

Presentation of MAR-ECO Students

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Working title of project: Identification and Quantification of Gelatinous Zooplankton as Energy Sources in Oceanic Food-webs

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Summary of Project: Understanding the food-web structure and organic cycling of deep-pelagic ecosystems requires integrated methods in order to identify and quantify the gut contents of a species in question. Due to the rapid digestion rate of gelatinous zooplankton in predatory fishes, the role of the former in deep-pelagic ecosystems is poorly understood. The MAR-ECO project presents us with the opportunity to gather further information about the trophic interactions between gelatinous zooplankton and the predatory fishes that consume them. One such fish, *Bathylagus euryops*, was found to be the biomass dominant deep-pelagic species in the 2004 MAR-ECO expedition and is a known gelativore. As part of a current US National Science Foundation-funded project, we will incorporate molecular methods in order to identify and quantify the gelatinous material that is often found in the gut contents of

B. euryops. In collaboration with a Census of Marine Life Zooplankton (CMarZ) molecular barcoding project led by Dr. Ann Bucklin, a sequence database for gelatinous zooplankton has been created using the ribosomal 28S gene. Group-specific primers will then be designed and used to amplify a shortened DNA sequence from the gut contents of *B. euryops*. DNA sequences will likely be degraded due to the rapid digestion rate of gelatinous material. Using this shortened sequence, it is then possible to match the molecular fingerprints with those in the database compiled with CMarZ along with the already established GenBank database. Based on a percent similarity of the sequences within the databases, the gut contents will then be identified to species level. The ability to detect gut contents to species level will greatly increase our understanding of the deep-pelagic ecosystem and the role that gelatinous zooplankton play in it. This method of gut content analysis via molecular methods could further be applied to other taxa in which questions of the food-web structure exist.