P-110 - NEW INSIGHTS ON MECHANISMS OF SULFONAMIDE BIO-TRANSFORMATION BY ENVIRONMENTAL BACTERIA

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Background

Since 1935, when sulfonamides were first introduced as antimicrobials, resistance to this class of drugs was observed in a variety of bacteria. In contrast to beta-lactam antibiotics that are hydrolyzed by resistant bacteria, bacterial sulfonamide resistance occurs through mutations in chromosomal DHPS gene (*fol*P) or acquisition of an alternative DHPS gene (*sul*) involved in the biosynthetic folate pathway. While partial mineralization or transformation of sulfonamides by bacteria have been recently reported, these processes seem by far more uncommon than sulfonamide-resistance, and eventually not related with resistance. This study aimed at investigating the capacity of aquatic-bacterial isolates to transform sulfonamides and assess if such capacity could be associated with resistance.

Method

Forty-seven Gram-negative isolates from wastewater (WW, n=4), surface-water (SW, n=7) and drinking-water (DW, n=36) able to grow in the presence of 50 mg/L SMX were included in this study. The presence of sulfonamide-resistance genes (*sul*1, *sul*2) was investigated. Biotransformation assays were conducted in mineral or in rich media supplemented with SMX(50 mg/L). Identification of the SMX-transformation product was carried out by LC-MS.

Results & Conclusions

SMX-tolerance could be explained by the presence of one or both of the analyzed *sul* genes in only 15 of the isolates, and only 14 were able to transform SMX. Interestingly, only 3 isolates able to transform SMX carried one of these antibiotic-resistance genes (*sul*1), and most (n=13) were recovered from drinking-water. None of these SMX-transforming isolates could use the antibiotic as the sole source of carbon and energy, being the biotransformation only possible through co-metabolism, with accumulation of acetylated SMX. Bacteria able to transform SMX were affiliated to *Pseudomonas* (n=12), *Brevundimonas* (n=1), and *Stenotrophomonas* (n=1). Among the transforming-strains, *Pseudomonas mandelii* McBPA4 converted up to 81% of the initial SMX concentration after 48 h incubation in a feed-batch reactor. *N*-Acetylation of SMX by these fresh-water bacteria might contribute to their environmental adaptation, especially to those tested negative for sulfonamide-resistance genes, but further studies are needed to rule out other mechanisms of sulfonamide-resistance.

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