Bacteria feeding on antibiotics – eating the poisonous

Philippe Corvini, Boris Kolvenbach, Hans-Peter Kohler, Benjamin Ricken, Institute for Ecopreneurship, School of the Environment, FHNW Gruendenstrasse 40, CH-4132-Muttenz, Switzerland TEL: +41-61-467-4344, philippe.corvini@fhnw.ch

Micropollutant removal from wastewater is of high concern in Europe and is regulated by the EU "Water Framework Directive" (WFD) and the "Swiss Water Protection Law". It has been shown that the presence of antibiotics in the environment contributes to the formation and spread of resistance genes among bacterial strains (1). Especially wastewater treatment plants (WWTP) are proposed to be a hubs for the emergence of resistant bacterial strains and one of the major sources for the input of bactericidal micropollutants into the environment (2, 3). Among these substances, sulphonamide antibiotics are the second most used antibiotics worldwide in human and in veterinary medicine with a release of ~20,000 tons year⁻¹ (1). The photo- and thermally stable sulframethoxazole (SMX) as one representative of this chemical group, is often detected in significant concentrations reaching several µg/L (4). The biodegradation pathways are poorly understood and several studies report insufficient sulphonamide removals by conventional sewage treatment (5).

We report here on the isolation of bacterial strains, which are not only resistant to the sulphonamide antibiotics, but also degrade and mineralize them. One of these isolates, namely Microbacterium sp. strain BR1 is able to feed on SMX as sole carbon and energy source. In this bacterium, the degradation of SMX and structurally related compounds is initiated by an ipso-substitution, catalysed by a flavin-dependent monooxygenase acting in concert with a FMN reductase (6). The resulting p-aminophenol enters the central metabolism through a second monooxygenase activity, which leads to products amenable to ring opening (7). The cluster of genes involved in this degradation process was identified and each of these three enzymes could be heterologously expressed in E. coli (8). The presence of this gene cluster might represent an additional, yet unknown resistance mechanism for bacteria against sulfonamides. Even though the classic sul1 gene is present as well in Microbacterium sp. strain BR1, its additional capacity to feed on SMX might represent a superior mechanism conferring to the bacterium clear advantages over a modified protein target especially in nutrient limited environments but also in case of human infection.

References

Sci. Rep. 7(1): 15783 doi: 10.1038/s41598-017-16132-8

Keywords
Sulfonamides; ipso-substitution; flavin dependent monooxygenase; wastewater treatment