



Small Ruminant Lentiviruses (SRLVs): Genetic Diversity, Pathogenicity and Diagnostic Approach

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Message from the Guest Editor

Dear colleagues,

Lentiviruses and their hosts have worldwide distribution and are known to cause a wide range of slowly progressive diseases affecting humans, nonhuman primates, crows, sheep, goats, and other animal species. Numerous studies have been devoted to the high genetic diversity and the pathogenesis of the diseases caused by SRLVs. The latter are able to cross the interspecies barrier, infecting sheep and goats through horizontal and lactogenic routes. Regarding infection among domestic and wild small ruminants, phylogenetic reconstructions support the existence of SRLV cross-species transmission. Infection of SRLVs usually leads to reproductive losses, reduction in growth rate and milk production, etc. It also appears that different strains present analogous clinical and gross, histopathological, and immunohistochemical pattern. Thus, SRLVs represent an interesting, albeit murky research topic.





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Message from the Editor-in-Chief

The worldwide impact of infectious disease is incalculable. The consequences for human health in terms of morbidity and mortality are obvious and vast but, when infections of animals and plants are also taken into account, it is hard to imagine any other disease that has such a significant impact on our lives—on healthcare systems, on agriculture and on world economics. *Pathogens* is proud to continue to serve the international community by publishing high quality studies that further our understanding of infection and have meaningful consequences for disease intervention.

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