Cospesciation of Whale Lice 
(Crustacea: Amphipoda: Cyamidae) 
and Their Hosts (Cetacea: Eubalaena)

Whale lice are Amphipod crustaceans in the family Cyamidae (Leung, 1967). Right whales carry three recognized species of cyamids: Cyamus ovalis, C. gracilis and C. erraticus. There are two long-recognized species of right whales: The northern right whale (Eubalaena glacialis) and the southern right whale (Eubalaena australis). Since cyamids stay on one host (the whale) their whole lives, and the northern and southern populations are no longer in contact with each other, the cyamids would also be expected to have speciated. If so, the three recognized species of right whale cyamids might really be six species. To test this hypothesis, we generated and analyzed DNA sequences for all three cyamid species from the North Atlantic and the two populations of South Atlantic right whales.

As in many other species, the COI gene is extremely well conserved, with Ks/Ka ratios between 50 and 200. (Ks is synonymous [silent] base substitutions per position in DNA, and Ka is non-synonymous [amino-acid changing] substitutions per position.) There is a great deal of synonymous sequence

Hemispheres, but almost no non-synonymous divergence. The synonymous divergences for North and South Atlantic C. ovalis, C. gracilis and C. erraticus are 0.29, 0.39, and 0.37 respectively. These values are large, and they do not differ significantly from each other, so they would appear to correspond to when the Atlantic right whale stopped crossing the equator and separated into two different species. COI molecular-clock calibrations for other marine crustaceans suggest that this split occurred around six million years ago.

Until recently we had assumed that all cyamids of a given species from one whale would have identical mitochondrial sequences. But this summer we sequenced several C. ovalis and C. gracilis from individual whales and found that they differ from each other as much as cyamids from different whales in the same ocean! Interestingly the diversity within both the Northern and Southern C. ovalis populations is greater (Ks up to 0.1) than is the diversity within C. gracilis populations (Ks up to 0.04), and there seems to be almost no variation within C. erraticus populations. These differences in genetic variation may reflect differences of population size and life history.