## Effect of climate change on the microbiome of the blue mussel

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Marine environments are being threatened by global change. Increased atmospheric CO<sub>2</sub> concentrations lead to global warming on the one hand, and on the other hand to a decrease in ocean pH. Moreover, marine coastal areas are increasingly used for the production of marine renewable energy, mainly by installing offshore wind farms. As such, artificial hard substrates are being introduced in areas that are otherwise characterized by sandy sediments. These artificial hard substrates are being colonized by a fouling fauna: for instance, the bivalve Mytilus edulis. They can serve as a predictable and resource-rich surface for microbial communities and are to be considered as biogeochemical hotspots in the aquatic environment producing considerable amounts of N<sub>2</sub>O, and in this way affecting the N-cycle. N<sub>2</sub>O is considered a highly potent greenhouse gas, and thus also contributing significantly to global warming. In the PERSUADE project (BELSPO) 16S rRNA gene sequencing will be conducted to detect and identify these  $N_2O$  producing sources in biofilms associated with the shell of the mussel. The microbiome and some functional genes will be screened between the current natural situation and acidified and warmer conditions, and a combination of both. In this way, we can try to predict if climate change has an influence on the bacterial composition of biofilms and if this change in composition may have an effect on the N-cycle. Preliminary results show that the microbial communities present in the microbiomes of the mussels, and the denitrification rates, differ between the control and all climate change treatments. These results indicate that climate change may influence the N-cycle and may have an impact on the production of an important greenhouse gas. The new hard substrates created by offshore wind farms in the North Sea may thus influence communities and nutrient cycles more than previous expected.

Keywords: Offshore wind farm; Microbiome; Climate change; N-cycle