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Abstract

The aim of the present work was to investigate the dynamics of microbial community at DNA and RNA level and the role of *bamA* and *mcrA* gene during anaerobic digestion of phenol and p-cresol. Anaerobic digestion was conducted in batch reactors and microbial community dynamics was analysed. Results showed that active microbial community was quite dissimilar in comparison to the total microbial community. *Syntrophorhabdus* and *Bacillus* were the dominant active bacterial genera whereas *Methanosaeta* together with *Methanobacterium* showed the highest potential activity in the *Archaea* domain indicating a relevant role of these microorganisms in the anaerobic process. Ecological Networks revealed dissimilar interactions