

Nuclear techniques for surveillance and monitoring of antimicrobial and antimicrobial resistance in soil and the environment

Introduction

- Antimicrobials (AM) play a critical role in the treatment of human and animal diseases.
- pathogens.
- to develop guidance to managing it cost effectively.

Antimicrobial movement from agricultural areas to the environment

- efflux or decreased permeability; and (4) general cell adaption (Figure 1).
- veterinary medicine.
- contain antibiotics from veterinary medicine.
- concentrations and the abundance of pathogenic antibiotic-resistant bacteria (Figure 2).

Existing conventional methods for monitoring antimicrobials

- conventional methods used for monitoring antimicrobials.
- hybridization.

Nuclear techniques and tools for determining the source and transport of AM

- distribute.

- changes in the stable isotope composition of a contaminant (Elsner et al., 2005).
- enrichment factor.
- 2016).

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• Globally, about 700 000 deaths/year arise from resistant infections because AM drugs are less effective at killing resistant

* AM chemicals that are present in environment can trigger the development of antimicrobial resistance (AMR). * A better understanding of how AMR moves from agricultural areas to the environment through soil and water is important

* We examined the potential of nuclear techniques—the application of compound-specific stable isotope analysis (CSIA) to determine the origin, production process and transport of AM through soil and water to the environment.

Antibiotic resistance can originate from: (1) the transformation of antibiotics; (2) changes in bacterial target site; (3) active

Antibiotics enter the environment when discharged into wastewater or into surface water, or through human and

Soil is the most important vector when antibiotics are used as pesticides, or when manure and slurry used as fertilizers

Important knowledge gaps exit on interdependency of antibiotics concentrations, antibiotic resistance genes (ARGs)

* Liquid chromatography, mass spectrometry, and bioanalytical quantification of antibiotics are currently some of the

The quantification, detection, typing and characterization of ARGs in environmental samples are possible using molecular biological methods that are based on nucleic acid amplification tests (NAATs), DNA sequencing, or DNA

* Nuclear techniques trace the antibiotic medicine – the chemical, not the antimicrobial resistance which is the pathogen in question. Once a selection pressure is imposed, AMR genes may potentially originate, amplify and

CSIA is a powerful tool that provide answers when existing monitoring methods fall short. It may reveal different sources of an identical chemical and may detect when a given chemical has been transformed or degraded. Successful applications have focused on the sources and fates of many common groundwater contaminants such as chlorinated solvents and BTEX (benzene, toluene, ethylbenzene, and xylene) compounds (Fischer et al., 2016). A decrease in concentration of a contaminant can result from transformation, dilution or sorption, pronounced

• Observed isotope fractionation in situ is compared with laboratory observations, to determine a pathway-specific

An analysis of stable isotope patterns can be used to determine the source of a contamination, because the ground stocks and synthesis pathway used during production can leave a typical 'stable isotope fingerprint' (Nijenhuis et al.,





Figure 2. Pathways for antibiotics, antibiotic resistance and antibiotic-resistant pathogens into the environment and the food chain (left) and current knowledge gaps about their concentration behaviour throughout the process (right).

Conclusions and the way forward

Antibiotics kill bacteria, healing infections that cause diseases and death, hence an urgent need to understand the sources and environmental fate of antibiotics, antibiotic resistance genes and the pathogens carrying the resistance genes and develop a stepwise methodology to monitor AM and AMR in the environment.

References

Fischer et al (2016) Curr Opin Biotech, 41: 99-107. Elsner et al (2005) Environ Sci Technol, 39: 6896-6916. Nijenhuis et al (2016) Trends Environ Anal, 11: 1-8.