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New insight on the population structure of *Calanus finmarchicus* in the North Atlantic using Next-Generation Sequencing technologies

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Genetic differentiation between populations of marine species with high dispersal potential has been the subject of long-standing discussions primarily due to the complexity of the marine habitat and the limited number of genetic markers employed. Next-generation sequencing has revolutionized population genetics and allowed genome-wide high throughput genotyping– even for non-model species. Here we used and compared traditional genotyping (microsatellites) with genotyping by sequencing approaches (ddRAD and targeted-resequencing) in natural populations of *Calanus finmarchicus*, an ecologically important planktonic copepod species, to examine large-scale population genetic diversity and structure. These approaches allow cost effective genotyping of a large number of SNPs (Single Nucleotide Polymorphism markers). We analyzed samples covering most of the distributional range of the species. Our results show that SNPs have a greater resolution power than microsatellites and indicate population structure of *C. finmarchicus* in the North Atlantic.

Keywords: Next-generation sequencing . population structure . genotyping . microsatellites . ddRAD . targeted-resequencing . copepod . SNP

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