

Characterization of an ibuprofen-eater bacteria

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The presence of pharmaceutical compounds (PhCs) in drinking water, treated wastewater, groundwater, surface water, and soil around the world is an emerging challenge. The bioremediation of organic pollutants by microbial degradation is a proven method for counteracting the contamination caused by these recalcitrant substances.

We have isolated a bacterium belonging to the genus *Sphingomonas*, able to grow with ibuprofen as sole carbon and energy source. This strain was isolated from a Wastewater Treatment Plant of a pharmaceutical company (Almirall). Its genome sequence contains genes previously described as necessary for the biotransformation of ibuprofen. The ipf cluster is flanked by transposon sequences and its GC content is lower than the average of the genome, suggesting that this cluster could have been horizontally acquired.

We performed a transposon mutagenesis with a miniTn5 derivatives and selected mutants unable to use ibuprofen as a nutrient. Three different phenotypes were detected: (i) mutants unable to grow that do not modify the growth medium, (ii) mutants unable to grow that give a brown colour to the medium and (iii) leaky mutants able to poorly grow on ibuprofen. Sequencing of the region flanking the insertions mapped the insertions as follows: the non-coloured mutants (i) were mainly located into the ipf cluster, the brown mutants (ii) in a different genomic region that contains genes belonging to aromatics degradation pathway and the leaky mutants (iii) in a Propionyl-CoA carboxylase carboxyl transferase subunit. We have constructed a genomic library to complement those mutant and the results suggest that only these regions are involved in ibuprofen degradation.

We propose a complete ibuprofen degradation pathway that seems to have been formed by combination of different biodegradation pathways, some of which acquired by horizontal gene transfer.

14 de Octubre de 2020 a las 12:30