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Summary of current and planned genetic  
data to resolve the breeding and feeding  
ground structure in North Atlantic  
humpback whales, *Megaptera  
novaeangliae*

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INTERNATIONAL  
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# Summary of current and planned genetic data to resolve the breeding and feeding ground structure in North Atlantic humpback whales, *Megaptera novaeangliae*

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Since the last comprehensive assessment of North Atlantic humpback whales in 2001-2002 the number of samples has increased from ~3,700 to ~ 8,600 samples, and the data per sample increased from 6 to 21 microsatellite loci. In other words, the data set has increased from ~ 22,000 to ~180,000 microsatellite genotypes. In addition, a *de novo* reference genome has been sequenced, assembled and published. All samples genotyped prior to 2001 have been re-sequenced and re-genotyped. In addition to some additional low coverage whole genome sequencing (x10) and RADSeq-based data, we are also working on greatly increasing the number of microsatellite loci genotyped in each specimen.

## ***Current DNA samples***

Table 1: Sample sizes and areas

North Atlantic region (and latitude)	No of samples
western North Atlantic	
high-latitude	3,226
mid-latitude	89
low-latitude	
western Caribbean	4,588
eastern Caribbean	15
Central North Atlantic	
high-latitude	170
mid-latitude	7
eastern North Atlantic	
high-latitude	436
mid-latitude	35
low-latitude	56
Mediterranean Sea	2
Grand Total	8,624
<u>Additional samples awaiting shipping</u>	<u>~500</u>

Notes: Samples were collected and provided by; US National Marine Fisheries Service, Center for Coastal Studies, Allied Whale, Memorial University, Mingan Island Cetacean Study Inc., Greenland Institute of Natural Resources, Iceland Marine Research Institute, Norwegian Marine Research Institute, Norwegian Polar Institute, Utrecht University, Slovenian Marine Mammal Society, Irish Whale and Dolphin Group, Marine and Environmental Sciences Centre, University of Barcelona, Brest University, Réserve naturelle de Saint-Martin, Florida Fish and Wildlife Conservation Commission, Georgia Department of Natural Resources, Virginia Aquarium, Members of the Northeast and Southeast U.S. Marine Mammal Stranding Networks, including: Atlantic Marine Conservation Society, College of the Atlantic, IFAW, Hubbs-Seaworld Research Institute, Marine Mammal Stranding Center, Maryland Department of Natural Resources, MERR Institute, Mystic Aquarium, New England Aquarium, Riverhead Foundation, University of North Carolina at Wilmington.

### ***Current genetic data***

- Collected from current samples
  - For all in-house samples in Table 1 (8,624)
    - Genotypes at 21 microsatellite loci.
    - Sex.
    - DNA sequence of first 450 base pairs of the mitochondrial control region (mtCR).
- *De novo* genome assembly from one [Gulf of Maine] female.
- RAD data from 67 individuals.
  
- ***Additional genetic data planned in next 1-2 years***
  - Legacy mtDNA, microsatellite and sex data (as above)
  - mtDNA whole genome
  - Additional RAD data from key winter and summer areas
  - x10 whole genome sequencing of pedigrees
  - eDNA individual identification

### ***Desirable samples***

- Mid-latitude migratory corridors
- Eastern Caribbean
- Low-latitudes in eastern North Atlantic
- Winter areas between Silver Bank and St. Martin
- Low-latitude wintering areas off western Africa
- Northern Hemisphere summer samples from low-latitude areas