

Isolation and characterization of small ruminant lentiviruses (SRLV) circulating in Swiss goats in the post- CAEV-eradication era as a precondition to design novel, genotype-specific diagnostic tools.

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Key words

Caprine arthritis encephalitis virus (CAEV), Maedi-Visna virus (MVV), small ruminant lentiviruses (SRLV), field strain, phylogenetic analysis, cell culture, qRT-PCR, sequencing

Aim of the study

The Swiss caprine arthritis encephalitis virus (CAEV) eradication campaign was a pioneering effort and, as far as the clinical manifestations of the disease in the Swiss goat population are concerned, was a complete success. This program permitted a reduction in seroprevalence from about 60 to 80% to less than 1%. Unfortunately, however, seroconversions still occur, causing important economic losses to the breeders. The aim of this study was to characterize the viruses involved in these seroconversions events and to test the suitability of the currently used diagnostic tools for the detection of animals infected with these particular SRLV.

Material and methods

Macrophage cultures from milk and PBMC, product enhanced reverse transcriptase assay, qRT-PCR

Results and significance

A number of field isolates of small ruminant lentiviruses (SRLVs) were derived from flocks located in different cantons. The phylogenetic analysis of pol sequences permitted to classify these isolates as A4 subtype, providing evidence for the prominence of this particular subtype in the post-eradication phase. None of the animals involved showed clinical signs of SRLV infection, confirming previous observations which had suggested that this particular subtype is highly attenuated, at least for goats. Three of these isolates, derived from a mixed flock of goats and sheep certified for many years as free of CAEV, were characterized in details. A quantitative real time PCR strategy based on primers and probes derived from a highly variable env region permitted us to classify the animals as uninfected, singly or doubly infected. The performance of different serological tools based on this classification revealed their profound inadequacy in monitoring animals infected with this particular SRLV subtype. *In vitro*, the isolates showed differences in their cytopathicity and a tendency to replicate more efficiently in goat than sheep cells, especially in goat macrophages. By contrast, *in vivo*, these viruses reached significantly higher viral loads in sheep than in goats. Both subtypes infected goats and sheep with equal efficiency. Sequencing of the LTRs of these isolates provided strong evidence that a series of mutations in this particular region are responsible for the attenuated phenotype of these SRLV.

In conclusion, we isolated several field strains of SRLV and characterized three isolates of the subtype A4 that efficiently circulate in a mixed herd of goats and sheep in spite of their apparent attenuation and a strict physical separation between goats and sheep. The poor performance of the serological tools applied indicates that, to support an SRLV eradication campaign, it is imperative to develop novel, subtype specific tools.

Publications, posters and presentations

Cardinaux, L.; Molecular analysis of avirulent, albeit successful, small ruminant lentiviruses; Meeting of Master- and Doctoral Students in Virology, Schloss Münchenwiler, November 1-2, 2012

Cardinaux, L.; et al. (2012) "Virological and phylogenetic characterization of attenuated small ruminant lentivirus isolates eluding efficient serological detection" Vet. Microbiol., in press.

Cardinaux, L.; Dr. med. Vet. Thesis, Vetsuisse Faculty Bern (submitted).

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