

Estimating sequence diversity of prion protein gene (PRNP) in Portuguese populations of two cervid species: Red deer and Fallow deer

George C. Pereira^{1,4,5*}, Nuno Gonçalves-Agu^{1,6*}, Estela Bastos¹, Leonor Orge^{1,6}, Ana C. Matos¹, Adélna Gama¹, Anabela Alves¹, Alexandra Esteves¹, Sara Rocha¹, Luis Figueira¹, Carla Lima¹, Filipe Silva¹, Fernanda Soutar¹, Isabel Pires¹, João Silva¹, Madalena Vieira-Pinto¹, Maria L. Pinto¹, Paula Mendonça¹, Paulo Carvalho¹, Paula Tavares¹, Roberto Sargo¹, Maria A. Pires¹



ABSTRACT

Among the transmissible spongiform encephalopathies (TSEs), chronic wasting disease (CWD) is currently one of the most serious to wildlife. In Europe, after the first case was detected in Norway in 2016, it is still unclear and still unclear (2021), a total of 30 cases were described in Norway, Sweden and Poland. The study of the genetic diversity of the prion protein gene, PRNP, has been proposed as a valuable tool for determining the relative susceptibility to TSEs. In the present study we analyzed the exon 3 of PRNP gene in 134 animals from two species: red deer (*Cervus elaphus*) and fallow deer (*Dama dama*). Three single nucleotide polymorphisms (SNPs) were found in red deer samples and compatible with the ones found in previous studies in Europe. The comparison of our population with North American populations suggest that the first-arriving deer from the north may possess susceptibility to CWD, although lack of experimental data and the necessity of large surveys are necessary to evaluate these populations.

INTRODUCTION

Chronic Wasting Disease (CWD) belongs to the family of Transmissible Spongiform Encephalopathies (TSEs), specific to cervids, and characterized by an infectious, misfolding of the prion protein (PrP^C) into a protease-resistant form (PrP^{Sc}). Originated in North America and widespread in USA and Canada, the first case of CWD appeared in Europe in 2016 in a free-ranging reindeer in Norway and further cases were later reported in red deer and moose, ultimately reaching other countries like Finland and Sweden (Vilén et al 2019; Arfola et al 2021). The study of susceptibility/resistance of cervids to CWD is essential to predict that certain populations are less susceptible to infection than others (Haworth et al 2021). The variability in the prion protein (PRNP) gene is one of the methodologies used to predict that certain populations are less susceptible to infection than others (Haworth et al 2021). The analysis of the PRNP diversity in European cervid species is still limited but some studies carried out in Britain, Norway and Sweden, showed that some PRNP genetic variations can be related with CWD susceptibility/resistance. Genetics studies, in Europe and Portugal, to evaluate the variation of PRNP gene in cervid populations are of extreme importance in order to estimate potential susceptibility populations to emerging CWD and informing risk assessment and control/surveillance strategies.

MATERIAL AND METHODS

Samples

- Total Number of Samples 134 animals
- Red deer (*Cervus elaphus*) - 57
- Fallow deer (*Dama dama*) - 77

Genomic DNA Extraction

- Frozen Muscle and Lymphoid tissues
- NZY Tissue gDNA Isolation kit (NZYTech, Lda - Genes and Enzymes)

PCR Amplification

- Full exon 3 of PRNP gene (771 bp)
- Primers F223-ACACCCCTCITTAITTTGCAAG and R224-AGAAGATAATGAAAACAGGAAG

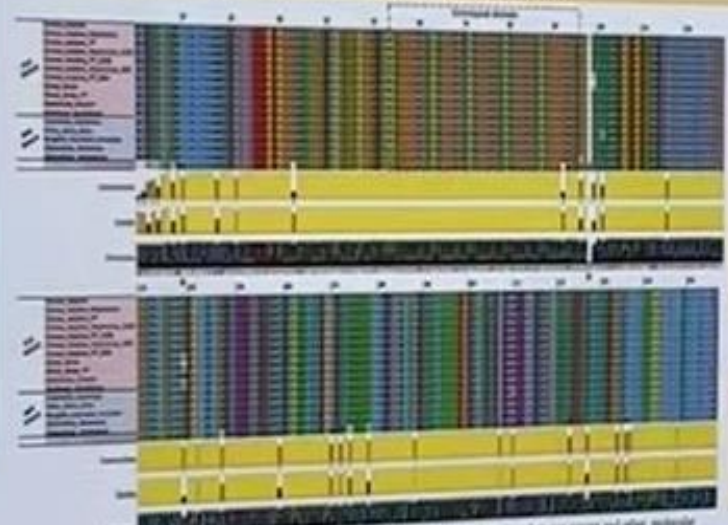
Sanger Sequencing and Analysis

- Eurofins Genomics GmbH in Germany
- SnapGene Viewer v. 5.1.5
- Unipro UGENE v. 40.0
- Jalview 2.11.1.4

FINDINGS

- I. The comparison of coding region PRNP gene (771 bp) and protein sequence - PrP^C (256 aa) showed:
 1. Red deer (57 samples) - high conservation in protein sequence;
 2. Fallow deer (77 samples) - no sequence diversity was found corresponding to the red deer haplotype T₄₀₈F₁₃₆ (TF) with an amino acid variation in codon 138, asparagine (N) for serine (S) (highlighted in Figure 2).

- II. Presence of the terminal signals and the octorepeat domain (5 peptide repeats with 3 octapeptides of PHGGGWGQ flanked by 2 nonapeptides of P(Q)/HGGGGWGQ) (highlighted in Figure 2).



- III. Three single-nucleotide polymorphisms (SNPs) were identified:
 1. One synonymous SNPs - position 408 (codon 136) (gC/T/p.C);
 2. Two non-synonymous mutations: position 292 (Acc/Gcc)/T98A and position 676 (Cag/Gag)/Q226E (Table 1 and 2).

- IV. The synonymous mutation at position 408 (codon 136) showed to be linked to the non-synonymous mutations at position 676 (codon 226).

Figure 2. Protein sequence alignment of New and Old World cervid showing conserved homologies between species and other molecules conserved domains.

Table 1. Amino acid variations within the exon 3 and haplotype frequencies of cervid PRNP in red deer populations.

Nucleotide Change	Amino Acid		Total	Total	Frequency	Frequency	Frequency	Frequency
	gC/T	p.C						
408	1	56	57	100	1.75	98.25	1.75	3.12
676	1	56	57	100	1.75	98.25	1.75	3.12
Total	2	112	114	100	1.75	98.25	1.75	3.12

Table 2. Coverage frequencies of PRNP polymorphisms in Portuguese red deer populations.

SNP	gC/T	p.C	Frequency		Linkage	
			gC/T	p.C	gC/T	p.C
408	1	56	1.75	98.25	1.75	3.12
676	1	56	1.75	98.25	1.75	3.12
Total	2	112	3.5	196.5	3.5	6.24



Figure 1. Map of the southern of Portugal (Distrito Beira Interior) showing the geographic locations where different samples were obtained.

CONCLUSION

In summary, it is our opinion that multi-disciplinary approaches including genotyping, PrP^{Sc} detection, identification of risk factors and others, are of great importance to evaluate the risk of occurrence of CWD in European and more specific in Iberian Peninsulas. In this way a synergistic collaborative project (Project 029947ICAT R2/SAICT/2017-SAICT) was established between the University of Trás-os-Montes and Alto Douro (UTAD), the National Institute for Agricultural and Veterinary Research (INIAV) and the Polytechnic Institute of Castelo Branco (IPCBr) with the aim of evaluating the risk of a potential occurrence of CWD in cervid Portuguese populations.