## **Marine Microbial Diversity and Genomics**

Frank Oliver Glöckner

Seas and oceans cover over 70% of the Earth's surface and account for 97 percent of the biosphere. Marine ecosystems provide energy resources, and the basis for maritime transport, and recreation. The oceans contain the highest biological diversity on Earth; marine organisms live throughout the water column, to an extreme depth of up to 11 km, and in ocean sediments up to a further 400 m below the seafloor. Marine microorganisms in particular play a central role in the global cycling of matters and energy, for they are both a driver and indicator of global climate change. Furthermore, they are an inevitable genetic resource for new enzymes and reactions which can be used for pharmaceutical and industrial applications. Current estimates show that a millilitre of sea water hosts around 1 million cells. In sediments total cell numbers of up to 1 billion per gram

against databases of functionally described genes. Alternatively, the respective clone libraries are initially screened for specific enzymatic functions (activity or functional screening) and only if activity is found are the corresponding clones sequenced and further processed. The most prominent large-scale metagenomic studies carried out in the marine environment were the shotgun sequencing of the Sargasso Sea and the Global Ocean Survey by Venter et al. (10, 12). These two investigations have delivered several million new enzymes and currently represent the largest sequenced reservoir of functional genes from the marine environment. Since only a part of the samples have been analysed to date more data can be expected soon.

Coinciding with the

Prochlorococcus marinus