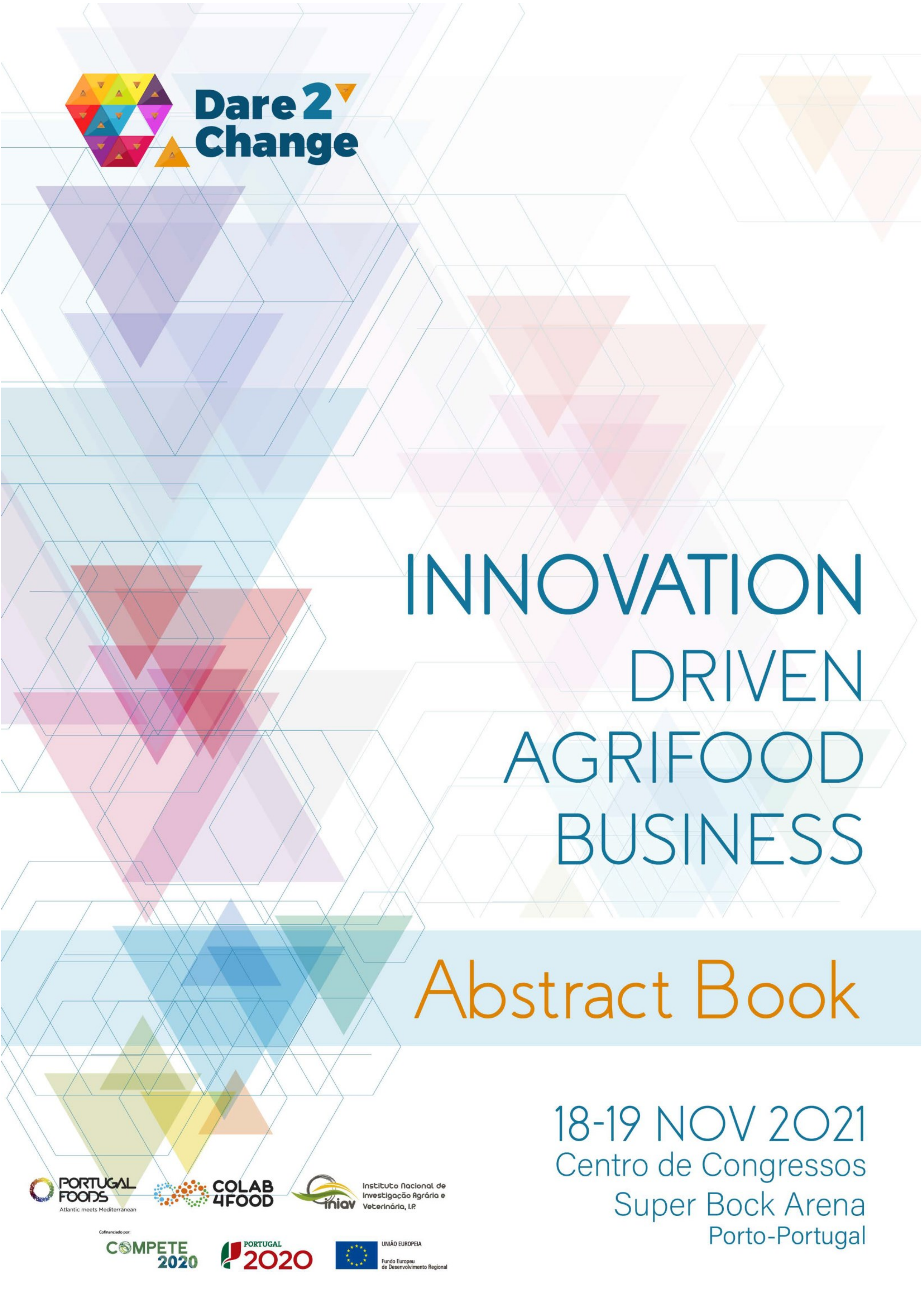

Dare 2 Change

INNOVATION DRIVEN AGRIFOOD BUSINESS

Abstract Book

18-19 NOV 2021
Centro de Congressos
Super Bock Arena
Porto-Portugal

PORTUGAL FOODS
Atlantic meets Mediterranean
COLAB 4FOOD
iniav Instituto Nacional de Investigação Agrária e Veterinária, I.P.
Cofinanciado por:
COMPETE 2020
PORTUGAL 2020
UNIÃO EUROPEIA
Fundo Europeu de Desenvolvimento Regional

[SBE 6]

Metagenomic assessment of the microbial diversity of swine carcasses

Marta Carvalho[1]*, Márcio Moura-Alves[2], Cristina Saraiva[2], Alexandra Esteves[2], Deise Ribeiro[3], Inês Carvalho Leonardo[4],[5], Frédéric Bustos Gaspar[4],[5], Maria Teresa Barreto Crespo[4],[5], Paula Teixeira[1]
[1]Universidade Católica Portuguesa, CBQF - Centro de Biotecnologia e Química Fina e Laboratório Associado, Escola Superior de Biotecnologia.
[2]Universidade de Trás-os-Montes e Alto Douro, Centro de Ciência Animal e Veterinária (CEVAV), School of Agrarian and Veterinary Sciences, Vila Real, Portugal.
[3]Universidade Federal de Santa Catarina, Centro de Ciências Agrárias, Departamento de Ciência e Tecnologia de Alimentos. Florianópolis, SC, Brazil.
[4]Food Safety and Microbiology Laboratory, Food & Health Division, iBET - Instituto de Biologia Experimental e Tecnológica, 2781-901 Oeiras, Portugal
[5]ITQB NOVA - Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa, 2780-157 Oeiras, Portugal
*e-mail: mpcarvalho@ucp.pt

Contamination, cross-contamination, or carcass recontamination can mainly occur along the slaughtering processes due to contact between animals during their transportation, steps of slaughter carcass preparation, slaughterhouse environment, clothing, and poor slaughter and hygiene practices [1]. Evaluating the microbiological profile is important to verify hygiene conditions during the slaughter processes and ensure the food safety of the final product [2]. The purpose of this study was to characterize the microbial community of swine carcasses and environmental samples - knives and drains - using a metagenomic approach. Gauze swabs were used to collect samples from drains and from five animals before and after evisceration, and water from the knives sterilizer was collected in sterile tubes before and after eviscerations. Samples were prepared for Illumina Sequencing by 16S rRNA gene amplification of the bacterial community. All 16S rRNA data were analysed with Kraken v1 using the pre-built MiniKraken 8Gb database (https://ccb.jhu.edu/software/kraken/) with default parameters. Twenty-five genera with abundance above 1% were found. The most abundant genus on carcasses was *Anoxybacillus* (52% of the total microbiome) and on environmental samples *Oenococcus* (15%). *Enterobacteriaceae* were detected in 13 collected points (prevalence ranging from 0.001% to 0.02%), with different genera found: *Citrobacter* (18.0%)*,* *Klebsiella* (14.0%), *Erwinia* (12.1%), *Enterobacter* (9.99%), *Trabulsiella* (5.99%), *Providencia* (4.0%), *Serratia* (4.0%), *Salmonella* (4.0%) and *Morganella* (1.99%). It is important to highlight that *Salmonella* spp. was found in only two samples, one from the carcass and the other from the drain sampled on the same day. Other genera of interest in food microbiology were also detected, namely, *Pseudomonas*, *Lactobacillus*, *Campylobacter*, *Clostridium*, *Bacillus*, *Staphylococcus*, and *Lactococcus*. Such diversity suggests possible interventions to extend shelf life hampered by the microbial consortia with pork products. Otherwise, it may be useful for developing microbial traceability to a slaughterhouse.

Acknowledgments: This work was supported by the projects UIDB/50016/2020 and UIDB/CVT/00772/2020 funded by the Fundação para a Ciência e Tecnologia (FCT)

References:

[1] Pandey, P.K., Biswas, S., Kass, P. Microbial pathogen quality criteria of rendered products. Applied Microbiology and Biotechnology, 100 (2016) pp. 5247-5255,
[2] Pandey, P.K., Vidyarthi, S.K., Vaddella, V., Venkitasamy, C., Pitesky, M., Weimer, B., Pires, A. Improving biosecurity procedures to minimize the risk of spreading pathogenic infections agents after carcass recyclying. Frontiers in Microbiology, (2020).