Poster Abstract - C.72

GENETIC VARIABILITY IN *TRIGLA LUCERNA* BY SSR ISOLATION AND mtDNA POLYMORPHISMS IDENTIFICATION

M. D'ANDREA*, S. REALE*, A. RONCARATI**, N. GUARAGNELLA***, F. PILLA*

*) Department of S.A.V.A., University of Molise, Via de Sanctis, 86100 Campobasso, Italy **) Department of Veterinary Science, University of Camerino, 62032 Camerino, Italy ***) Department of S.pe.S., University of Molise, Via de Sanctis, 86100 Campobasso, Italy

microsatellite markers, mtDNA, Trigla lucerna

The tube gurnard (*Trigla lucerna L.*) is a teleost species of great commercial importance to European fishing nations bordering the Atlantic and Mediterranean Sea. This species is highly esteemed in many countries on account of its firm white flesh. In order to diversify the production after the rapid increase in the number of fish farms that produce sea-bass and sea-bream, the researchers and operator turned their interest to other valuable marine species like the tube gurnard. The successful performance of *Trigla lucerna* in aquaculture and the lack of knowledge about the genetic population structure has prompted the attention on the evaluation of its genetic variability. Early studies on fishery using molecular genetics focused primarly on the structure of proteins and enzymes. Nowadays research has switched to the study of DNA segments.

Microsatellite markers and mtDNA analysis have been elected to characterise the species. Even though microsatellite isolation is time-consuming and expensive, they are widely used as genetic markers since they are co-dominants, multiallelic, easy to score and highly polymorphic. Microsatellite have never been described neither in tube gurnard fish nor it species from the same suborder. To isolate them from the tube gurnard, the FIASCO (Fast Isolation by AFLP of Sequences COntaining repeats) protocol was chosen. The method, based on a digestion-ligation reaction of the amplified fragment length polymorphism procedure, allowed to isolate a microsatellite loci panel. Further investigations throughout screening of wide population in order to verify the informativity of the microsatellite loci has been accomplishing.

Moreover mtDNA variation has been used in this research because already successfully employed to study the phylogenetic inference and population structure in other teleost. Homologous primers were designed on the armored gurnard (*Satyrichthys amiscus*) fish taking advantage of the interfamiliar relationship, because no useful sequence data were available in the database. The subunit 16S and the cytochrome B mitochondrial gene were studied by direct sequencing. So far alignment of sequences from individuals belonging to different populations harvested interspecific SNPs. More genes sequence will be covered and the analysis will be extended to other populations.