
Woods Hole Oceanographic Institution
Biology Department Seminar

Thursday, November 8, 2012
Redfield Auditorium - 12:00 Noon

**Population genetic structure and gene expression
patterns of the copepod *Calanus finmarchicus* in
the North Atlantic Ocean**

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The planktonic copepod *Calanus finmarchicus*, found throughout Sub-Arctic waters of the North Atlantic, is among the most abundant marine species. Geographic variations in behavior, ecology and timing of life history events have been the subject of many studies. Spatial/temporal patterns of population genetic variation were examined over basin- and small-scales using Single Nucleotide Polymorphisms (SNPs) in nuclear protein-coding genes. The results confirmed that *C. finmarchicus* is a high-gene flow species, and yielded evidence of large-scale population differentiation consistent with two to four distinct populations. Small but significant levels of sub-regional scale structuring were observed among area populations. Preliminary analysis of interannual variation using time-series collections from the Gulf of Maine indicated the presence of significant variation in SNP allele and genotype frequencies among years. Temporal patterns appeared related to North Atlantic Oscillation (NAO) variation. Differential gene expression analysis of *C. finmarchicus* populations in the Gulf of Maine revealed upregulation of genes involved in protein synthesis, cell-cycle and tissue buildup in females and juveniles collected in deeper strata (130m); genes related to protein turnover, cellular homeostasis, activity, and stress/immunity responses were upregulated in females collected at the surface. Future studies are planned to examine small- to large-scale patterns of time/space variation using next-generation sequencing analysis of transcriptome-wide patterns of gene expression.