Predominance of ß-proteobacteria in summer melt pools on Arctic pack ice

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ABSTRACT: The diversity and community structure of bacteria in melt pools on Arctic pack ice floes were dominated by bproteobacteria. Thirty-five percent of the pure cultures isolated in 1997 from pack ice floes north of Svalbard and in the Fram Strait were from the ß-proteobacteria group. Within this group, there were only two phylotypes clustering within the widespread Beta I cluster, also known as the Comamonadaceae clade. One phylotype, most closely related to *Aquaspirillum arcticum* (96.0-97.3% identical), was frequent among cultures isolated from 10 melt pools. A 16S ribosomal RNA (rRNA) gene clone library, constructed from a melt pool that was sampled 2 yr later in the Fram Strait, was also dominated by ß-proteobacteria, in particular the same recurrent isolate phylotype designated □MP-Beta□. Fluorescence in situ hybridization of 20 melt pools corroborated the cultivation and cloning data. b-Proteobacteria were the most abundant bacterial group, constituting ~49% of the bacteria that were stained by 496-diamidino-2-phenylindole (DAPI). α- and γ-proteobacteria accounted for only 2% each, the *Cytophaga-Flavobacterium* group accounted for 9%, and the *Actinobacteria* spp. accounted for 9%. Approximately 63% of the ß-proteobacterial fraction that was found in the melt pools was determined with a newly developed probe to be the recurrent ß-proteobacterial MP-Beta1 phylotypes, indicating that it is particularly adapted for success in this extreme environment.