

New orthobunyavirus detected in cattle in Germany



SCOFCAH Brussels 6 December 2011

Background

During summer 2011 following symptoms were observed in dairy cows in North Rhine-Westphalia (similar to those described by NL):

- increased body temperatures ($>40^{\circ}\text{C}$)
 - impaired general condition
 - anorexia
 - reduced milk yield (by up to 50%)
- **symptoms disappeared after several days**

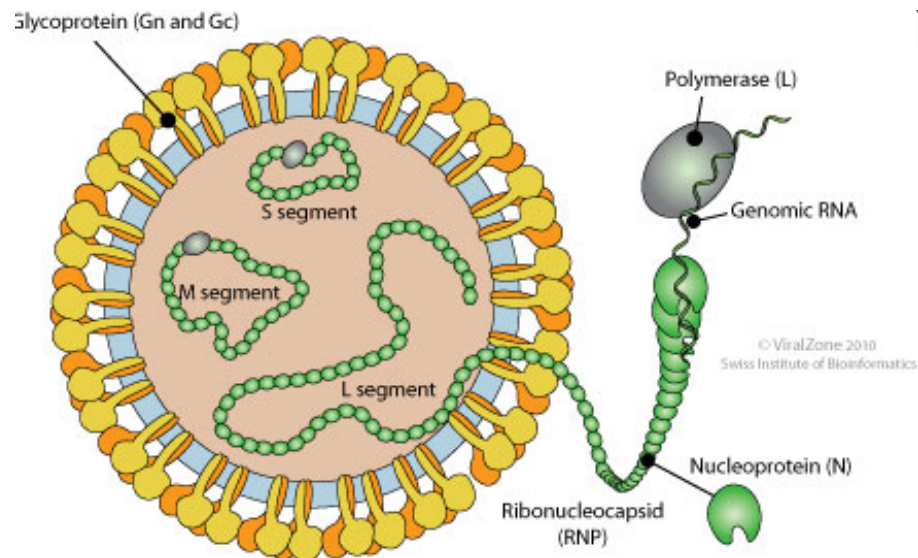
Laboratory investigations at the Friedrich-Loeffler-Institut (FLI)

- diagnostic screenings allowed to exclude infections with BTV, FMDV, EHDV, BVDV and other pestiviruses, BHV-1 and other herpesviruses, RVF and bovine ephemeral fever
- new technologies – **next generation sequencing and metagenome data analysis** – revealed Orthobunyavirus-like sequences

Sequences obtained were most closely related to Akabane, Aino and Shamonda viruses (Simbu-Serogroup of Orthobunyaviruses)

Orthobunyaviruses

- Family: *Bunyaviridae*
- Genome: segmented, single stranded negative-sense RNA
- 3 Segments: L (encodes for RNA dependant RNA polymerase)
M (encodes for two surface glycoproteins Gn and Gc)
S (encodes for the nucleocapsid protein)
- Transmission: through mosquitoes and *Culicoides* biting midges



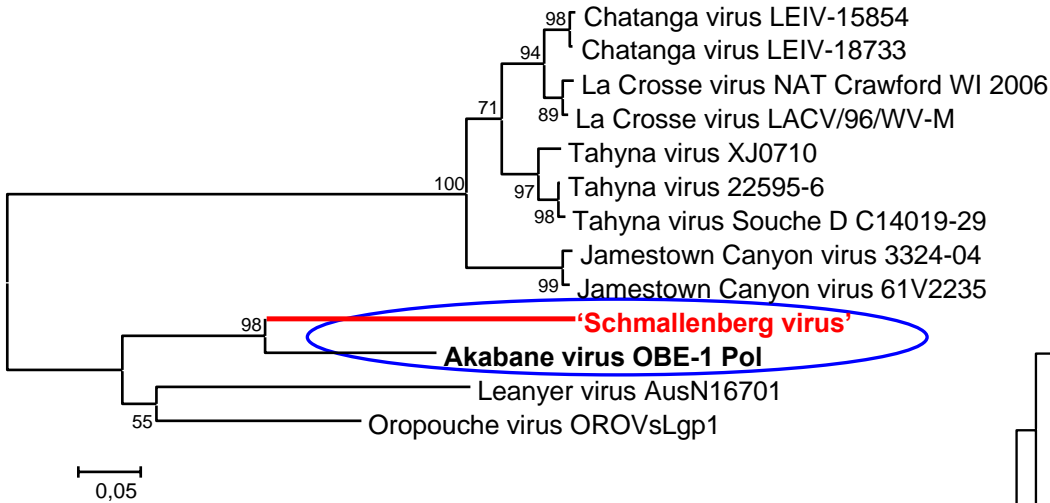
Full genome sequencing results (GS FLX, Roche)

Sequences obtained from all three segments:

Contig name	Length [bp]	Gene	
Contig1	1140	L	} ~ 70% coverage of Akabane L segment
Contig2	1005	L	
Contig3	653	L	
Contig6	451	L	
Contig8	413	L	
Contig9	302	L	
HCBT6XI02H8QXY	384	L	
HCBT6XI01DSD6S	237	L	
Contig4	757	M	} ~ 50% coverage of Aino M segment
Contig5	504	M	
HCBT6XI01AQTNF	400	M	
HCBT6XI01ARRX1	371	M	
Contig7	451	S	→ ~ 50% coverage of Shamonda S segment

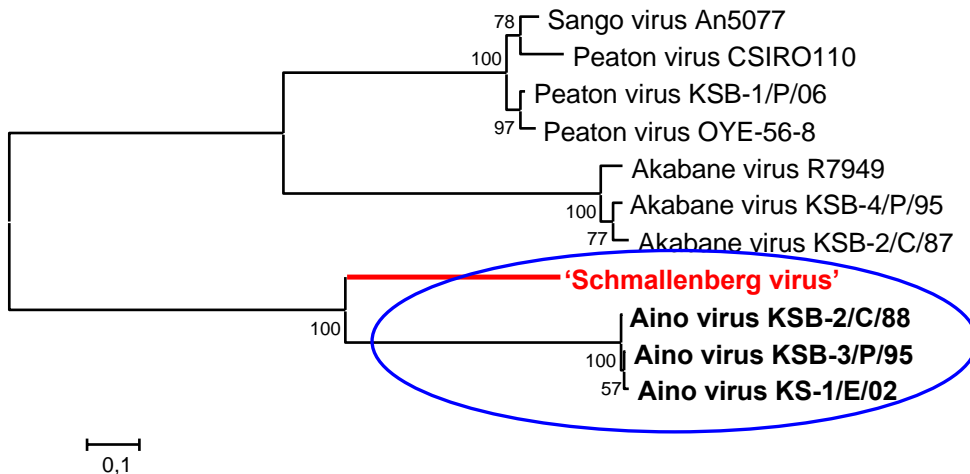
L segment

145 amino acids / 70% similarity to Akabane virus



M segment

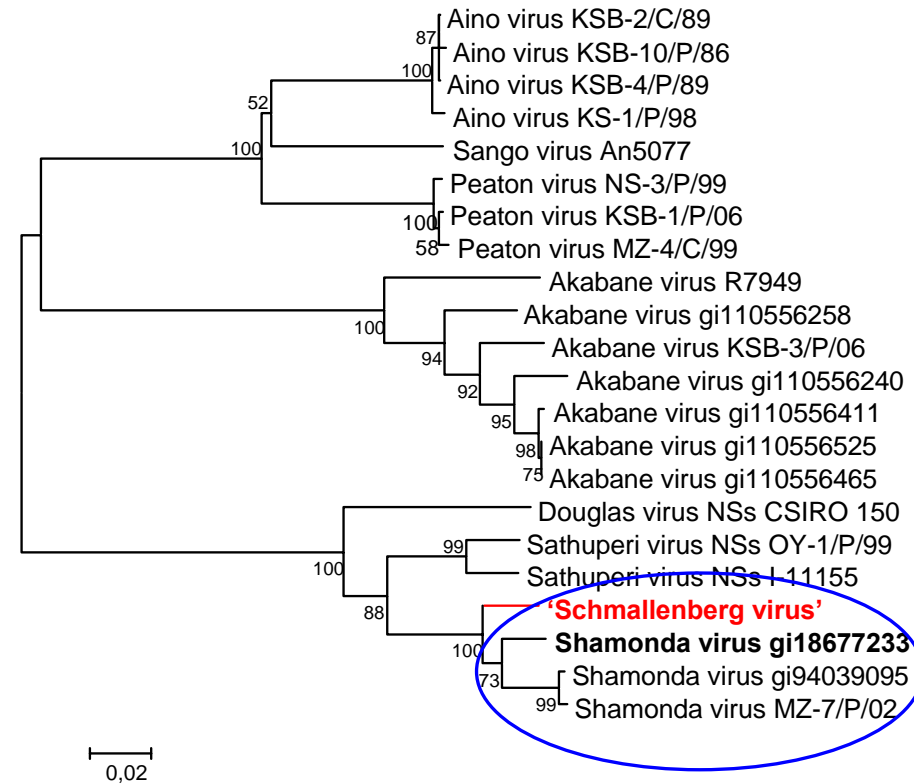
251 amino acids / 48% similarity to Aino virus



Phylogeny

S segment

451 nucleotides / 96% similarity to Shamonda virus



Orthobunyaviruses – Simbu-Serogroup

- 25 different viruses
- Isolated from insect vectors, cattle, (humans)
- Most are not infecting humans!
- Normally mild clinical disease
- But: fetal infections can induce e.g. abortion or congenital disorders

Sequence analysis:

Most related viruses (Shamonda, Aino, Akabane) are only infecting cattle

Samples from abortions and diseased new born calves are investigated at the moment

First results of investigations at FLI

- Nine PCR-positive cattle in four holdings detected between August and October
- Virus provisionally designated „Schmallenberg virus“ according to the origin of samples
- First 90 samples from holdings in unaffected regions (southern part of Germany, Mecklenburg-Western Pomerania) are negative

Ongoing activities in FLI

- further epidemiological examination of cattle holdings in the affected area
- laboratory testing of blood samples of acute affected animals as well as abort material; the PCR protocol was also transferred to laboratories in The Netherlands and Belgium
- determination of a correlation between the virus findings and the clinical symptoms
- inoculation experiment with cattle has started
- Virus isolation in cell culture ongoing
- development of tools for serological testing of cattle for Schmallenberg virus;
- Simbu-serogroup reference viruses were ordered from the World Reference Center for ARBO viruses (Dr. R. Tesh, UTMB, Texas, USA)

Thank you for your attention!