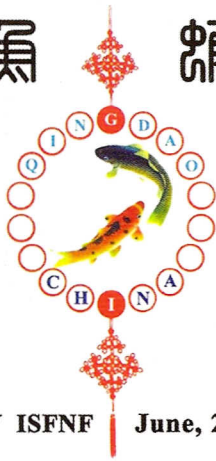


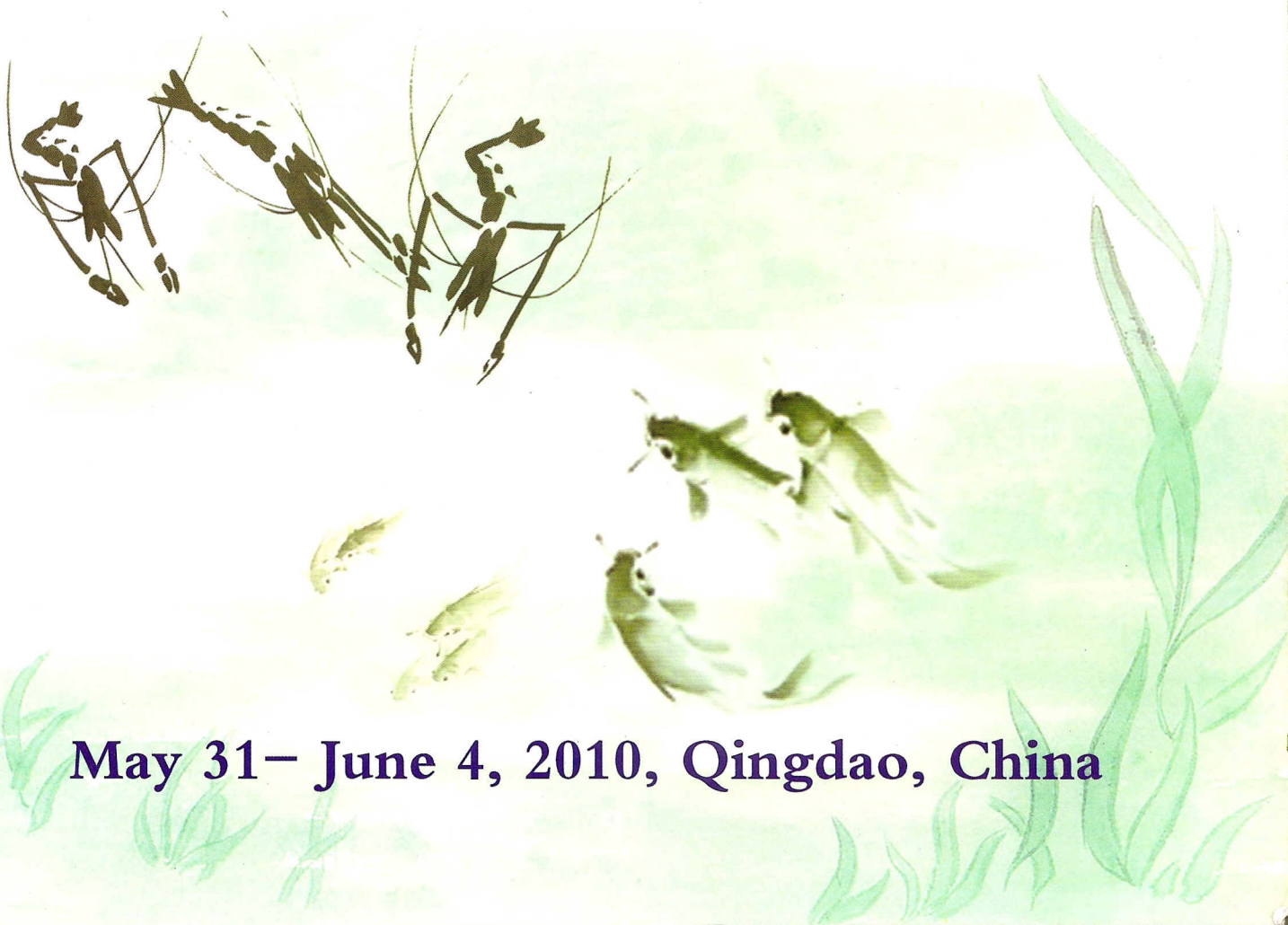
魚 蝦



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# Program & Abstracts



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**P-103****Inclusion of protein hydrolysates in the diet of white seabream (*Diplodus sargus*) larvae: impacts on skeleton quality and larvae proteome expression****Nadège Richard<sup>1\*</sup>, Mahaut de Vareilles<sup>1</sup>, Paulo J. Gavaia<sup>1</sup>, Tomé S. Silva<sup>1</sup>, Odete Cordeiro<sup>1</sup>, Manuel Yúfera<sup>2</sup>, Pedro M. Rodrigues<sup>1</sup> and Luis E.C. Conceição<sup>1</sup>**<sup>1</sup> Centro de Ciências de Mar do Algarve (CCMAR), Campus de Gambelas, 8005-139 Faro, Portugal<sup>2</sup> Instituto de Ciencias Marinas de Andalucía (CSIC), 11510 Puerto Real, Cadiz, Spain**Abstract**

In order to investigate the effects of dietary protein hydrolysate content on larval skeleton quality and larvae proteome expression, triplicate groups of white seabream (*Diplodus sargus*) larvae were co-fed from first-feeding onwards with live feed and three microencapsulated diets differing only on the molecular weight of their protein hydrolysate fraction. The protein hydrolysate fractions were: commercial hydrolysate (control diet), a high amount in larger molecular weight hydrolysates (3-20 KDa peptides, diet H) and a high amount in smaller molecular weight hydrolysates (<500Da, tri-, di-peptides and free amino acids, diet L). At 15 days after hatching (DAH), proteome expression changes were assessed in entire larvae by two-dimensional gel electrophoresis and the quality of larval skeleton was analysed at 28 DAH through double staining of cartilage and bone. Dietary protein hydrolysate fractions tested did not affect the incidence of deformed larvae, nor the number of deformities per fish. Nevertheless, larvae fed diet L presented a higher proportion of deformities in the pre-haemal region, where the incidence of deformed neural arches was higher compared to the two other groups. Vertebral fusions affecting the cephalic part were only observed in control group larvae. Two-dimensional analysis of larvae proteome, performed with PDQuest 2-D analysis software, allowed the detection and the comparative quantification of a total of 709 protein spots having a pI between 4 and 7. From these spots, 339 showed significant variations (Mann-Whitney U test,  $p < 0.05$ ) depending on the dietary treatment. Among them, 126 were significantly differentially expressed between group control and both groups L and H (100 spots under-expressed and 26 spots over-expressed in group control). A total of 98 spots displayed significant variation between groups H and control (45 spots under-expressed and 53 spots over-expressed in group H) and 84 spots were significantly differentially expressed between groups L and control (15 spots under-expressed and 69 spots over-expressed in group L). Proteome expression of larvae from groups L and H were differentiated by the expression of 93 spots (49 spots under-expressed, 44 spots over-expressed in group H). Some of the spots differentially expressed among the groups were analysed by liquid chromatography-tandem mass spectrometry and identified as proteins involved in cellular contractile system, energetic metabolism, collagen maturation process or chaperoning. These results revealed that the molecular weight of the dietary protein hydrolysate fraction had a strong effect on proteome expression of white seabream larvae. Another set of mass spectrometry analysis will extend the results.

**Keywords:** Seabream; larvae; protein hydrolysates; skeletal deformities; proteomics

\* E-mail address: nrichard@ualg.pt (N. Richard).