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Prion Protein Gene Diversity in European Cervids

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Chronic Wasting Disease (CWD), a Transmissible Spongiform Encephalopathy caused by the misfolding of a cellular prion protein (PrP^{C}) into its pathological isoform (PrP^{CWD}), has been endemic in North American cervids since the 1960s. However, the disease has recently also emerged in Scandinavia not only in its contagious but also in a novel 'atypical' form. CWD now threatens to spread throughout the European continent. Since susceptibility to this disease is largely determined by the structure of the prion protein gene (*PRNP*) of the host, it is necessary to know the diversity of the *PRNP* to estimate the threat CWD poses to the European deer population. Therefore, samples from 3000 red deer (Cervus elaphus), roe deer (*Capreolus capreolus*) and sika deer (*Cervus nippon*) were collected throughout Germany and in smaller numbers from neighbouring states. Sequencing of the Open Reading Frame (*ORF*) of the *PRNP* will provide information on the variations in genotype frequencies and their geographical distribution. The identified genotypes will be interpreted in the context of previously known sequencing data from North American and European studies, as well as the results of experimental deer challenge studies. This study will provide new insights into the vulnerability of European cervid populations and improve European surveillance and control measures.