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Quality and safety in oysters (*Crassostrea gigas*) and mussels (*Mytilus galloprovincialis*) reared in Orbetello lagoon (Central Italy)

Anna Messini, Giuliana Parisi, Glenda Fratini

Dipartimento di Biotecnologie Agrarie, Università di Firenze, Italy
Corresponding author: anna.messini@unifi.it

Shellfish are perishable products due to their biochemical composition. Under refrigerated storage conditions, the shelf life of these products is limited by microbiological and enzymatic spoilage. Aim of the work was the evaluation of the influence of culture site on quality and safety of oysters and mussels, during the post-harvest refrigerated storage. In this study, 145 oysters and 90 mussels, sampled in Orbetello Lagoon (Italy), at March and at September respectively, were monitored during the storage at 4°C. The shellfish were analysed at 1, 3, 7 and 10 days from the harvesting by counting of aerobic psychrotrophic bacterial, pseudomonads, coliform bacteria and *Escherichia coli*. In order to deepen the knowledge about the role of pseudomonads, the significant number of strains from oysters and mussels were isolated. Total DNA was extracted from the isolates and 16S rDNA was PCR-amplified using FD1 and RD1 primers. Amplicons were subjected to ARDRA analysis using the restriction endonuclease CfoI. Representative strains of ARDRA groups were identified by 16S rDNA sequencing. In oysters, the aerobic psychrotrophic bacterial counts was 4.5 and 6.0 log $CFUg^{-1}$ on the 1st and the 10th day, respectively; the pseudomonads values was 3.2 and 5.3 log $CFUg^{-1}$ on the 1st and the 10th day respectively. In mussels, the aerobic psychrotrophic bacterial count was 5.8 and 6.2 log $CFUg^{-1}$ on the 1st and the 10th day, respectively; the pseudomonads value was 4.2 and 6.2 log $CFUg^{-1}$ on the 1st and the 10th day respectively. The coliform number was always below the limit permitted by the Italian law and *Escherichia coli* was always undetected. 16S rDNA sequencing indicated that the analysed isolates (pseudomonads), from oysters and safety mussels, belong to *Pseudomonas spp*.. Oysters and mussels maintained appreciable quality and safety characteristics during ten days of refrigerated storage.

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Molecular cloning and expression analysis of genes involved in the compensatory growth of sea bass (*Dicentrarchus labrax*)

Samuela Corà, Genciana Terova, Simona Rimoldi,
Elena Preziosa, Micaela Antonini, Marco Saroglia

Dipartimento di Biotecnologie e Science Molecolari, Università dell'Insubria, Varese, Italy
Corresponding author: genciana.terova@uninsubria.it

There are several descriptions of compensatory growth (a phase of accelerated growth when food levels are restored after a period of growth depression) in fish, but the mechanisms involved in such rapid recovery from fasting are still not fully understood. Such mechanisms have principally been searched for at the level of total fish growth, but only little information is available at the molecular level. Accordingly, the present study has focused on identifying candidate genes which are involved in the compensatory growth induced by fasting and subsequent refeeding in sea bass (*Dicentrarchus labrax*). In particular, we report on the molecular cloning and sequencing of genes such as Δ6 desaturase, lipin, peroxisome proliferator-activated receptor (PPARγ) and oligopeptide transporter (PepT-1) involved in lipid and protein metabolism. We have also analyzed fasting- and refeeding -induced changes in the expression of the aforementioned genes, in different tissues, by using real-time RT-PCR quantification. In sea bass liver, 35 days without feed contributed to a significant increase in Δ6 desaturase transcript levels as compared to ad libitum fed controls, whereas recovery from fasting (21 days of refeeding) was associated with a significant decrease in Δ6 desaturase mRNA levels. The mRNA levels of lipin and PPARγ in sea bass liver followed the same pattern: a significant increase after fasting, and a significant decrease at the end of refeeding. PepT1 was highly expressed in the proximal intestine, and fish nutritional status significantly influenced its mRNA copy number inducing a down-regulation during fasting and an up-regulation during the refeeding. In conclusion, our findings offer new information about the dietary regulation of Δ6 desaturase, lipin, PPARγ, and PepT1 genes expression supporting their involvement in sea bass compensatory growth induced by refeeding.

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Effects of *postmortem* storage temperature on sea bass (*Dicentrarchus labrax*) muscle protein degradation: analysis by 2D DIGE and mass spectrometry

Elena Preziosa, Samuela Corà, Genciana Terova,
Maria Filippa Addis, Tonina Roggio, Marco Saroglia

Dipartimento di Biotecnologie e Scienze Molecolari, Università dell'Insubria, Varese, Italy
Corresponding author: elena.preziosa@uninsubria.it

Given the recognized importance of storage conditions for postmortem deterioration of fish muscle, this study has focused on the storage temperature, which is considered the factor with the strongest impact in this process. Differences in the abundance of muscle proteins, due to biological *post mortem* processes, were studied by 2D DIGE and MS in 6 sea bass (710±157.87 g) kept at either 1°C or 18°C for 5 days. The results demonstrated that sea bass muscle proteins within the molecular weight and pI values investigated here are proteolysed to a relatively less degree as compared to *post mortem* mammalian muscle. The greatest alterations in sea bass filet protein composition can be ascribed to the 18°C *post mortem* storage, and distinct changes appear after 5