

Indigenous and spoilage microbiota of farmed sea bream stored in ice identified by phenotypic and 16S rRNA gene analysis

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Abstract

Investigation of the initial and spoilage microbial diversity of iced stored sea bream was carried out. Culture dependent methods were used for bacterial enumeration and phenotypic identification of bacterial isolates, while culture independent methods, using bacterial 16S rRNA gene amplification, cloning and sequencing of DNA extracted directly from the flesh were also employed. The culture dependent approach revealed that the initial microbiota was dominated by *Acinetobacter*, *Shewanella*, *Pseudomonas* and *Flavobacterium*, while at the end of shelf-life determined by sensory analysis (16 days), the predominant microbiota was *Pseudomonas* and *Shewanella*. Culture independent approach showed that initially the sea bream flesh was strongly dominated by *Acinetobacter*, while *Pseudomonas*, *Aeromonas salmonicida* and *Shewanella* were the predominant phylotypes at the end of shelf-life. Initial and spoilage microbiota comprised of phylotypes previously identified by others using traditional or molecular techniques. However, *Aeromonas* has not been reported as part of the dominant microbiota of sea bream at the time of spoilage. Combination of classical and molecular methodologies better reveals the microbiota during storage by revealing bacteria that escape standard approaches and, thus, provides valuable complementary information regarding microbiological spoilage.

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