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The sea surface microlayer is a thin surface film located at the interfacial point between the sea surface and the atmosphere. Compared to the underlying water (UW) below it, the SML is a unique but harsh environment; with elevated meteorological stresses and biologically and chemically enriched. Thus, it is widely recognized that the physical, chemical and biological processes in the SML are very different compared to UW even with just a few centimeters difference in depth. The proximity of this thin layer to the atmosphere also makes this layer highly dynamic and one of the most important layer to control the air-sea biogeochemical exchanges and climate-related processes. This biofilm-like thin layer with a depth of less than 1000  $\mu\text{m}$ , this layer have found to exist in most aquatic habitat and oceanic environments. This layer was found to be composed of hydrated gelatinous layer entangled in a matrix of dissolved organic matter composed mainly of transparent exopolymer particles (TEP). While few research have shown that the bacterial community in the SML possessed different functional genes compared to the underlying water others, in mesocosm experiments, have shown that bacterioneuston responded differently when introduced to experimentally-induced carbon dioxide loading scenarios in mesocosm experiments. However, little is still known about the microbial structure in this layer and their contribution towards the global biogeochemical cycles. In our research, bacteria community structure in the SML (bacterioneuston) at Aburatsubo Inlet, Misaki during summer and winter were examined using high throughput sequencing. In contrast to conditions in UW that remained constant throughout the sampling period, SML was highly dynamic with fluctuations in biological matter concentrations and bacterial communities. At times when the SML was enriched with biological matter and distinct bacterioneuston communities were formed. When the SML was enriched, rare bacterial groups including those that could play a role in biogeochemical cycles were more abundantly found in the SML and the diversity of these groups increased in proportion to the magnitude of biological matter enrichment in the SML.

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