New Approach for Active Biomass Measurement and Dynamics of Bacterial Communities in Sediment

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The degradability of chemicals in different environmental compartments is one of the major determinants of their environmental fate and therefore plays a crucial role in regulatory decision making. In the study of chemicals degradability, simulation tests present several uncertainties with regard to performance, evaluation and data interpretation. In this context, this work aimed to evaluate an alternative method, based on the 16 S RNA, to measure sediments microbial activity, responsible of biodegradation through sediment-associated microorganisms.

Two natural sediments, with different textures, were selected to simulate the biodegradation of four different test substances (Aniline, Pyriproxyfen, Voriconazol, Celecoxib). For every sediment/test substance, four tests were conducted in parallel including: a setting according OECD 308, OECD 308 modified (with a thinner, ideally fully aerobic sediment layer), OECD 309 and OECD 309 modified (with higher sediment content). Biomass was measured, at the beginning of and at the end of test by fumigation and also using reverse transcriptase quantitative PCR (qRT-PCR). Additionally the microbial diversity of the sediments was studied with polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE). Eubacterial primers were used, in both, qRT-PCR and DGGE (GC clamped primers). In order to monitor the function of the microorganism in each test system the mineralization of ^{14}C-Aniline as reference standard was measured. This way a huge data set will be finally available to compare the different methods for microbial activity determination.

The results obtained so far showed no correlation between the mineralization, fumigation and qRT-PCR results, and in most cases biomass was overestimated when using the fumigation method. The results of the qRT-PCR did not show significant differences between the different test settings, however different microbial profiling was observed in the DGGE pattern. This analysis of microbial diversity gives first indications of a possible shift of individual microorganism populations, which might explain the biodegradation results better than a total estimation of the active microbial population. Studies are not yet finished but it can be concluded already that a deeper analysis of microbial diversity is needed and further studies to evaluate in deep the differences observed, should be conducted.