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Coupling deep-water circulation and microbial communities of the North Atlantic

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The movement of deep-water masses in the Atlantic is one of the major factors driving the oceanic conveyor belt. During the last decades, oceanographers have identified the physical properties and general flow patterns of the main water masses of the Atlantic Ocean. These water masses differ greatly in their physical properties as well as in age and nutrient concentrations. However, little is known about the microbial communities inhabiting these waters. The low prokaryotic abundance observed in deep waters makes it difficult to measure their activity, thus leading many oceanographers to think that the deep water masses of the ocean are more or less evenly populated by starving prokaryotes with no biogeochemically significant activity. Here we present measurements of microbial activity and community structure along a ˜4,000 km transect covering meso- and bathypelagic layers of the Atlantic Ocean. Our results show that, despite their low abundance, deep-water prokaryotes are active and present different patterns of activity in different water masses. Moreover, the different water masses harbor characteristic prokaryotic communities with some prokaryotes being specific to a certain water masses. These data suggest that deep-water prokaryotes are well adapted to their environment and may play a much bigger role in the biogeochemical cycling of carbon than hitherto assumed.