A comparison of the antimicrobial resistance of fecal *Bacteroides* isolates and assessment of the composition of the intestinal microbiotas of carbapenem-treated and non-treated persons from Belgium and Hungary

József Sóki, Ingrid Wybo, Roland Wirth, Edit Hajdú, Mária Matuz, Katalin Burián, on behalf of the ESCMID Study Group on Anaerobic Infections

PII: S1075-9964(21)00163-3

DOI: https://doi.org/10.1016/j.anaerobe.2021.102480

Reference: YANAE 102480

To appear in: Anaerobe

Received Date: 24 July 2021

Revised Date: 14 November 2021

Accepted Date: 15 November 2021

Please cite this article as: Sóki Jó, Wybo I, Wirth R, Hajdú E, Matuz Má, Burián K, on behalf of the ESCMID Study Group on Anaerobic Infections, A comparison of the antimicrobial resistance of fecal *Bacteroides* isolates and assessment of the composition of the intestinal microbiotas of carbapenem-treated and non-treated persons from Belgium and Hungary, *Anaerobe* (2021), doi: https://doi.org/10.1016/j.anaerobe.2021.102480.

This is a PDF file of an article that has undergone enhancements after acceptance, such as the addition of a cover page and metadata, and formatting for readability, but it is not yet the definitive version of record. This version will undergo additional copyediting, typesetting and review before it is published in its final form, but we are providing this version to give early visibility of the article. Please note that, during the production process, errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

© 2021 Published by Elsevier Ltd.



- Journal Pre-proof
- 1 A comparison of the antimicrobial resistance of fecal *Bacteroides* isolates and assessment
- 2 of the composition of the intestinal microbiotas of carbapenem-treated and non-treated
- 3 persons from Belgium and Hungary
- 4
- József Sóki^a*, Ingrid Wybo^b, Roland Wirth^c, Edit Hajdú^d, Mária Matuz^e and Katalin Burián^{a,f} on behalf
 of the ESCMID Study Group on Anaerobic Infections
- ⁷ ^a Institute of Clinical Microbiology, Faculty of Medicine, University of Szeged, Szeged, Hungary
- ^b Department of Microbiology and Infection Control, Universitair Ziekenhuis Brussel, Vrije Universiteit
 Brussel, Belgium
- ^c Department of Biotechnology, Faculty of Sciences and Informatics, University of Szeged, Szeged
- 11 Hungary
- ^d Division of Infectious Diseases, First Department of Internal Medicine, Faculty of Medicine,
- 13 University of Szeged, Szeged, Hungary
- ^e Department of Clinical Pharmacy, Faculty of Pharmacy, University of Szeged, Szeged, Hungary
- ^f Department of Microbiology and Immunobiology, Faculty of Medicine, University of Szeged, Szeged,
 Hungary
- 17
- 18 **Running title**: Antibiotic resistance of *Bacteroides* and microbiomes of carbapenem-treated persons
- 19 Keywords: antibiotic resistance, *Bacteroides*, *B. fragilis*, carbapenems, microbiome
- 20
- 21 * Corresponding author:
- 22 Dr. József Sóki
- 23 Institute of Clinical Microbiology, Albert Szent-Györgyi Clinical Centre, Faculty of Medicine,
- 24 University of Szeged
- 25 Semmelweis 6
- 26 H-6726 Szeged, Hungary
- 27 Tel.: 36 62 545399
- 28 Fax: 36 62 545712
- 29 e-mail: <u>soki.jozsef@med.u-szeged.hu</u>
- 30
- 31
- 32

33 Abstract

34	The antimicrobial susceptibilities of <i>Bacteroides</i> strains isolated from the feces of imipenem-treated
35	patients from Belgium and Hungary were compared with those isolated from the normal microbiota
36	from these two and five other European countries and assessed. Of the 10 antibiotics tested, highly
37	significant differences were found with cefoxitin (decrease for Belgium and for this two and the five
38	countries from the previous study), clindamycin (decrease for Belgium and for this two and the five
39	countries from the previous study) and moxifloxacin (increase for Belgium and for this two and the
40	five countries from the previous study) relative to normal microbiota strains reported earlier.
41	Imipenem treatment brought about modest, but notable differences in the compositions of the
42	microbiomes where there was less diversity in the treated group relative to the non-treated group.
43	
44	
45	
46	
47	
48	
49	
50	
51	
52	
53	
54	
55	
56	
57	
58	

59 Bacteroides species are important and, also common participants of the normal human gut 60 microbiota. Together or separately their phylum (Bacteroidetes), order (Bacteroides), and genera 61 (Bacteroides and the similar Parabacteroides species) usually comprise 15-30 %-s colonic microbiome suggested from the results of earlier studies ^[1, 2]. With these, they exert important interactions with 62 63 the same (digestive) or other organ systems like immune, cardiovascular, and central nervous 64 systems. In the gut, they digest carbohydrates or glycoproteins such as mucin, produce short-chain fatty acids, conjugate bile, and they can exert immune-modulatory effects through the capsular 65 polysaccharides (CPS) of *Bacteroides fragilis*^[1]. *B. fragilis* may produce an enterotoxin that mainly 66 affects children, it can harm the mucosal epithelium, and hence it has a tumorigenic potential ^[3]. The 67 68 immunomodulatory effects of the CPSs of B. fragilis outside the gut can induce abscesses and B. fragilis also has a high oxygen tolerance ^[4, 5]. With these, they can be opportunistic pathogens and 69 70 may be the most prevalent taxon in infections caused by anaerobic bacteria. They are also the most 71 antibiotic-resistant anaerobes that have many resistance mechanisms and they have the highest 72 resistance rates compared with other known anaerobic pathogens. To facilitate their antibiotic 73 treatment, resistance surveys are conducted to guide empiric therapies and direct antimicrobial susceptibility tests (most often Etest) can be used for targeted therapies ^[6]. Our knowledge of the 74 75 antimicrobial susceptibilities of the clinical isolates is quite good, at least in the developed countries, but it is more limited when it comes to the normal microbiota isolates. Therefore, after the 2010 76 European Bacteroides antimicrobial susceptibility survey ^[7], a new study on fecal Bacteroides strains 77 isolated between 2014-2016 was carried out ^[8]. This study included persons who were treated or not 78 79 treated with carbapenems (in Belgium and Hungary to carry out antimicrobial susceptibility tests) 80 and these results are now presented along with the normal microbiome compositions of patients 81 who were treated or not treated with imipenem in Hungary.

Patients treated with meropenem (the standard regimen of 1g-2g *iv*/8 h) in Belgium (n=6) and
imipenem (the standard regimen of 500 mg *iv*/6 h) in Hungary (n=7) were included in the study
(ethical permissions: Regional Research Ethical Board of the University of Szeged, permission no.

70/2015-SZTE and Commissie Medische Ethiek O.G.016 Reflectiegroep Biomedische Ethiek in
Hungary and Belgium, respectively).

Strain isolation, cultivation, storage, antibiotic susceptibility testing, and the statistical evaluation
were performed as described previously and we compared our new data with those obtained in the
previous one ^[8]. The number of subjects/patients and the isolated strains are listed in Table 1 for the
earlier and the present study.

91 DNA samples from feces of the Hungarian patients, with or without imipenem treatment, for next 92 generation sequencing were isolated using the Qiagen Stool DNA Mini Kit. 16S rDNA amplification 93 and sequencing (V3-V4 region, 466 bp) were carried out by the Illumina 150 bp paired-end method 94 (Novogene, Hong Kong), the datasets were uploaded to the EZ Bio Cloud (www.ezbiocloud.net) 95 database and they were evaluated as described earlier using a local in-house application ^[9, 10]. 96 Comparative datasets on the antibiotic resistance levels of Bacteroides strains isolated from normal 97 microbiota and carbapenem-treated patients can be seen in Table 2. Statistically significant 98 differences were obtained for cefoxitin (increased from about 16% to 51%), clindamycin (decreased 99 from about 49% to 31%), and moxifloxacin (increased from about 10% to 41%) in cases where the 100 merged data of Belgium and Hungary or the data for the five European countries of the previous 101 study were analyzed [8]. The significance levels for these data values lay in the range of <0.001-0.006, 102 which are beyond doubt. There were also some differences that were seen in the Belgian strains. For 103 instance with tetracycline, an increase (from 59.5% to 89.5%) in the resistance rate was observed 104 with a moderate significance (p=0.044), but for moxifloxacin it was more pronounced (an increase 105 from 5.4% to 52.6%, p<0.0001) and for clindamycin a pronounced but adverse effect (from 75.7% to 106 31.6%, p=0.004) was noted (Table 2). Interestingly, no significant difference was found for imipenem, 107 contrary that carbapenems were applied, but the actual values displayed a high variance (0 to 10.5% 108 in Belgium and 2 to 10.3% for all countries, Table 2). Møller Hansen et al. studied the short-term 109 effects of antibiotic treatments (piperacillin/tazobactam, meropenem, metronidazole, and 110 clindamycin) on the enrichment of antibiotic-resistant Bacteroides in the gut in of patients from

111 Denmark. A significant increase (p=0.0001), contrary to our expectations, was found for the 112 carbapenem meropenem (but here the number of the strains involved differed significantly i.e. 197 113 vs. 10 patients and 357 vs. 39 strains in Denmark and this study, respectively) ^[11]. 114 We should mention that in our study clinical-to-normal flora differences were experienced for 115 amoxicillin/clavulanic acid, cefoxitin, imipenem, clindamycin and moxifloxacin, where the resistance 116 levels for cefoxitin, imipenem and clindamycin increased, and for moxifloxacin only species-specific differences were found^[8]. This latter study offered a possible explanation for this, namely that the 117 118 origin of the strains might differ – more precisely, the clinical strains originating from the mucosa and 119 the fecal strains originating from the lumen where vertical and horizontal strain/gene spread may also differ^[8]. At present it is thought that imipenem might act as an influencer of the proportion of 120 121 antibiotic-resistant strains in the microbiota. An enhancement of the conjugation frequencies was 122 described for the tetracycline resistance conjugative transposons and mobilizable elements of Bacteroides by tetracycline ^[12] and Tn916 of Firmicutes by ribosome targeting antibiotics ^[13]. It is 123 124 conceivable that imipenem has similar effects as well since it can induce resistance in some 'silently' 125 resistant, cfiA-positive B. fragilis strains (according to our preliminary, unpublished observations). In 126 our investigations, detecting the prevalence of corresponding resistance genes/genetic elements in 127 our laboratory may take us closer to finding the reasons for the above-mentioned differences. 128 The microbiome examinations by 16S rDNA amplicon sequencing and principal component analysis 129 of the fecal samples taken from Hungarian patients revealed no marked differences between the 130 normal and imipenem-treated individuals (Fig S1). As expected, the usual Firmicutes and 131 Bacteroidetes species were found in the core microbiomes (Fig. S2) and the ten top species displayed 132 a near-even distribution between the two groups (Fig. S3). However, out of the simpler α -diversity 133 measures, (using the Shannon and Chao formulas which use different calculations to be able to 134 compare different species compositions), with the Chao formula there was a difference with a low 135 significance value (p=0.02, Fig. S4). This may be because in the imipenem-treated group there was a 136 tendency for one taxon to dominate (e.g. B. fragilis, Clostridioides difficile, enterococci), as was

137 noticed in an inspection of the species composition bars (not shown). Imipenem attains a good concentration (0-8 µg/ml)^[14, 15] in the intestine during use in *iv* treatments but still, from the low 138 139 disturbance of the intestinal microbiome with imipenem observed in this study, a resilience to this 140 drug due to the production of carbapenemase can be expected. As regards the latter, we note that 141 there is a significant proportion of carbapenem resistant strains in the gut (about 1% of the 142 Bacteroides which are not exclusively B. fragilis) that can mediate this resilience ^[8]. Although 143 antibiotic treatment may have short and long-term effects on the composition of the intestinal microbiota especially for cultivable bacteria ^[16], now it seems from several studies that it has some 144 145 resilience to such disturbance indeed. This latter phenomenon can vary between microbiotas of 146 different individuals, it may depend on the diet, the content of the main species, and different environmental factors [17-19]. It was also expected that the differences in antibiotic resistance values 147 148 might be due more to imipenem than the composition of the microbiotas. 149 In summary, it can be stated that carbapenem treatment induced antibiotic resistance level changes 150 of Bacteroides isolates obtained from the intestinal microbiotas of the treated individuals. In spite of this, the whole microbiotas of the imipenem-treated patients displayed no marked adverse effects, 151 which can be attributed to the resilience of the intestinal microbiota. However, in view of the low 152 153 number of individuals involved in this present study, we think that larger sample sizes sould provide 154 more reliable results.

155

156 Acknowledgements

157 We would like to thank Glória Stefán and Katalin Ördög for their technical assistance.

158 Funding

This study was supported by grants from the ESCMID Study Group on Anaerobic Infections and the GINOP-2.3.2-15-2016-00006 and GINOP-2.3.2-15-2016-00011 grants. The GINOP grants were funded by the European Regional Development Fund of the European Union and managed in the framework

- 162 of the Economic Development and Innovation Operational Program by the Ministry of National
- 163 Economy, National Research, Development, and Innovation Office, Budapest, Hungary.
- 164

165 Transparency declarations

- 166 The authors hereby declare that they have no conflict of interest.
- 167

168 References

- 169 1. Wexler HM. Bacteroides: the good, the bad and the nitty-gritty. *Clin Microbiol Rev* 2007;
- 170 20(4):593-621.
- 171 2. Kurilshikov A, Medina-Gomez C, Bacigalupe R, Radjabzadeh D, Wang J, Demirkan A, et al. Large-
- 172 scale association analyses identify host factors influencing human gut microbiome composition.
- 173 *Nature Genetics* 2021; 53(2):156-165.
- 174 3. Sears CL. Enterotoxigenic Bacteroides fragilis: a rogue among symbiotes. *Clin Microbiol Rev* 2009;
- 175 22(2):349-369, Table of Contents.
- 176 4. Erturk-Hasdemir D, Kasper DL. Finding a needle in a haystack: Bacteroides fragilis polysaccharide
- 177 **A as the archetypical symbiosis factor**. *Ann N Y Acad Sci* 2018; 1417(1):116-129.
- 178 5. Yekani M, Baghi HB, Vahed SZ, Ghanbari H, Hosseinpur R, Azargun R, et al. Tightly controlled
- 179 response to oxidative stress; an important factor in the tolerance of Bacteroides fragilis. Res
- 180 *Microbiol* 2021:103798.
- 181 6. Nagy E. Anaerobic infections: Update on treatment considerations. *Drugs* 2010; 70(7):841-858.
- 182 7. Nagy EU, E.; Nord, C. E. on behalf of the ESCMID Study Group on Antimicrobial Resistance in
- 183 Anaerobic Bacteria. Antimicrobial susceptibility of *Bacteroides fragilis* group isolates in Europe 20
- 184 **years of experience**. *Clinical Microbiology and Infection* 2011; 17(3):371-379.
- 185 8. Sóki J, Wybo I, Hajdú E, Toprak NU, Jeverica S, Stingu CS, et al. A Europe-wide assessment of
- 186 antibiotic resistance rates in Bacteroides and Parabacteroides isolates from intestinal microbiota of
- 187 healthy subjects. *Anaerobe* 2020; 62:102182.

- 188 9. Yoon SH, Ha SM, Kwon S, Lim J, Kim Y, Seo H, et al. Introducing EzBioCloud: a taxonomically
- 189 united database of 16S rRNA gene sequences and whole-genome assemblies. Int J Syst Evol
- 190 *Microbiol* 2017; 67(5):1613-1617.
- 191 10. Wirth R, Maróti G, Lipták L, Mester M, Al Ayoubi A, Pap B, et al. Microbiomes in supragingival
- 192 biofilms and saliva of adolescents with gingivitis and gingival health. Oral Diseases; n/a(n/a).
- 193 11. Hansen KCM, Schwensen SAF, Henriksen DP, Justesen US, Sydenham TV. Antimicrobial resistance
- 194 in the Bacteroides fragilis group in faecal samples from patients receiving broad-spectrum
- 195 **antibiotics**. *Anaerobe* 2017; 47:79-85.
- 196 12. Salyers AAS, N. B.; Li, L.-Y. In the driver's seat: The Bacteroides conjugative transposons and the
- 197 elements they mobilize. J Bacteriol 1995; 177(20):5727-5731.
- 198 13. Scornec H, Bellanger X, Guilloteau H, Groshenry G, Merlin C. Inducibility of Tn916 conjugative
- 199 transfer in Enterococcus faecalis by subinhibitory concentrations of ribosome-targeting antibiotics.
- 200 Journal of Antimicrobial Chemotherapy 2017; 72(10):2722-2728.
- 201 14. Kager L, Brismar B, Malmborg AS, Nord CE. Imipenem concentrations in colorectal surgery and
- impact on the colonic microflora. Antimicrob Agents Chemother 1989; 33(2):204-208.
- 203 15. Salmon-Rousseau A, Martins C, Blot M, Buisson M, Mahy S, Chavanet P, et al. Comparative
- review of imipenem/cilastatin versus meropenem. *Med Mal Infect* 2020; 50(4):316-322.
- 205 16. Jernberg C, Löfmark S, Edlund C, Jansson JK. Long-term ecological impacts of antibiotic
- administration on the human intestinal microbiota. *Isme j* 2007; 1(1):56-66.
- 207 17. Ng KM, Aranda-Díaz A, Tropini C, Frankel MR, Van Treuren W, O'Loughlin CT, et al. Recovery of
- 208 the Gut Microbiota after Antibiotics Depends on Host Diet, Community Context, and
- 209 Environmental Reservoirs. Cell Host Microbe 2019; 26(5):650-665.e654.
- 210 18. Chng KR, Ghosh TS, Tan YH, Nandi T, Lee IR, Ng AHQ, et al. Metagenome-wide association
- analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. Nat Ecol
- 212 *Evol* 2020; 4(9):1256-1267.

- 213 19. Lavelle A, Hoffmann TW, Pham HP, Langella P, Guédon E, Sokol H. Baseline microbiota
- 214 composition modulates antibiotic-mediated effects on the gut microbiota and host. *Microbiome*
- 215 2019; 7(1):111.

216

Journal Proposi

217 Table 1. Patients and Bacteroides strains

	Be	elgium	Hung	gary	Both ^a		All ^b
	NΜ ^c	Treated ^c	NM	Treated	NM	Treated	
Number of patients	5	6	12(+1) ^d	4(+3) ^d	17	10	42
Species distribution of Isolates							
All	40	19	62	20	102	39	241
B. fragilis	2	1	14	-	16	1	24
B. thetaiotaomicron	1	4	9	4	10	8	19
B. ovatus/xylanisolvens	8	4	14	6	22	10	48
B. vulgatus/dorei	6	4	9	5	15	9	36
B. uniformis	1	5	5	1	6	6	14
P. distasonis	3	-	5	2	8	2	12
Other ^d	19	1	20	2	39	3	49

218

^a Merged values of Belgium and Hungary. ^b All the strains from the five European countries including

220 the isolates from the imipenem-treated patients. ^c NM – Normal microbiota, Treated – imipenem

221 treated patients. ^d The number of patients are shown in parentheses where *Bacteroides* isolation has

not been carried out, and their fecal samples were only used for DNA extraction to perform

223 microbiome composition sequencing. ^d We placed the following species *B. cacae*, *B. celulosilyticus*, *B.*

224 clarus, B. coprocola, B. eggerthii, B. faecis, B. finegoldii, B. nordi, B.stercoris, Parabacteroides

johnsonii and *P. merdae* in the 'other' category.

Table 2. A comparison of antibiotic susceptibilities of *Bacteroides* strains isolated from normal and carbapenem-treated microbiotas

Antibiotic		Control				Treated				
	Countries	Range	MIC ₅₀	MIC ₉₀	R (%)	Range	MIC ₅₀	MIC ₉₀	R (%)	pª
Ampicillin	Belgium ^₅	8->256	256	>256	100	16->256	>256	>256	100	-
	Hungary	2->256	128	>256	100	4->256	>256	>256	100	-
	Both ^c	2->256	128	>256	100	1->256d	N 256	N256	100	-
	All	1->256	128	>256	96.6	4-2250-	~250	2250	100	n.s
Amoxicillin/clavulanate	Belgium	0.125->256	1	8	2.7	0.25-4	1	4	0	n.s.
	Hungary	0.125-32	1	8	7.9	0.064-2	0.5	0.5	0	n.s.
	Both	0.064-32	1	8	6.2	0 064-4	0.5	4	0	n.s.
	All	0.064-32	0.5	4	4.5	0.004-4	0.5	7	0	n.s.
Cefoxitin	Belgium	0.5-128	4	16	2.7	2-256	128	128	52.6	<0.001
	Hungary	0.5-128	32	64	25.0	1-128	32	128	50.0	n.s.
	Both	1-128	8	64	17.7	1-256	32	128	513	0.003
	All	0.5-256	16	64	14.9	1 250	52	1120	51.5	<0.001
Imipenem	Belgium	0.125-2	0.5	1	0	0.5->32	1	32	10.5	n.s.
	Hungary	0.125-16	0.5	4	3.9	0.064-4	2	4	0	n.s.
	Both	0.064-16	0.5	2	2.7	0.064-	1	16	10.3	n.s.
	All	0.032-32	0.5	2	2.0	>32		10	10.5	n.s.
Clindamycin	Belgium	0.125->256	16	>256	75.7	0.25-32 0.064-	16	32	31.6	0.004
	Hungary	0.064->256	2	>256	36.8	>256	1	>256	30.0	n.s.
	Both	0.064->256	8	>256	50.4	0.064-	1	>256	30.8	0.004
	All	0.064->256	4	>256	47.3	>256	T	~230	30.8	0.006
Metronidazole	Belgium	0.064-1	0.5	0.5	0	0.5-1	0.5	0.5	0	-
	Hungary	0.032-4	0.5	1	0	0.064-1	0.5	1	0	-
	Both	0.032-4	0.5	0	0	0.064-1	0.5	0	0	-
	All	0.032-4	0.5	1	0	0.004-1	0.5	0	0	-
Moxifloxacin	Belgium	0.125-32	1	2	5.4	0.5->32 0.25-	16	32	52.6	<0.001
	Hungary	0.064-32	1	4	9.2	>32	1	>32	15.0	n.s.
	Both	0.064-32	1	4	8.0	0.25-	4	>32	41.0	<0.001
	All	0.064-64	1	8	11.4	>32	•	, <u>5</u> 2	11.0	<0.001
Tetracycline	Belgium	1->256	16	32	59.5	0.5-64	32	64	89.5	0.014
	Hungary	0.125-128	16	32	63.2	0.5-64	32	32	70.0	n.s.
	Both	0.125->256	16	32	62.8	0.5-64	32	64	82.1	0.044
	All	0.064->256	32	128	66.2					n.s.
Tine e velie e	Deleium	0.004.00	0.5	0	2.7	0.032-	1	0	F 0	
ngecycline	Beigium	0.064-32	0.5	8	2.7	10	1	8	5.0	n.s.
	Hungary	0.032-4	0.25	2	0	0.125-8	0.25	2	0	n.a.
		0.032-32	0.5	2	0.9	0.032-	0.25	8	2.6	n.s.
Chloromphonical	All	0.032-32	0.5	4	1.5	20	0	0	0	n.s.
Chioramphenicol	Beigium	0.125-8	ð 1	ð	U	۲-۵ ۲ ۹	ð 1	ð	U	-
		0.25-8	4	ð	0	Z-8	4	ð	U	-
		0.125-8	4 1	o Q	n	2-8	8	8	0	-
		0.123-0	4	0	U					-

^a Significance of the differences. ^b These numerical replace those presented in Sóki *et al.* ^[8], which
 otherwise does not affect the evaluations and conclusions given in that study. ^c Normal microbiota
 values from the two (Belgium and Hungary) and all five European countries investigated earlier were
 compared with the values of two countries in this study. ^d Merged values for Belgium and Hungary.

Highlights

Bacteroides strains from the feces of imipenem-treated and non-treated patients were isolated.

Out of 10 antibiotics, cefoxitin, clindamycin, moxifloxacin, and tetracycline gave different resistance values between the above two groups of strains.

Imipenem-treatment caused a decrease in the diversity of the patients' microbiomes.

Journal Pression

TITLE OF MANUSCRIPT SUBMITTED TO ANAEROBE: "COMPARISON OF THE ANTIMICROBIAL RESISTANCE OF FECAL *BACTEROIDES* ISOLATES AND THE COMPOSITION OF THE INTESTINAL MICROBIOTAS OF HEALTHY AND CARBAPENEM-TREATED PERSONS FROM BELGIUM AND HUNGARY"

by

József Sóki, Ingrid Wybo, Roland Wirth, Edit Hajdú, Mária Matuz, Katalin Burián

We declare no conflict of interests.

József Sóki Corresponding author

or Providence of the second se