

POPULATION PROTEOMICS: PROTEIN DIVERSITY IN HAKE (*MERLUCCIUS MERLUCCIUS*) POPULATIONS

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Population proteomics is becoming a powerful tool enabling the study of the population structures and functional adaptations to environment from human settlement to animal natural populations. The present communication deals with preliminary results of a high throughput, large-scale study of hake (*M. merluccius*) proteome across and within populations. The aim of this study is the search for proteins that exhibit differences in abundance and mobility in order to trace frequencies distribution and differential features across populations.

Approximately 150 µg of liver proteins of eighteen individuals (six replicas) from three different sampling sites (two from the Atlantic Ocean and one from the Mediterranean Sea) were labelled with cyanine dyes (Cy3, Cy5) and separated on a two dimensional differential gel electrophoresis (2D-DIGE). The obtained gel images were analyzed using the DeCyder and BVA software modules. Gels were grouped according to their geographical source and data used for further analyses were filtered. Up to 335 spot features exhibited statistically significant (ANOVA $p < 0.05$) changes in abundance on all 9 gels. PCA analyses of this filtered data set showed that samples segregated in three geographical groups and hence sample distribution did factor into the differential abundance of proteins observed. These differences in proteomic profiles have future potential application for the identification of hake genetic stocks.