



Modelling the seasonal occurrence and distribution of humanpathogenic bacteria within the German Bight, southern North Sea

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In recent years, the occurrence of human-pathogenic bacteria of the genus *Vibrio* in the North Sea and the Baltic Sea has come into the focus of many marine research activities, as different *Vibrio* strains caused harmful infections, especially in summers 2003, 2006, 2010 and 2014. Furthermore, it is anticipated that under global warming conditions, the risk of the occurrence of human-pathogenic in summer season will increase very likely.

To present knowledge temperature and salinity are the most powerful predictors of the occurrence of *Vibrio* spp. in coastal waters. However, studies support the interaction of human-pathogenic *Vibrio* spp. with different host and vector organisms like chitinous zooplankton or with predator organisms such as *Vibrio*-specific bacteriophages.

A modeling system has been developed to understand and predict the occurrence and distribution of harmful *Vibrio* spp. within the North Sea with a special focus on the German Bight including the shallower Wadden Sea areas and the estuaries of Ems, Weser and Elbe. On the one hand, this modeling system is based on the unstructured-mesh hydrodynamic model FVCOM, which can predict the oceanic circulation and distributions of temperature and salinity within the German Bight for appropriate present and future climate conditions. On the other hand, a biological module has been attached, which can simulate the distribution and abundances of *Vibrio* spp.. In detail, apart from specific *Vibrio* strains, this biological module incorporates functional groups of phyto- and zooplankton and bacteriophages as potential host- and predator-organisms.

In a first study, this modeling system has been applied to a hot summer season in 2006. It has been demonstrated that this system can reproduce the valid hydrodynamic conditions within the North Sea region of interest including temperature and salinity distribution patterns. In addition, reasonable temporal and spatial patterns of *Vibrio* abundances have been obtained.