P4.28 - ASSESSING THE VIRULENCE POTENTIAL OF DIFFERENT *LISTERIA MONOCYTOGENES* CLONAL COMPLEXES WITH *GALLERIA MELLONELLA* LARVAE MODEL

Mariana Sousa [1(*)]***, Sónia Silva*** [2,3]***, Daniela Araújo*** [2]***, Joana Castro*** [2,3]***, Gonçalo Almeida*** [2]***, Catarina Ventura*** [1]***, Rui Magalhães*** [1]***, Vânia Ferreira*** [1]***, Paula Teixeira*** [1]

[1] *Universidade Católica Portuguesa, CBQF - Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Porto, Portugal*

[2] *National Institute for Agrian and Veterinary Research (INIAV, I.P.), Vairão, Vila do Conde, Portugal*

[3] *Centre of Biological Engineering (CEB), University of Minho, Campus de Gualtar, Braga, Portugal*

[(*)] *e-mail: marsousa@ucp.pt*

Keywords: bacterial pathogenesis; infection; nonvertebrate animal model; foodborne.

ABSTRACT

Listeria monocytogenes is a highly diverse species, exhibiting differential virulence potential within strains from different clonal complexes (CCs). Hypervirulent CCs strains tend to be associated with higher frequency in clinical cases and severe outcomes, while hypovirulent CCs are characterized by a reduced level of virulence and are often associated with food-related contamination. Recently, researchers have employed *Galleria mellonella* larvae as an *in vivo* model to characterize these variable virulence patterns among *Listeria* strains. Although it has only been utilized once to study CC-related virulence thus, there is still uncertainty about its relevance as an *in vivo* model. Infection studies with *G. mellonella* larvae were performed to evaluate the virulence potential of 16 *Lm* strains from CC1, CC2, CC4, CC6, CC388, CC87, CC9 and CC121. Hence, the survival rate and health index scores of larvae were used to quantify the virulence capacity of this pathogen. Results obtained indicate that: the CC2 strain exhibited a hypovirulent phenotype in the larvae with the highest survival rate and health index scores, followed by two strains from CC1 and CC6. In contrast, another CC6 strain exhibited reduced larvae survival rates, followed by the CC4 strain. Furthermore, strains from CC9, which is considered hypovirulent, caused around 47% mortality (Figure 1). Our findings revealed clear variations in virulence patterns that were previously determined with other *in vitro* and *in vivo* models. Moreover, it was observed a strain-dependent intra-clonal complex virulence difference in the infection of *G. mellonella* larvae. Additionally, by eliminating the dependence of *L. monocytogenes* strains on the *inlA* gene for host cell invasion, it was observed that hypovirulent clones demonstrated an infection potential equal to or greater than that of hypervirulent strains. Hence, there are still virulence markers that need to be characterized to improve the genotypic distinction of these CCs.

Acknowledgements:
This work was supported by National Funds from FCT - Fundação para a Ciência e a Tecnologia through project GenoPhenoTraits4Persitence - Genomic and phenotypic traits contributing to persistence of Listeria monocytogenes in food processing environment (PTDC/BAA-AGR/4194/2021).