MOCNESS sampling: MB95-03, MB95-06

Sampling and Analytical Methodology:

$1m^2$ MOCNESS net. The $1m^2$ MOCNESS system carries nine nets and is designed to fish with a $1m^2$ net mouth area when towed at a 45^o angle (Wiebe et al., 1976). A flow meter mounted on the frame, just ahead of the net mouth, allowed calculation of the volume of water sampled (Wiebe et al., 1976). The data-acquisition software used angle information when calculating volume of water filtered. The $1m^2$ MOCNESS was fitted with 153um mesh nets and included, in addition to the standard conductivity (Sea-Bird SBE 4) and temperature (Sea-Bird SBE 3) sensors, a transmissometer (SeaTech, 25cm beam) and an oxygen probe (Sea-Bird SBE 13). The $1m^2$ MOCNESS was towed behind the ship at a speed of 1.5 to 2 knots (2.8-3.7 km h^{-1}) through the water. Winch speed generally ranged from 10 to 25 m min^{-1} during deployment and 5 to 15 m min^{-1} during recovery. Target sampling depths for this report were 1000-750m, 750-500m, 500-250m, 250-200m, 200-150m, 150-100m, 100-50m, and 50-surface.

The $1m^2$ MOCNESS samples collected were split with a Folsom splitter, with half of the sample preserved in 4% buffered formaldehyde/seawater solution for laboratory measurement of displacement volume (Smith et al., 1998; Lane and Smith, 1997) and taxonomic analysis. Other fractions were shared with other cruise participants.

Laboratory analysis. The samples reported here were split one to four times, depending on the amount of plankton present, in a Folsom splitter at the Rosenstiel School of Marine and Atmospheric Science (RSMAS), University of Miami. Subsamples were concentrated to 20 to 100ml and were transported to Ukraine (Russia) for enumeration and identification at the Institute for Biology of the Southern Seas (IBSS) in Sevastopol. Treatment of the samples at IBSS depended on the amount of plankton present in each sample. When the sample contained only a small amount of plankton, the entire split was analyzed for all species. In most cases, however, organisms smaller than ~1.5mm were identified and counted in smaller subsamples collected with a 1, 2 or 5ml Stempel pipette. Two replicate subsamples were withdrawn and counted and the data were averaged for calculation of abundance; generally 1-40 individuals per taxon were identified and sometimes more when a taxon was particularly abundant. Organisms ranging in size from ~1-2mm were counted in another part of the subsample collected with a 5ml Stempel pipette or by splitting the subsample into two or four equal parts. The entire subsample originating at RSMAS was then analyzed for abundance of organisms larger than 2mm, including copepods, euphausiids, amphipods, fish larvae, ostracods and any rare, large organisms. A total of 300 to 500 organisms per entire split were identified and counted. The identifications were performed with the aid of Leningrad Optic-Mechanics Company (LOMO) binocular microscopes using various magnifications depending on the sizes of the individuals being identified. Copepod species are listed in alphabetical order. All copepod adult stages, copepodite stages and nauplii found in each sample are listed. The taxonomic notations are: c1 = copepodite stage I of the species; c2 = copepodite stage II of the species; c3 = copepodite stage III of the species; c4 = copepodite stage IV of the species; c5 = copepodite stage V of the species; c = undetermined copepodite stage of the species; m = adult males of the species; f = adult females of the species. Total length is the average length in mm measured microscopically for that taxon.