



Pharmaceutical Biotransformation of Comamonas and Aeromonas Species

Minghui Yao*

Xinchuang Biotechnology (Xiamen) Co., Ltd., Xiamen, Fujian, China

ABOUT THE STUDY

Contamination of natural niches by pharmaceutical residues has become a major concern. The discharge of untreated waste water from pharmaceutical, hospital and domestic facilities has been identified as an important source of the massive spread of antibiotics. The unnecessary existence of pharmaceutical residues, including antibiotics, is associated with an increased risk of selection for resistance between pathogenic and non-pathogenic microorganisms. To date, several methods have been proposed to remove these pollutants from wastewater, but their implications on a larger scale are not feasible due to the complexity and high cost of the processes, especially in developing and underdeveloped countries. This study aimed at isolating and characterizing bacterial strains from domestic and pharmaceutical wastewater that are bio transformable to most persistent antibiotics.

The discovery of antibiotics played a crucial role in the treatment of life threatening infections and drastically altering the mortality and morbidity rates associated with them. Since then, these biologically active compounds have become indispensable in the maintenance of human health and improvement of quality of life. Besides human medicine, antibiotics have extensive application in aquaculture research and veterinary medicine to treat infections and promote growth in animals [1,2]. Such widespread usage of antibiotics has given rise to concerns related to their persistence in the environment for longer periods of time. This is attributed to their partial metabolism in humans and animal body which results in their discharge in active form. The unnecessary persistence of antibiotics results in the development of drug resistance in human, animals and pathogenic microorganism, rendering the drugs ineffective against the diseases. Apart from pathogenic resistivity, antibiotics also have adverse effects on structure and functions of ecological system. Biological diversity plays key role in the maintenance of ecological functions and biogeochemical cycles, which are generally mediated by a consortium of microorganisms. Antibiotics reduce biodiversity by eliminating or inhibiting non-target microbial species, ultimately affecting

normal biological processes such as nitrogen fixation, biomass production and functional stability.

Domestic, pharmaceutical and hospital effluents are the primary sources of antibiotic disposal and are considered as the hot spots for their widespread release in the environment. If these effluents are not properly treated in sewage treatment plants for the degradation and elimination of such active compounds, they ultimately find their way into the natural environment such as soil, surface water and ground water. Several studies have reported the presence of multiple antibiotics in natural water sources as well as in treatment plants. Various chemical and abiotic methods have been invented and used to date for the removal of organic pollutants, including advanced oxidation and adsorption processes. The complexity, high cost and difficulty of chemical sludge treatment of such processes make them ineffective for large-scale application. Over the years, bioconversion has become a safe and cost-effective tool for environmental adaptation and is used to transform a wide range of organic pollutants including metals, pharmaceuticals, and chemicals products and hydrocarbons [3]. This is mainly due to the observed catabolic diversity, growth rate, and horizontal gene transfer characteristics of the bacteria, presenting them as suitable candidates for this process. Most biotransformation studies have used mixed cultures isolated from sewage sludge or soil sources. The biodegradation of sulphonamides was achieved by bacterial strains isolated from wastewater sludge, including *Achromobacter denitrificans* PR, *Pseudomonas* and *Arthrobacter* species. Liao and sewage sludge investigated the ability of a mixed culture consisting of bacterial strains of the classes Bacteroidia, Gamma proteobacteria and Beta proteobacteria to degrade ciprofloxacin. A complex called AMQD4 was found to remove gentamicin from the waste products generated during its production. However, a limited number of studies have reported biotransformation of individual antibiotics by pure culture other than fungal isolates [4].

The current study is based on the isolation and molecular identification of antibiotic-resistant bacterial strains from domestic and pharmaceutical effluents, having the potential to carry out significant degradation of most persistent antibiotics in

Correspondence to: Minghui Yao, Xinchuang Biotechnology (Xiamen) Co., Ltd., Xiamen, Fujian, China, E-mail: yaminghui@xmu.edu.cn

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the environment. Optimization of parameters such as pH, temperature, and inoculum size and growth time was carried out to achieve maximum degradation of antibiotics. Furthermore, biotransformation efficiency of these isolates was evaluated to develop an efficient and cost-effective strategy for large scale remediation of polluted environments [5].

Moreover, studies can be conducted to reveal the genetic basis of the transformation mechanism. Determining the genes and metabolic pathways involved in the transformation of antibiotics will help develop genetically engineered microbes with additional qualities and more controlled regulation.

REFERENCES

1. Deb P, Md. Mollab MAKM, Rahmanc S. An update to monoclonal antibody as therapeutic option against COVID-19. *Biosafety and Health*. 2021;87-91.
2. Kim PS, Derek E, Chensue W. Effect of monoclonal antibody therapy on the endogenous SARS-CoV-2 antibody response. *Clin Immunol*. 2022; 236:108959.
3. Ghotlooa S, Golsaz-Shirazia F, Amiria M, Shokri M. Neutralization of tetanus toxin by a novel chimeric monoclonal antibody. *Toxicol*. 2021;201:27-36.
4. Böttinger K, Esser-Skala W, Herwig C. At-line quantitative profiling of monoclonal antibody products during bioprocessing using HPLC-MS. *Analytica Chimica Acta*. 2022;1207:339813.
5. Michelchen S, Micheel B, Hanack K. In vitro immunization approach to generate specific murine monoclonal IgG antibodies. *J Immunol*. 2021; 499:113149.