Metaproteomic and 16S rRNA Reveal Rapid Shifts in Functional Responses of Native Polar Bacterial Communities to Organic Carbon Inputs: Does Taxonomy matter?

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The cycling of organic carbon in marine systems is primarily catalyzed by microbes, and is particularly important in the polar oceans where primary production is temporally offset from upper trophic level consumption. We examined the response of native bacterial communities in the Bering Strait chlorophyll maximum and Chukchi Sea bottom waters to marine derived organic carbon input using using mass spectrometry-based metaproteomic and 16S rRNA analysis to trace cellular function responses and community taxonomic composition at 0°C. Major organic component analysis measured the impact of proteomic expression on organic carbon composition. Bacteria from both locations and under both treatments showed rapid community responses and changes in proteomic expression, accompanied by distinct changes in the concentration and distributions of multiple organic components. In the Bering Strait surface community, protein translation was an important immediate cellular response under marine POM addition and its absence, while specific metabolic processes were more distinct between treatments over 6 days. Surface and bottom waters showed distinct responses and substrate-specific transporter activity with the Chukchi Sea community higher than in the Bering Strait, especially under low organic conditions. The patterns of functional responses contrasted with taxonomic analysis which revealed 3 classes + inconclusives classes dominate well over 90% of changing cellular functions with activities across all taxonomic classes highly variable. An important observation was that less dominant bacterial groups exhibited similar proteomic functional responses over time.