



[Puumala hantavirus genetic variability in an endemic region \(Northern Sweden\).](https://arctichealth.org/en/permalink/ahliterature158643)

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Abstract:

Puumala hantavirus (PUUV), naturally harboured and shed by bank voles (*Myodes [Clethrionomys] glareolus*), is the etiological agent to nephropathia epidemica (NE), a mild haemorrhagic fever with renal syndrome. Both host and virus are found throughout much of the European continent and in northern Sweden NE is the second most prevalent serious febrile viral infection after influenza. The reliability of diagnostics by PCR depends on genetic variability for the detection of viral nucleic acids in unknown samples. In the present study we evaluated the genetic variability of PUUV isolated from bank voles in an area of northern Sweden highly endemic for NE. Genetic variability among bank voles was also investigated to evaluate co-evolutionary patterns. We found that the viral sequence appeared stable across the 80km study region, with the exception of the southernmost sampling site, which differed from its nearest neighbour by 7%, despite a geographical separation of only 10km. The southernmost sampling site demonstrated a higher degree of genetic similarity to PUUV previously isolated 100km south thereof; two locations appear to constitute a separate PUUV phylogenetic branch. In contrast to the viral genome, no phylogenetic variance was observed in the bank vole mtDNA in this study. Previous studies have shown that as a result of terrestrial mammals' postglacial re-colonization routes, bank voles and associated PUUV of a southern and a northern lineage established a dichotomous contact zone across the Scandinavian peninsula approximately 100-150km south of the present study sites. Our observations reveal evolutionary divergence of PUUV that has led to dissimilarities within the restricted geographical scale of the northern host re-colonization route as well. These results suggest either a static situation in which PUUV strains are regionally well adapted, or an ongoing process in which strains of PUUV circulate on a geographical scale not yet reliably described.

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