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UNIVERSITY OF CONNECTICUT

Department of Marine Sciences  
Presents a Seminar By

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## **Next generation genomics for fisheries management and marine conservation**

In face of accelerated rates of climate change and other growing anthropogenic pressure, it is important that we get a better understanding of how different organisms respond to altered environmental conditions. Historical DNA samples can be an important resource for this endeavor because they provide unique insights into the past and can help recover detailed information about how natural populations have responded to previous impacts. In this talk, I will explain how we have used DNA extracted from extensive collections of archived otoliths ('ear stones') to assess how the genetic composition of Atlantic cod (*Gadus morhua*) populations in Greenland and Canada have changed over the past 80 years. By analyzing >900 gene-linked single nucleotide polymorphisms (SNPs) in contemporary and historical samples, we obtained unprecedented power to detect weak population structure in this species and observed that the spatial distribution of certain populations had remained stable over decades, while substantial geographical distribution shifts were evident in other populations. We also detected strong signatures of divergent adaptation among the populations and found evidence for ongoing selection acting on specific parts of the cod genome over decadal time scales. This recent selection may reflect evolutionary changes induced by the intense fishing pressure that these cod populations have endured. A growing body of evidence suggests that the strong mortality on particular size and age groups imposed by fishing have caused large changes in heritable life history traits of many exploited populations. However, in wild fish stocks it is often difficult to fully disentangle genetic from phenotypic changes and to distinguish selection caused by fisheries as opposed to other potential drivers. To get a basic understanding of how fisheries selection may affect the exploited populations at the molecular level, I have returned to a seminal experiment that under highly controlled conditions demonstrated substantial evolution in growth rates and a suite of correlated traits in response to size-selective fishing over just five generations in the Atlantic silverside (*Menidia menidia*). I will present results from an exome-wide scan for genomic changes in fish from the original experiment. These results provide a first look into the genomic basis for fisheries-induced evolution and shed light on what types of genetic variation and physiological pathways fisheries-selection acts on, how extensively it impacts the genome through direct and indirect effects, and how reversible the changes are once fishing stops. These insights should provide a better understanding of how fisheries-induced selection operates and what signatures we may expect in affected natural populations.

**Host:** Hannes Baumann

**Time & Date:** 11:00 am, Friday, November 11, 2016

**Place:** Marine Sciences Building, Seminar Room 103

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email [marinescienceseminars@uconn.edu](mailto:marinescienceseminars@uconn.edu), or call 860-405-9152 or 860-405-9151