecular techniques. The 16S rRNA gene sequence analysis is currently the most common approach for studying seafood microbiota that grown on plates [2-4]. On the other hand recent studies have concluded that many potential fish spoilage microorganisms are overlooked, while other are unable to grow on media used [5]. Using traditional culture techniques, the population level and the diversity of the bacterial populations reflect those that are able to growth on culture media. The lack of selective media or non-efficient media for enumeration of various spoilage microorganisms illustrates the challenges of using modern culture-independent approaches for examining the biodiversity of initial and spoilage fish micro-biota [3,6,7].

The microbial growth constitutes the main cause of fresh seafood rejection and the currently used microbiological methods are retrospective and time consuming. Hence, there is an emerge towards the development of rapid indirect monitoring of microbial growth by determining the activity of the microorganisms based on the determination of microbial metabolites produced during storage in order to assess fish freshness/spoilage status.

Various compounds such as Trimethylamine (TMA), total volatile base nitrogen (TVB-N), sulphuric compounds, aldehydes, ketones, esters, etc., are being produced by various microorganisms during the fish spoilage [1]. Traditional chemical methods to monitor microbial activity in fish include the determination of TVB-N and TMA. However, TVB-N and TMA increase in fish occurs only at the late stages of storage, making them suitable only as acceptance/rejection criterion and not suitable for freshness indicators [8]. Volatile organic compounds (VOCs) have been exploited as potential CSIs for spoilage/freshness evaluation. Solid Phase MicroExtraction coupled with gas chromatography/mass spectrometry (SPME-GC/MS) is an analytical method which has been used to study the VOCs in seafood in order to evaluate the degree of seafood spoilage and can be used for rapid quality assessment and estimation of the remaining shelf-life [9-11].

The current approaches help us to increase our knowledge towards the elucidation of fish spoilage mechanism [12]. The determination of spoilage micro-biota and the metabolites produced during fish storage allow us to determine which microorganisms are the key spoilage players and which metabolites are suitable CSIs; hence allow the rapid evaluation of fish freshness/spoilage at any stage of production and distribution chain.

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