

# Novel Respirovirus in Alpine Chamois

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The Alpine chamois is a free-living wild ruminant distributed across the mountainous areas of France, Italy, Switzerland, Liechtenstein, Germany, Austria, Slovenia and Croatia. This wide distribution favours interactions with other wild ruminants and livestock, implying the risk of cross-transmission of pathogens. Due to the impact of lung diseases on chamois populations, the investigation of respiratory pathogens is important for wildlife conservation and for the understanding of infection transmission at the livestock–wildlife interface. A novel respirovirus was isolated from a chamois with lung lesions in Italian Alps. The genome characterization of this novel virus revealed similarities to domestic ruminant respiroviruses, mainly of caprine and ovine origin. Overall, phylogenetic analyses indicated that the chamois virus is distinct from already defined species and suggested that it is a putative novel member of the genus *Respirovirus*. The present investigation contributes to the knowledge of respiratory infections in wild ruminants and raises questions on the epidemiological link between chamois and other animal species.

Keywords: novel respirovirus ; Paramyxoviridae ; chamois ; wild ruminants ; pneumonia

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## 1. Introduction

In recent years, novel respiroviruses have been identified in goats suffering respiratory syndrome in China <sup>[1]</sup>,<sup>[2]</sup> and in the Sri Lankan Giant squirrel introduced in Germany <sup>[3]</sup>. To date, the *Respirovirus* genus in the family *Paramyxoviridae* includes six species: human respirovirus 1 and 3 (HRV1, HRV3; formerly human parainfluenza virus 1 and 3), porcine respirovirus 1 (PRV3, formerly porcine parainfluenza virus 1), bovine respirovirus 3 (BRV3, formerly bovine parainfluenza virus 3), caprine respirovirus 3 (CRV3, formerly caprine parainfluenza virus 3) and murine respirovirus (MRV, formerly Sendai virus), as recently revised <sup>[4]</sup>.

CRV3 (formerly CPIV3) was first identified in goats <sup>[2]</sup> and recently also in sheep in China <sup>[5]</sup>. To date, CRV3 has not been reported in other countries.

BRV3 (formerly BPIV3) is a worldwide cattle respiratory pathogen involved in bovine respiratory disease (BRD) <sup>[6]</sup>, a multifactorial disease for which viral pathogens have a prominent role as primary agents <sup>[7]</sup>. Serological evidence of BRV3 infection has been reported in several wild ruminant species, including Alpine chamois in Italy <sup>[8]</sup>. Due to the impact of the pneumonia complex on chamois populations, investigation on respiratory pathogens is of considerable interest <sup>[9]</sup>.

The Alpine chamois is the most abundant subspecies of *Rupicapra* spp. with nearly 500,000 individuals distributed among France, Italy, Switzerland, Liechtenstein, Germany, Austria, Slovenia and Croatia <sup>[10]</sup>. This expansion favours the interactions between livestock and wild ruminants, implying an increased risk of cross-transmission of pathogens. Indeed, some of the major outbreaks reported in chamois in Europe have been triggered by pathogens initially cross-transmitted at the interface with livestock <sup>[11]</sup>.

## 2. Specifics

A novel RV3 was recently isolated from a hunted chamois with lung lesions in Italian Alps. The absence of other respiratory agents in the lungs of the RV3-positive and other chamois supports the hypothesis that the novel virus in chamois may be the etiological agent of the lung lesions that could either be interstitial pneumonia and/or catarrhal bronchopneumonia. Nevertheless, the negative results for other viral or bacterial respiratory pathogens could be biased by the storage condition of lung samples and by an analytical protocol focused on viral isolation. The phylogenetic analyses based on the full-length genome sequence of the novel isolate and reference respirovirus strains showed that chamois RV3, named ChamoisRV/IT2014, significantly clustered with CRV3 but formed a separated branch. The nucleotide identity for the ChamoisRV/IT2014 complete genome with respirovirus reference strains, including CRV3, was 80% or below and the current species demarcation criterion for *Respirovirus* genus <sup>[12]</sup> shows that ChamoisRV/IT2014 possesses sequence differences from the other respirovirus species.

Overall, the results of the full genome phylogenetic tree, sequence identities with other respirovirus and species demarcation criterion for the Respirovirus genus, indicate that ChamoisRV/IT2014 is distinct from already defined species and suggest that it is a putative novel member of the genus Respirovirus.

This new isolate in a new host species raises several questions to be addressed. Studies on the epidemiological role of chamois, the risks of cross-transmission between wild ruminant and livestock and the evolution mechanisms, including genomic changes driven by the adaptation of viruses to new hosts, are suggested. The new powerful methods for genomic characterization will contribute to increase the availability of whole genome sequences to deepen the understanding of the origin and evolution of respiroviruses.

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