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THE HEPATIC PROTEOME OF GILTHEAD SEABREAM (SPARUS AURATA) ACCLIMATED TO TWO SALINITY CONDITIONS

Varó^{1,2}, I; Navarro², J; Del Ramo¹, J.; Torreblanca¹, A.

¹ Departamento de Biología Funcional Biology, Facultad de Ciencias Biológicas, Universidad de Valencia. Dr. Moliner, 50, 46100 Burjassot (Valencia, Spain); ²Instituto de Acuicultura de Torre de la Sal (CSIC), 12595 Ribera de Cabanes, Castellón (Spain)

The gilthead seabream (Sparus aurata) is valuable euryhaline specie in the Mediterranean aquaculture, adapted to survive in a wide range of salinity. The aim of this study was to identify, by a proteomic approach, changes in the liver as response to acclimation to salinity that may be indicative of metabolic adjustments to the physical and chemical environmental conditions.

Gilthead seabream of 350 g were acclimated to high (37 %) and low salinity (18-20 ‰) for 5 months. Difference Gel Electrophoresis Technology (2D-DIGE) was used to study the effect salinity in liver protein profile. Resulting gels images were analized by DeCyderTM (V. 6.5) software and the statistical module EDA (V.1.0) was used for multivariate statistical analysed of data. The results showed significant changes in the expression of 24 proteins between high and low salinitiy group (p≤0.02). Among these proteins, a total of 11 increased in abundance and 13 decreased in the group accimated at high salinity. Mass spectrometry and database research is being performed to identify these differentially expressed proteins involved, presumably, into some homeostatic processes that would explain the gilthead seabream tolerance to a broad salinity range.

Keywords: Proteomics, DIGE, Salinity, Biomarkers, Liver gilthead seabream

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