

Evolution of bacterial community in isopropanol-degrading biotrickling filters by fluorescence in situ hybridization (FISH).

M.C. Pérez, F. J. Álvarez-Hornos, P. San-Valero, C. Gabaldón.

Univ. Valencia, Dep. Chemical Engineering, Av. de la Universidad s/n, 46100 Burjassot, Spain. Tel: +34963543169, fax: +34963544898, e-mail: maria.c.perez@uv.es

One of the most important industrial pollutant sources is the emission of volatile organic compounds (VOCs) from the use of solvents. Biological treatment technologies, such as biofilters (BFs) and biotrickling filters (BTFs), for controlling VOC emissions are attractive techniques because of their efficiency and cost-effectiveness. BTFs use a specified inert packing material and involve a liquid phase, which trickles through the bed providing nutrients. The biofilm is developed on the packing surface. Removal efficiency in BTFs depends on multiple parameters, being the microbial community a key parameter in the performance of this process.

In this study, the bacterial population of two biotrickling filters (BTFs) treating isopropanol by using fluorescence in situ hybridization (FISH) is analyzed. The experimental system consists in two identical laboratory-scale BTFs named as BTF1 and BTF2. The two bioreactors were operated in parallel during an experimental period of one year working under intermittent feeding conditions. Operating conditions and maintenance were identical in both BTF.

The FISH technique was carried out following the procedure described by Álvarez-Hornos et al. (2011) with a Cy5-labelled EUBmix probe for most bacteria and Cy3-labelled specific probes (Thermo Fisher Scientific, Germany). Specific probes were quantified as a proportion of EUBmix labeled bacteria using image analysis with the methodology developed by Jubany et al (2009).

The FISH technique was applied in order to study the changes of the microbial population within the different operational conditions applied in the BTFs during days 64 to 276. For example, the relative abundance of the general groups of bacteria in BTF1 is shown in Figure 1; in particular, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Actinobacteria* (high G+C Gram-positive bacteria) and *Firmicutes* (Low G+C gram-positive bacteria) are expressed as percentage of EUB338mix stained cells. It can be observed a variation in the composition of the bacterial community with time of operation.

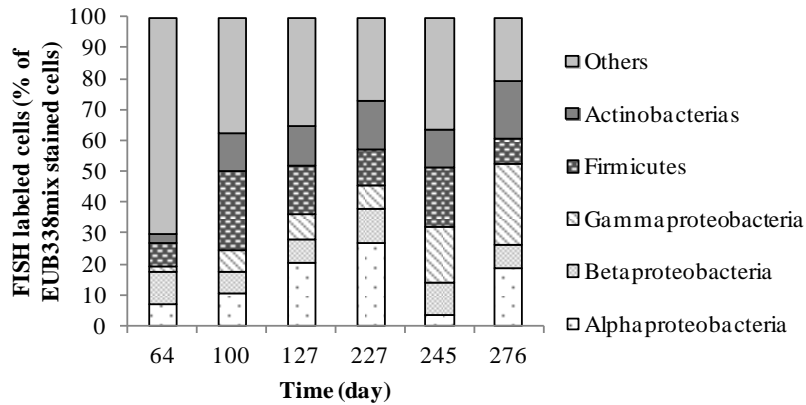


Fig.1. Evolution of bacterial community composition in BTF1.

Acknowledgments

The research leading to these results has received funding from the People Programme (Marie Curie Actions) of the European Union's Seventh Framework Programme FP7/2007-2013/ under *REA* grant agreement n° 284949. Financial by Ministerio Ciencia e Innovación (Spain, research Project CTM2010-15031) is also acknowledged. M.C.Pérez has a FPU grant from Ministerio de Ciencia e Innovación, Spain.

References

- Álvarez-Hornos, F.J., Lafita, C., Martínez-Soria, V., Peña-Roja, J.M., Pérez, M.C., Gabaldón, C. (2011). *Biochemical Engineering Journal*, 58-59: 154-161.
- Jubany, I., Lafuente, J., Carrera, J.Baeza,J. (2009). *Journal of Chemical Technology and Biotechnology*, 84: 1140-1145.