Antimicrobial susceptibility profile of *Faecalibacterium prausnitzii* DSM 17677 – a novel probiotic candidate

Daniela Machado [a #], Joana Barbosa [a #], Melany Domingos [a], Diana Almeida [a], José Carlos Andrade [b], Ana Maria Gomes [a], Ana Cristina Freitas [a]

[a] Universidade Católica Portuguesa, CBQF – Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Rua Diogo Botelho 1327, 4169-005 Porto, Portugal
[b] CESPU, Instituto de Investigação e Formação Avançada em Ciências e Tecnologias da Saúde, Rua Central de Gandra, 1317, 4585-116 Gandra PRD, Portugal

[#] Both authors with equal contribution

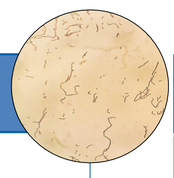
Objectives

Faecalibacterium prausnitzii is a common resident of healthy human intestine and it has been proposed as a **novel probiotic** with high application potential in the **food** and **pharmaceutical markets**. Despite its multiple benefits, detailed data regarding its antimicrobial susceptibility profile remains limited. However, this information is an important requirement in terms of **safety assessment** of probiotic strains.

This work aimed to characterize **antimicrobial susceptibility profile** of *F. prausnitzii* DSM 17677 strain using **phenotypic** and ***in silico*** approaches.

Methods

Growth conditions

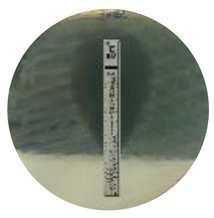


Strain: *F. prausnitzii* DSM 17677
Medium: sBHI
Temperature: 37ºC
Atmosphere: 85% N_2, 5% H_2 and 10% CO_2
Incubation time: 16h (1st culture) and 9-10h (2nd culture)

I) Antimicrobial phenotypic testing

- **Broth microdilution**

- **E-test®**



II) *In silico* analysis

- **Databases:** PATRIC; CARD
- **Bioinformatic tools:**
  ICEfinder
  IslandViewer
  ResFinder

Results

I) Phenotypic

Table 1. Antimicrobial susceptibility profile of *Faecalibacterium prausnitzii* DSM 17677

Antimicrobial	MIC (µg/mL) in broth microdilution	MIC (µg/mL) in E-test®	EFSA cut-off values (µg/mL)
Ampicillin	**> 2**	**> 3**	**1**
Vancomycin	≤ 1	0.25 - 0.5	4
Gentamicin	**> 8**	**12**	**4**
Kanamycin	**> 32**	**16 - 32**	**16**
Streptomycin	**> 16**	**≥1024**	**8**
Erythromycin	**> 2**	**0.5-1**	**1**
Clindamycin	≤ 1	≤ 0.016	4
Tetracycline	≤ 0.5	0.023-0.047	2
Chloramphenicol	2-4	1-1.5	4

Note: MIC = minimum inhibitory concentration; EFSA = European Food Safety Authority

II) *In silico*

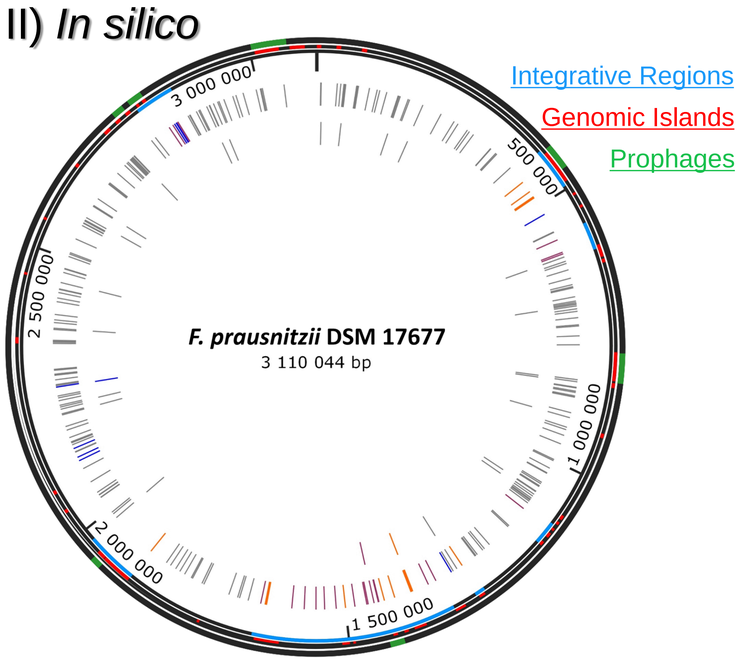


Figure 1. *Faecalibacterium prausnitzii* DSM 17677 genome map with a representation of the antibiotic resistance genes (**ARG**).

Main Findings:

- **Susceptible** to **vancomycin**, **clindamycin**, **tetracycline** and **chloramphenicol**.
- **Annotated ARG**: gentamicin, kanamycin, streptomycin and erythromycin.
- **Homology search** reveals ARG variants putatively involved in β-lactams and glycopeptides resistance.
- Only **streptomycin resistance** represents a risk concerning **horizontal transferability.**

Conclusion

This work provides important information regarding the antimicrobial susceptibility profile of ***F. prausnitzii* DSM 17677**, supporting its use in **probiotic** products for **human consumption**.

References

1. Andrade J. C. et al. Front Bioeng Biotechnol. 2020; 8:550.
2. Martín R et al. Front Microbiol. 2017; 8:1226.
3. EFSA-FEEDAP et al. EFSA J. 2018; 16 (3): e05206.

Acknowledgements

This work was supported by national funds through FCT/MEC (PIDDAC), project references IF/00588/2015, individual CEEC program (CEECIND/00520/2017/ CP1404/CT0001), and by Operational Program Competitiveness and Internationalization in its FEDER component and by the budget of the Foundation for Science and Technology, I.P. (FCT, IP) in its OE component, project reference POCI-01-0145-FEDER-031400 – PTDC/BAA-AGR/31400/2017. We would also like to thank the scientific collaboration under the FCT project UIDB/50016/2020.