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## A "HOT SPOT OF MUTATION" IN THE SCHMALLEMBERG VIRUS M-SEGMENT

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In autumn 2011, Schmallenberg virus (SBV), a novel orthobunyavirus of the Simbu serogroup, was identified by metagenomic analysis in Germany. Hereupon SBV was detected in ruminants all over Europe and since then investigations on phylogenetic relationship, clinical signs, and epidemiology were conducted. However, until now only comparative sequence analysis of SBV genome segments with other species of the Simbu serogroup were performed, and detailed data on the S- and M-segments, relevant for virus- host cell interaction, are missing.

### Purpose

In this study we investigated the S- and M-segment sequences obtained from 24 SBV-positive field samples from sheep, cattle and a goat collected from all over Germany.

### Methods

S- and M-segment sequences were generated via one-step RT-PCR and subsequent Sanger-sequencing. Comparative sequence analyses as well as statistical and phylogenetic investigations were performed.

### Results

Findings obtained in our study indicate that the overall genome variability of SBV is neither regionally nor host species dependent. Nevertheless, we characterized for the first time a region of high sequence variability ("hot spot of mutation") within the glycoprotein Gc encoded by the M-segment.

### Conclusions

Our study addressed for the first time the SBV genome diversity using more than 20 different SBV-positive field samples from Germany. The data suggest that the SBV-genome variability is especially high within the N-terminal part of the putative Gc protein. The process of mutation within this hot spot of mutation seems to be independent from host species and geographical region but may be limited to the individual level.

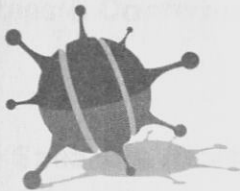
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