**Non-*Helicobacter pylori* in feline gastrointestinal neoplasia.**

Sara Campana1,2, José Catarino2,3,4,5, Margarida Alves2,6, Andreia Valença2,3,7,8, Joana Santos2,5, Ana Santana2,3,8,9, Pedro Faísca2,5,6, Adriana Belas2,3,7,8, Joana Ropio2,10, Rute Teixeira2,3

1 Universiti of Sassari, Department of Veterinary Medicine, Sassari, Italy

2 Faculty of Veterinary Medicine, Lusófona University, Lisbon, Portugal

3 Escola Superior de Saúde, Proteção e Bem Estar Animal, Instituto Politécnico da Lusofonia, Lisbon, Portugal

4 Comprehensive Health Research Centre (CHRC), Departamento de Desporto e Saúde, Escola de Saúde e Desenvolvimento Humano, Évora University, Évora, Portugal

5 DNATECH Veterenary Laboratory, Lisbon, Portugal

6 CBIOS – Universidade Lusófona's Research Center for Biosciences & Health Technologies

7 CIISA - Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, Lisbon University, Lisbon, Portugal

8 Associate Laboratory for Animal and Veterinary Sciences (AL4AnimalS), Lisbon, Portugal

9 Veterinary and Animal Research Center (CECAV), UTAD, Vila Real, Portugal

10 BRIC (BoRdeaux Institute of onCology), UMR1312, INSERM, University of Bordeaux, Bordeaux, France

**Objectives:** Over the last two decades, bacterial mucosal colonization, particularly involving non-*H. pylori* helicobacters (NHPH), has been highlighted as a potential oncogenic factor in feline gastric lymphoma and poorly differentiated large intestinal adenocarcinoma. Our aim was to validate simple molecular diagnostic techniques to identify the presence of specific *Helicobacter* species in feline gastrointestinal (GI) tract.

**Materials and Methods:** DNA was extracted from 25 paraffin-embedded tissue from any portion of the GI tract with a previous histopathological diagnosis of lymphoma or gastric adenocarcinoma. The presence of *Helicobacter* spp. was performed by PCR. All PCR-positive samples were sequenced, and the sequenced PCR products were compared to the GenBank/EMBL/DDBJ databases using the Basic Local Alignment Search Tool (BLAST).

**Results:** Six samples (33,3%) were *Helicobacter* spp. PCR-positive*. H. heilmannii* was the most frequent species, identified in 4 animals. *H. ailurogastricus* (n=1)*, H. felis* and *H. bizzozeronii*, were also detected. These last two *Helicobacter* species were identified in the same cat sample.

**Conclusions:** Our preliminary results confirm the occurrence of NHPH in distinct regions of the feline gastrointestinal tract. However, more samples will be needed in order to establish a correlation between specific *Helicobacter* species and feline gastrointestinal manifestations.

**Keywords:** non-*H. pylori* helicobacters, feline gastrointestinal carcinogenesis

**Funding:** This work is part of the exploratory project “Unveiling the Non-*Helicobacter pylori* role in feline gastrointestinal diseases”, funded by FMV-ULHT in 2022-2023.