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THE ENTEROCYTE PROTEOME OF GILTHEAD SEABREAM (*SPARUS AURATA*) ACCLIMATED TO TWO SALINITY CONDITIONS.

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The Mediterranean Sea and the coastal aquatic systems are, as a result of the climate change, experiencing a warming of the surface and deep waters. An increase in the average temperature and in the number of "heat waves" is predicted, in which the temperature of the surface waters may reach considerable levels, and not ruling out changes in the levels of salinity in some areas In fish, the acclimatization to changes in salinity and temperature is associated with changes in the composition of lipids and proteins. These changes can be detected at a molecular level and may constitute a useful tool for the tracking of the effects of the global changes on aquacultured fish species of interest. The gilthead seabream (*Sparus aurata*) is a valuable euryhaline species in the Mediterranean aquaculture, adapted to survive in a wide range of salinty. The intestinal epithelium is involved in osmoregulation in fish. In the present work we investigated the proteome of enterocytes, in order to search for new proteins that could be useful as biomarkers to evaluate the response of euryhaline cultured fish to salinity changes. Gilthead seabream of 350 g were acclimated to high (37 ‰) and low salinity (18-20 ‰) for 5 months. 2D difference gel electrophoresis (DIGE) was performed to identify protein profiles related to osmoregulation. Analyses of the gels image scaning were caried out with the DeCyder™ (V. 6.5) software, and the statistical module EDA (V.1.0) was used for multivariate statistical analysed of data. A total number of 34 proteins were differentially expressed as consequence of salinity acclimation ($p \leq 0.02$). Among these proteins, 16 increased in the group acclimated to high salinity, whereas 18 decreased. Mass spectrometry and database research is being performed to identify these differentially expressed proteins involved, presumably, into the acclimatory processes of the gilthead seabream to salinity changes.

Keywords: Proteomics, DIGE, salinity, Enterocytes, Biomarkers, gilthead seabream

Acknowledgements: This work was funded by project CTM 2006-14279-CO2-01/MAR and CTM 2006-14279-CO2-02/MAR MEC-FEDER. I. Varó was a recipient of a Ramón y Cajal contract MEC (Spain). DIGE analysis was performed in the proteomics service of University of Valencia (SCSIE), Valencia (Spain). We thank to Oreto Antúnez for their technical support.