

Molecular screening of equine herpesvirus in the southern Iberian Peninsula – Preliminary results

João Dias¹, Adriana Belas^{1,2,3,4}, André Pereira^{1,2,3,4,5}, Margarida Alves^{1,2,3,6}, Joana Simões^{1,2,3}, Andreia Valença^{1,2,4}

¹Faculty of Veterinary Medicine, Lusófona University, Lisbon University Centre, Lisbon, Portugal

²1-MVET (Research in Veterinary Medicine), Faculty of Veterinary Medicine, Lusófona University - Lisbon University Centre, Lisbon, Portugal

³Animal and Veterinary Research Center (CECAV), Faculty of Veterinary Medicine, Lusófona University - Lisbon University Centre, Lisbon, Portugal

⁴Superior School of Health, Protection and Animal Welfare, Polytechnic Institute of Lusophony, Lisbon, Portugal

⁵Global Health and Tropical Medicine (GHTM), Associate Laboratory in Translation and Innovation Towards Global Health (LA-REAL), Instituto de Higiene e Medicina Tropical (IHMT), Universidade NOVA De Lisboa (UNL), Lisbon, Portugal

⁶CBIOS - Research Center for Biosciences and Health Technologies, Lusófona University, Lisbon, Portugal

Objectives: Equine herpesviruses (EHV) are widespread respiratory pathogens that pose a major threat to equid health and have a considerable economic impact on the horse industry worldwide. The viruses' ability to establish latency allows for their persistence in the host, with potential reactivation during periods of immunosuppression throughout the animal's life. Among the nine identified EHV types, EHV-1, EHV-2, EHV-4, and EHV-5 are the most frequently detected in equid populations. Co-infection with multiple EHV types has also been reported in both clinically healthy and symptomatic animals. To our knowledge, there is a lack of published data on EHV infection and its association with equid health status in Portugal, likely due to the absence of routine diagnostic practices. This study aimed to investigate the presence of EHV DNA in equids from the southern Iberian Peninsula.

Material and Methods: DNA was extracted from 50 equid nasal swab samples. The presence of EHV DNA was screened using a nested-PCR assay with consensus primers targeting a conserved region of the herpesvirus *DNA polymerase* gene. Statistical analysis was performed to assess associations between EHV infection and selected epidemiological variables using the Chi-square (χ^2) and Fisher's exact tests.

Results: Preliminary results revealed that 42 out of 50 samples (84%) tested positive for EHV DNA. The frequency of EHV DNA was significantly higher in unvaccinated equids (100%; 22/22) compared to vaccinated ones (71.4%; 15/21) ($p = 0.006$).

Conclusion: These findings highlight a high frequency of EHV infection within the sampled population, particularly in unvaccinated animals, thus underscoring the crucial role of vaccination in mitigating viral circulation. This emphasizes the importance of active molecular surveillance practices to better understand the epidemiology of EHV infections and their potential impact on equid health and reinforces the strategic value of vaccination programs for effective disease control and improved animal health.

Keywords: Equine herpesvirus; molecular screening; polymerase chain reaction; equids; southern Iberian Peninsula.

Funding: This study was supported by Lusófona University, Research Grants 2024/2025