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## Chamois, healthier as more diverse



A new pestivirus has affected chamois populations from the Catalan Pyrenees, causing mortalities reaching sometimes 80%. UAB researchers have analyzed the MHC complex gene of 81 chamois from different National Game Reserves, from Cadi to Cerdanya-Alt Urgell, to establish the relationship between genetic variability and the impact of the disease. In general, the chamois affected had less genetic diversity than the healthy ones. So, along with other immune, epidemiological and ecological factors, genetic variability should be assessed when studying viral infections in wild ungulate populations.

The Pyrenean chamois (*Rupicapra pyrenaica pyrenaica*) is a mountain ungulate which inhabits the Pyrenees. Its populations are managed through hunting and may be affected by several diseases, as keratoconjunctivitis and chamois pestivirus, caused by a virus similar to that of border disease of sheep. This last disease has decimated the population of chamois in the Catalan Pyrenees during the last years, causing mortalities ranging between 40 and 85%.

The Major Histocompatibility Complex (MHC) is a sensitive marker of population genetic

variability, and studying MHC may help to understand the evolution of the chamois populations in the different areas of the Pyrenees as related to their relative isolation and diseases.

In this study the exon 2 of the DRB gene of the class II MHC of 81 Pyrenean chamois from the National Game Reserves (NGR) of Cadí, Alt Pallars-Aran, Freser-Setcases i Cerdanya-Alt Urgell was analyzed. Twenty-nine haplotypes were identified, 26 of them for the first time. Genetic variability was higher in the NGR of Freser-Setcases than in Cadí, and the pestivirus-affected chamois had overall less genetic variability than healthy chamois. Interestingly, No chamois pestivirus-related mortality has been registered in the NGR of Freser-Setcases, although the causal pestivirus has been detected in this NGR. Perhaps the higher genetic variability in this NGR could explain the resistance of this chamois population to this disease, together with other immunological, epidemiological and ecological factors.

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## References

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