

Resolving identification challenge of calanoid copepods *Calanus finmarchicus* and *C. glacialis*: molecular and morphological advances

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Recent advances in the Next Generation Sequencing technologies have brought new possibilities to develop genetic resources for non-model species, including zooplankton, and therefore, have high potential to answer long-standing questions in various fields including taxonomy. This could be illustrated on the example of ecologically important copepods *Calanus finmarchicus* and *C. glacialis* that are routinely used as climate indicators and beacons of climate-related changes in North Atlantic and Arctic ecosystems. Morphological identification of *C. finmarchicus* and *C. glacialis* is constrained by subtle morphological difference, overlap of distribution and possible hybridization. We present an example of genome- and transcriptome-assisted insertion/deletion marker (InDel) development for molecular identification of the two closely related species, utilizing massive parallel sequencing on Ion Torrent platform. Twelve InDel markers show species-specific amplicon length, allowing easy and robust molecular identification of *C. finmarchicus*, *C. glacialis*, and their hybrids, as well as co-occurring *C. helgolandicus*, *C. hyperboreus* and *C. marshallae* at any developmental stage. These markers were also used to validate a new morphological criterion – redness – that can easily separate live females of *C. finmarchicus* and *C. glacialis* by the red pigmentation of the antenna and somites. Overall, the identification methods we have developed set up the foundation for further research on *Calanus* and illustrate integration between different taxonomical methods.

Keywords: InDels, redness, Calanus, Ion Torrent, NGS, identification

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