mice reached a clinical score between 4 and 6 in the later stages of the disease and eventually succumbed without statistically significant differences in the survival time (204 ± 4, 202 ± 3, and 202 ± 6 days after the induction, for the prophylaxis, treatment, and control group respectively). To further characterize the disease progression, the AUC for the clinical scores vs time plots was calculated and found significantly reduced (p = 0,0225) for the treatment group. **Conclusions**: Our results indicate that although the glycodendrimer did not prolong the survival interval in the animal model used, it led to a delay in disease onset and disease burden. Further studies on the pharmacokinetics and pharmacodynamics of the compound are underway.

Determining prion protein gene (PRNP) genetic variability in portuguese cervidae population. An important task in chronic wasting disease (CWD) risk assessment projet in Portugal

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Aims: The chronic wasting disease (CWD) in cervids is now a rising concern in wildlife within Europe, since the first case detected in Norway in 2016, 40 more appear until May of 2022, in Norway, Sweden and Finland. The unclear origin of these new European cases and the risk that CWD poses to cohabiting animals or more importantly to humans is largely unknown, is very important for the establishment of risk assessment projects, even in countries with no cases of CWD to forecast possible infections. In this way, a synergistic collaborative project was established between the UTAD, INIAV and IPCB to evaluate the risk of a potential occurrence of CWD in cervid Portuguese populations. The study of prion protein gene, *PRNP*, has been proved to be a valuable tool for determining the relative susceptibility to TSEs since this is influenced by polymorphisms in this gene. The aim of this work is the screening for $PrP^{res}$and determination of the *PRNP* genotyping profile on Portuguese cervids, as the survey and georeferencing of these animals will contribute to delineating the risk of dissemination of CWD in Portugal.

Material and Methods: This study includes 200 animals of three different cervid species: red deer (*Cervus elaphus*), fallow deer (*Dama dama*) and roe deer (*Capreolus capreolus*). Masseter muscle and lymph node of each animal were collected for genomic DNA extraction and genetic analysis of prion protein gene, *PRNP*. The full exon 3 of *PRNP* gene (771 bp) was amplified by PCR using the primers F223-ACACCCTCTTTATTTTGCAG and R224-AGAAGATAATGAAAACAGGAAG. PCR products were purified, sequenced, and analyzed using SnapGene Viewer v. 5.1.5, Unipro UGENE v. 40.0 and Jalview 2.11.1.4.

Results: The comparison of the coding region of *PRNP* gene and protein sequence – PrP^{C}(256 aa) in red deer, fallow deer, and roe deer, showed high conservation. In red deer, three polymorphisms were identified: one synonymous, codon A136A and two non-synonymous codons T98A and Q226E. The synonymous mutation at codon 136 showed to be linked to the non-synonymous mutations at codon 226. Three haplotypes were identified based on the sequence variations: T98-Q226 (TQ), T98-E226 (TE) and A98-Q226 (AQ). In fallow deer and roe deer, no intra variation was found.

Conclusions: The multi-disciplinary approaches including genotyping, PrP^{res}detection, identification of risk factors, clinical and pathology evaluations, are of great importance to evaluate the risk of occurrence of CWD in Europe and more specifically in Iberian Peninsula. We did not find any positive cases of CWD in the animals under study and the genetic variations do not allow to conclude about its resistance to this disease.

Funded by: This work was supported by the project WastingPrionRisk [POCI-01-0145-FEDER-029,947/PTDC/CVT-CVT/29947/2017] funded by the Portuguese Foundation for Science and Technology (FCT). FCT PhD grant [SFRH/BD/146961/2019] financed by FCT through FSE (Fundo Social Europeu). This work was also supported by national funds [UIDB/CVT/00772/2020], [LA/P/0059/2020] and [UIDB/04033/2020] by FCT.