medical sciences forum

MDPI

Proceeding Paper

Putative Role of the YbhFSR Efflux Pump in Resistance of *Aliarcobacter butzleri* to Several Antimicrobials †

Inês Martins[1], Cristiana Mateus [1], Fernanda Domingues [1], Mónica Oleastro [2] and Susana Ferreira [1]

[1] CICS-UBI–Health Sciences Research Centre, University of Beira Interior, 6201-506 Covilhã, Portugal; cristianamateus@live.com.pt (C.M.); fcd@ubi.pt (F.D.)
[2] National Reference Laboratory for Gastrointestinal Infections, Department of Infectious Diseases, National Institute of Health Dr. Ricardo Jorge, Lisboa, Portugal; monica.oleastro@insa.min-saude.pt (M.O.); susana.ferreira@fcsaude.pt (S.F.)
* Correspondence: ines.margarida.martins@ubi.pt
† Presented at the The 2nd International Electronic Conference on Antibiotics—Drugs for Superbugs: Antibiotic Discovery, Modes of Action And Mechanisms of Resistance, 15–30 Jun 2022; Available online: https://eca2022.sciforum.net/.

Abstract: The genus *Aliarcobacter* belongs to the *Arcobacteraceae* family, with nine validly published species. Among them, the species *Aliarcobacter butzleri* is considered the fourth most frequently found *Campylobacter-like* microorganism in human diarrheal stool samples and has also been included in the list of microorganisms considered a serious risk to human health by the International Commission on Microbiological Specifications for Food. Increasing rates of multidrug resistance to different antimicrobials have been described in *A. butzleri* isolates, with efflux pumps being one of the described resistance mechanisms. Efflux pumps of the *ATP-binding cassette* (ABC) family are known to export a wide variety of substances and are ubiquitous in almost all organisms. Several genes coding for efflux pumps of this family were described in the *A. butzleri* genome. Despite the resistance associated with this specie being widely described, the research on the mechanisms involved in this process is scarce. Therefore, the objective of this work was to evaluate the role of an ABC family efflux pump system in the resistance of *A. butzleri*. To this end, a mutant was constructed by deletion of the *ybhF* gene from the *ybhFSR* operon, a transporter with relevance in the extrusion of antibiotics and metals in other bacterial species. After ensuring that the mutation did not modify bacterial growth, the resistance profile of the native and mutant strains to different antimicrobial agents was evaluated. This analysis included metals, disinfectants, antibiotics, germicides, and an efflux pump substrate. The evaluation was based on the determination of the minimum inhibitory concentration of the antimicrobials by the agar dilution method. The results show differences in susceptibility of the mutant strain to some compounds tested, namely heavy metals and antibiotics, compared to the native strain. It can therefore be assumed that the YbhFSR efflux pump contributes to resistance in *A. butzleri*

Citation: Martins, I; Mateus, C.; .Domingues, F.; Oleastro, M.; Ferreira, S. Putative Role of the YbhFSR Efflux Pump in Resistance of *Aliarcobacter butzleri* to Several Antimicrobials. *Med. Sci. Forum* **2022**, *2*, x. https://doi.org/10.3390/xxxxx

Academic Editor(s):

Published: date