

## IOW Press Release - September 19, 2011

### Marine scientists from Warnemünde succeed in deciphering the microbial world of the Baltic Sea

*...and prove that bacteria do not follow the textbook rules describing the salinity/ diversity relationship of aquatic animals and plants*

*...and discover the apparently most abundant organism of the Baltic Sea – a bacterium unknown until now.*

In a comprehensive measuring campaign, the microbiologists Daniel Herlemann, Matthias Labrenz and Klaus Jürgens, from the Leibniz Institute for Baltic Sea Research in Warnemünde, together with Swedish colleagues have succeeded in sampling microorganisms from the entire Baltic Sea, from the southwestern marine Skagerrag to the northern freshwaters of the Bothnian Bay. The respective bacterial communities were analyzed by means of state-of-the-art "high-throughput sequencing technologies." Thus, the Baltic Sea is the first sea in which all of the microbial inhabitants have been completely inventoried.

The results, which were published very recently, are astonishing: unlike the Baltic Sea's fauna and flora, its bacteria are unimpressed by the varying salinity that prevails in the Baltic. Indeed, while many organisms avoid the intermediate salinities (between freshwater and saltwater) that are characteristic of the central Baltic—which explains the minimal diversity under brackish water conditions—bacteria clearly differ in that under these conditions they show a constant species diversity.

Similarly, although typical marine or limnic bacterial assemblages become less diverse beyond the fully marine or limnic margins of the Baltic Sea, bacterial diversity remains high in the brackish water of the Baltic Proper because of the presence of species adapted to these conditions.

Among these, one bacterium was discovered that seems to thrive extraordinarily well in the Baltic Proper: this remarkably abundant organism belongs to the group of *Verrucomicrobia*, which was previously mainly found in lakes and soils. The function of this newly discovered and highly abundant bacterium is, at the moment, obscure. Moreover, in addition to the lack of cultivated representatives, specific sequences of the closest related isolate of



the *Verrucomicrobia* group and those of the newly discovered organism differ by 12%.

The results support the notion that bacteria are well-equipped to cope with the challenging transitional area between freshwater and saltwater in the Baltic Sea and that, in contrast to higher organisms, there is no decline in their number of species under these conditions. Thus, the rapid and flexible adaptability of bacteria enables them to occupy ecological niches to which higher organisms have only limited access.

The results were published in the article: **“Transitions in bacterial communities along the 2000 km salinity gradient of the Baltic Sea”** Daniel PR Herlemann, Matthias Labrenz, Klaus Jürgens, Stefan Bertilsson, Joanna J Waniek and Anders F Andersson. The ISME Journal, (published online 7 April 2011) | doi:10.1038/ismej.2011.41

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