

Microbial composition and diversity of mice colonized with a carbapenemase-producing *Klebsiella pneumoniae* strain

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Key words: microbiota, microbiome, horizontal gene transfer, antimicrobial drug

Introduction: Emergence and spread of multidrug-resistant bacteria represent a serious problem worldwide. The extended-spectrum β -lactamase (ESBL) and carbapenemase-producing Enterobacteriaceae (CPE) are in the critical category on the WHO antimicrobial resistance priority list. These bacteria are responsible for a large proportion of hospital-acquired infections. The therapeutic options for CPE are limited, therefore controlling the spread of these bacteria is important.

In this study our goal was to investigate the effect of different per os antibiotic treatments on the microbial composition and diversity of C57BL/6 mice colonized with *K. pneumoniae* (KP5825). This strain expressed a carbapenemase gene, a PMQR gene and an ESBL gene. We also examined the colonization rate and the resistance gene copy number changes in the colonized mice.

Methods: All experiments were carried out using 6–8 weeks-old C57BL/6 male mice. For colonization, 5×10^6 CFU of KP5825 was administered orally on the 14th and 15th days of ampicillin pretreatment. After the colonization mice were divided into 6 groups. These groups received two different doses of the following antibiotic treatments for 15 days: ampicillin (AMP), ceftazidime (CAZ), ciprofloxacin (CIP) (6th group: control). From collected fecal samples microbial DNA was extracted.

In the second phase of our experiments we used qPCR technique to determine the KP5825 DNA quantities and assess the resistance gene copy numbers. The V3-V4 region of the 16S rRNA gene was amplified and sequenced with the Illumina MiSeq platform to determine the microbiota composition and diversity in the intestines of colonized mice.

Results: Our results show that AMP and CAZ increased the colonization KP5825 and reduced the gut microbiome diversity originally characterized by *Bacteroides* dominance. In contrast, CIP did not increase the colonization rate.

Discussion and Conclusion: We observed strong negative correlation between the presence of Lachnospiraceae, Roseburia, Anaerostipes, Lachnospiraceae, Tyzzerella, Agathobacter genera and the colonization rate with KP5825.

Ethical Committee:

Semmelweis University (permission no. PE//EA/60-8/2018, PE/EA/964-5/2018)

Grants and financial support:

Supported by the ÚNKP-19-2-I-SE-06 New National Excellence Program of the Ministry for Innovation and Technology.

Acknowledgements:

E. Ostorházi, J. Domokos, M. Kapás