

Putative role of the YbhFSR efflux pump in resistance of *Aliarcobacter butzleri* to several antimicrobials

Martins, I.¹, Mateus, C.¹, Domingues, F.¹, Oleastro, M.², Ferreira, S.¹

¹ CICS-UBI – Health Sciences Research Centre, University of Beira Interior, 6201-506 Covilhã, Portugal.

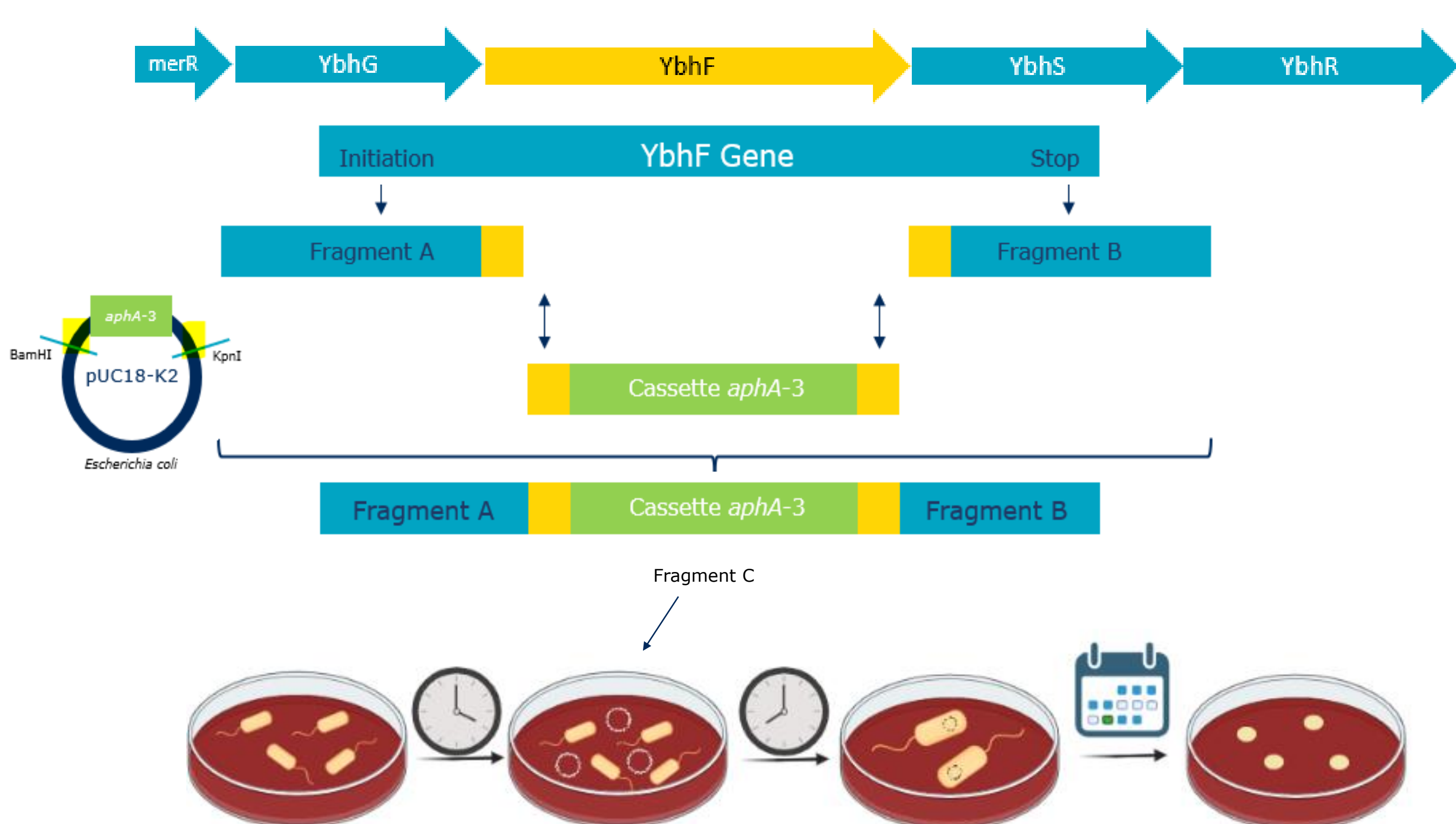
² National Reference Laboratory for Gastrointestinal infections, Department of Infectious Diseases, National Institute of Health Dr. Ricardo Jorge, Lisboa, Portugal.

Introduction

- Aliarcobacter butzleri* is considered the fourth *Campylobacter*-like microorganism most frequently found in human diarrheal stool samples. Increasing rates of multidrug resistance to different antimicrobials have been observed in isolates of this microorganism¹, with efflux pumps being one of the described resistance mechanisms². Efflux pumps of the *ATP-binding cassette* (ABC) family are known to export a wide variety of substances and are ubiquitous in almost all organisms³. Several genes coding for efflux pumps of this family have been observed in the *A. butzleri* genome².
- Despite the resistance associated with this specie being widely described, the research on the mechanisms involved in this process is scarce. Therefore, the **aim** of this work was to evaluate the role of an ABC family efflux pump system in the resistance of *A. butzleri*.

Experimental Design

A Construction of mutant strain by insertional mutagenesis and natural transformation



B Growth curves of parental and mutant strains



C Determination of the minimum inhibitory concentration (MIC) of antimicrobials by the agar dilution method



Results

Confirmation of Mutagenesis

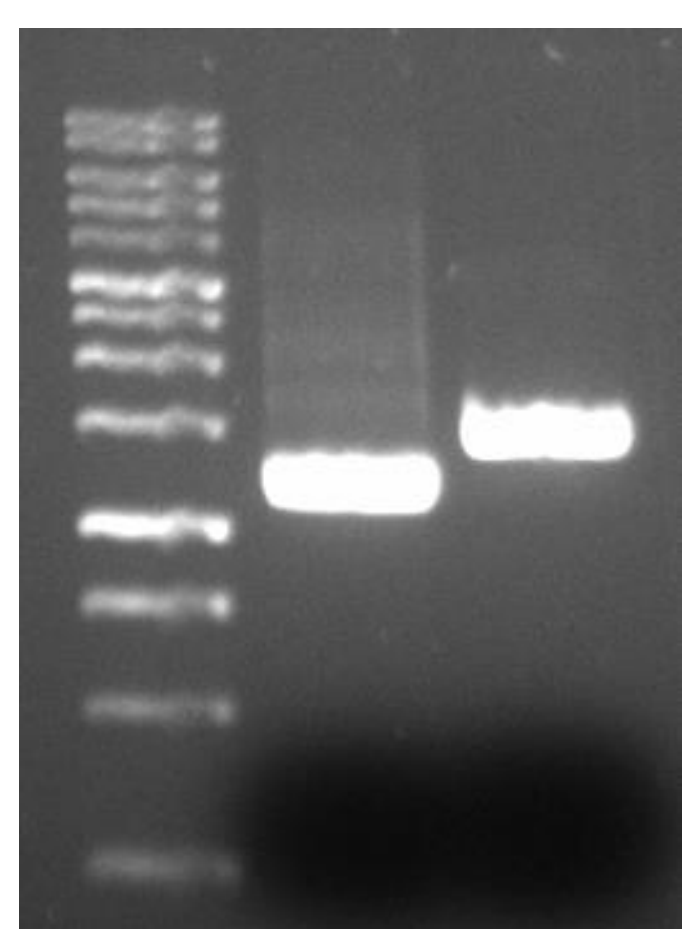


Fig 1. Electrophoresis agarose gel of the PCR products corresponding to the *ybhF* gene amplification in the parental and mutant strains.

- The transformation and mutant construction was confirmed by PCR and sequencing.
- Similar bacterial growth of both strains proves that **inactivation of the *ybhF* gene does not affect bacterial growth.**

Growth Curves

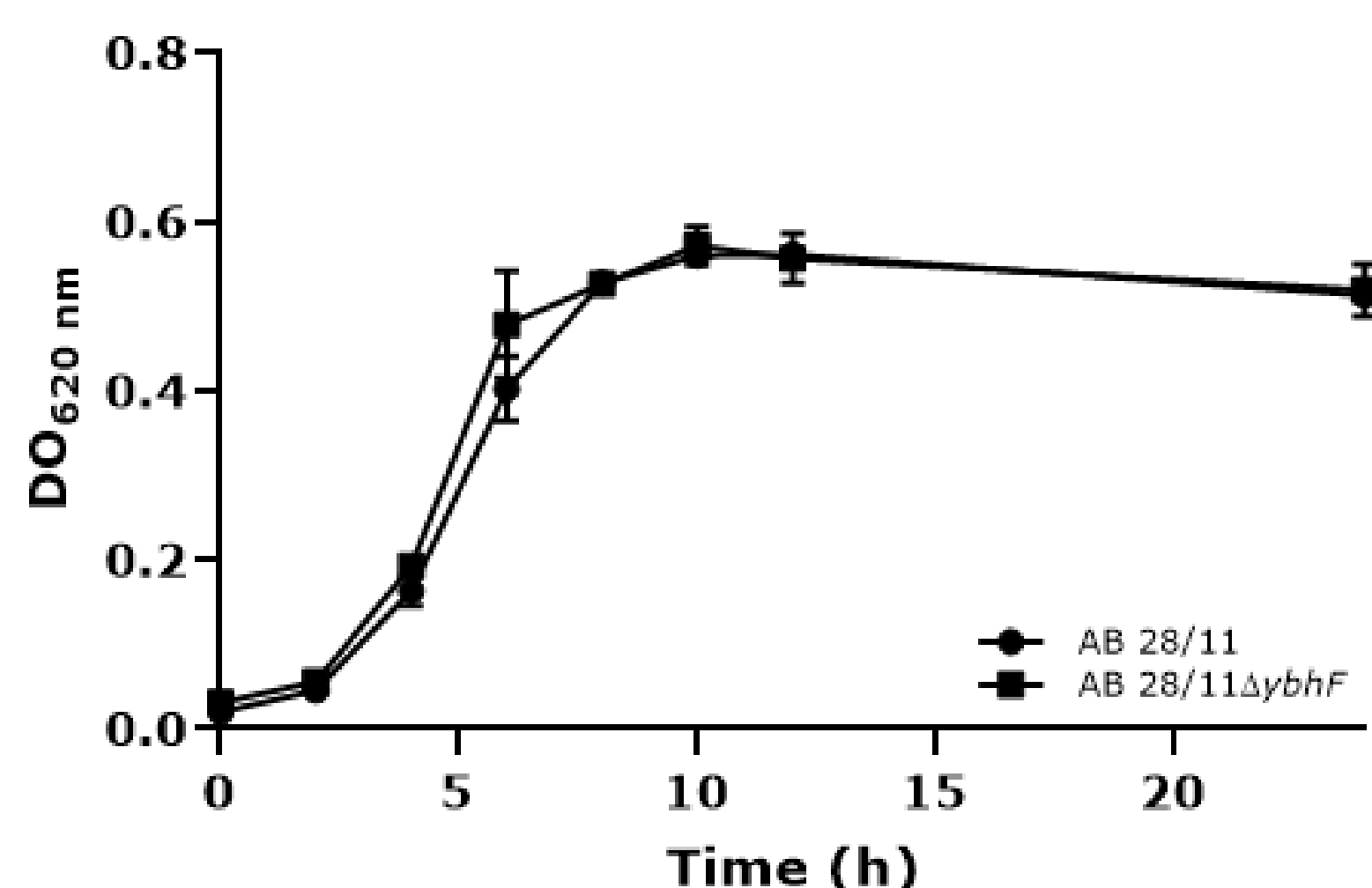


Fig 2. Growth curves of *A. butzleri* parental AB 28/11 strain and derived mutant.

Antimicrobial Resistance Profile

Table 1. Minimum inhibitory concentration of heavy metals for the parental and mutant strains of *A. butzleri*.

Strains	MIC (mM)												
	Ag	Cd	Co	Cr	Cu	Hg	Li	Na	Ni	Mn	Mo	Pb	Zn
AB 28/11	0.01	0.25	1	0.01	0.5	0.003	32	256	1	4	64	8	1
AB 28/11ΔybhF	0.01	0.03	1	0.01	0.25	0.003	32	128	1	2	64	8	0.5

(Ag: Silver; Cd: Cadmium; Co: Cobalt; Cr: Chrome; Cu: Copper; Hg: Mercury; Li: Lithium; Mn: Manganese; Mo: Molybdenum; Na: Sodium; Ni: Nickel; Pb: Lead; Zn: Zinc)

Table 2. Minimum inhibitory concentration of disinfectants and antibiotics, germicide and substrate of efflux pumps for the parental and mutant strains of *A. butzleri*.

Strains	MIC (µg / mL)											
	CHX	CLBZ	AMP	CFX	CHL	CIP	ERY	GEN	KAN	TET	ACR	EtBr
AB 28/11	1	64	64	32	128	16	32	0.5	1	8	32	64
AB 28/11ΔybhF	1	16	32	32	64	16	16	0.5	64	16	16	32

(CHX: Chlorhexidine; CLBZ: Benzalkonium chloride; AMP: Ampicillin; CFX: Cefotaxime; GEN: Gentamycin; KAN: Kanamycin; CIP: Ciprofloxacin; TET: Tetracycline; ERY: Erythromycin; CHL: Chloramphenicol; ACR: Acriflavine; EtBr: Ethidium Bromide)

- Inactivation of *ybhF* gene resulted in a **reduction of the MIC to some heavy metals and antibiotics**, as well as to **benzalkonium chloride, acriflavine and ethidium bromide.**

Conclusion

- Although it is likely that other efflux pumps are involved in tolerance or resistance in *Aliarcobacter butzleri*, **the inactivation of *ybhF* gene supports the role of YbhFSR efflux pump in intrinsic resistance of this bacterium.**

References

- ¹Ferreira, S., Queiroz, J. A., Oleastro, M., Domingues, F. C. (2014) Critical Reviews in Microbiology 42(3), 364-383
²Isidro, J., Ferreira, S., Pinto, M., Domingues, F., Oleastro, M., Gomes, J. P., Borges, V. (2020) Infection, Genetics and Evolution 80:104213.
³Garcia, I., Garcia, F., Pereira, P., Coutinho, H., Siyadatpanah, A., Norouzi, R., Wilairatana, P. (2022) Life Sciences 295, 120391.

Acknowledgments

Cristiana Mateus is recipient of a doctoral fellowship (UI/BD/151023/2021) under the scope of the CICS-UBI Programmatic Funding (UIDP/00709/2020). This work was developed within the scope of the CICS-UBI projects UIDB/00709/2020 and UIDP/00709/2020, financed by national funds through the Portuguese Foundation for Science and Technology/MCTES.