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Endemic Hantavirus in Field Voles, Northern England

Technical Appendix

Technical Appendix Table. Hantavirus detection by PCR of the viral genomic L segment in 48 voles, by sex and trapping site, northern England, March–September, 2015*

	Sex		Trapping sites				
Category	M	F	SCP	CHE	GRD	COL	RAV
No. voles infected	6	2	1	4	3	0	0
Total voles	34	14	12	18	12	2	4
% infected	17.65	14.29	8.33	22.22	25.00	0	0

*CHE, Cheese Sike (55°13′8.39″N, 2°32′26.50″W); COL, Coal Sike (55°14′08.35″N, 2°36′16.67″W); F, female; GRD, Geordies Knowe (55°11′1.61″N, 2°35′3.05″W); M, male; RAV, Ravenshill (55°14′30.55″N, 2°35′30.41″W); SCP, Scaup (55°15′44.18″N, 2° 32′41.05″W).

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Kielder            1 TGGTCTCCAGGAGATAACTCTGCAAAGTTTAGAAGATTTACTCAGGCTCT     50
                     |||||||||||||||||.||.|||||||||||||..||.|||||||||||
Tatenale           1 TGGTCTCCAGGAGATAATTCGGCAAAGTTTAGAAAGTTCACTCAGGCTCT     50

Kielder           51 GTATGACGGCCTAAGGGATGATAAGTTAAAAAATTGTGTGGTGGATGCGT    100
                     ||||||.||..||.|.||||||||.||||||||||||||.||.|||||.|
Tatenale          51 GTATGATGGTTTACGAGATGATAAATTAAAAAATTGTGTAGTAGATGCAT    100

Kielder          101 TAAGAAACATTTATGAAACAGAATTTTTTATGTCTCGAGAGCTACATCGA    150
                     |||||||.||||||||||||||.||.||||||||.||..|..|.|||||.
Tatenale         101 TAAGAAATATTTATGAAACAGAGTTCTTTATGTCCCGGAAATTGCATCGG    150

Kielder          151 TATATAGATGGAATGGAAGATTTATCTGAAAATGTGGAAGATTTTCTATC    200
                     |||||.||.||.|||||||||||||||||||||||.|||||||||.|.||
Tatenale         151 TATATTGACGGGATGGAAGATTTATCTGAAAATGTAGAAGATTTTTTGTC    200

Kielder          201 ATTTTTTCCTAATAATGTCTCCGCAATGATCAAAGGTAATTGGTTGCAAG    250
                     ||||||.||.|||||||||||.||||||||.||||||||.|||.|.||.|
Tatenale         201 ATTTTTCCCCAATAATGTCTCTGCAATGATTAAAGGTAACTGGCTACAGG    250

Kielder          251 GTAATTTAAATAAGTGCTCATCATTATTTGGTGCTGCAGTATCCCTGTTA    300
                     ||||||||||||||||.|||||||||||||||||||||||.||||||||||
Tatenale         251 GTAATTTAAATAAGTGTTCATCATTATTTGGTGCTGCAGTGTCCCTGTTA    300

Kielder          301 TTTAAGAGGGTATGGACAAATTTATTCCCTGAATTAGACTGTTTCTTTGA    350
                     ||.|||||.||.||||||||||||||||||||.|||||.|||||||||||
Tatenale         301 TTCAAGAGAGTGTGGACAAATTTATTCCCTGAGTTAGATTGTTTCTTTGA    350

Kielder          351 ATTTGCCCACCACTCAGACGA    371
                     .|||||.||||.|.|...|||
Tatenale         351 GTTTGCACACCCCGCTCTCGA    371
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Technical Appendix Figure 1. Pairwise nucleotide alignment of the genomic L segment sequence of the hantavirus found in Kielder Forest (145>A variant, GenBank accession no. KY751731) and Tatenale virus (GenBank accession no. JX316008.1). Sequences were aligned by using EMBOSS (*12*) on default settings. Alignment shows nucleotide similarity to be 86%.

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Kielder           1 WSPGDNSAKFRRFTQALYDGLRDDKLKNCVVDALRNIYETEFFMSRELHR     50
                    |||||||||||:||||||||||||||||||||||||||||||||||:|||
Tatenale          1 WSPGDNSAKFRKFTQALYDGLRDDKLKNCVVDALRNIYETEFFMSRKLHR     50

Kielder          51 YIDGMEDLSENVEDFLSFFPNNVSAMIKGNWLQGNLNKCSSLFGAAVSLL    100
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
Tatenale         51 YIDGMEDLSENVEDFLSFFPNNVSAMIKGNWLQGNLNKCSSLFGAAVSLL    100

Kielder         101 FKRVWTNLFPELDCFFEFAHHSD    123
                    ||||||||||||||||||||.:.
Tatenale        101 FKRVWTNLFPELDCFFEFAHPAL    123
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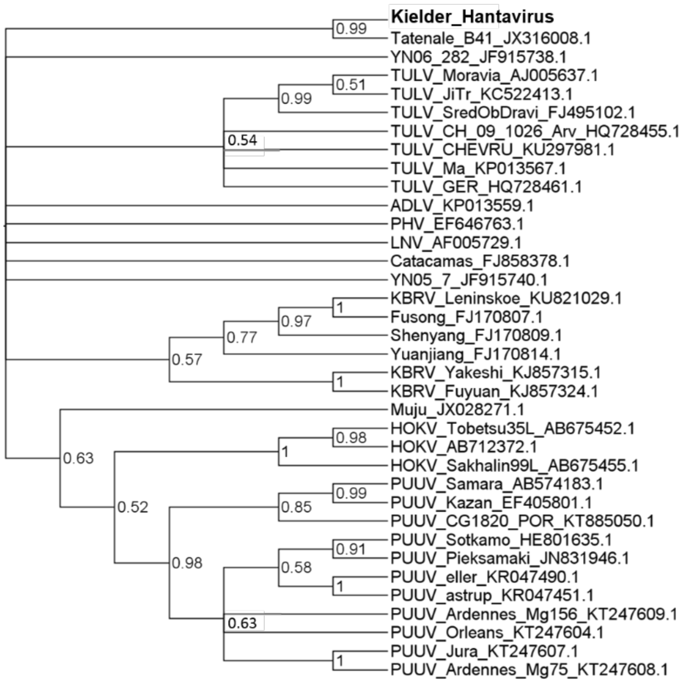
Technical Appendix Figure 2. Pairwise amino acid alignment of the L segment of the Kielder Forest hantavirus with that of the corresponding Tatenale virus. The Kielder Forest hantavirus 145>A variant (GenBank accession no. KY751731) and Tatenale virus (GenBank accession no. JX316008.1) nucleotide sequences were translated with MEGA7 (*11*) and aligned with EMBOSS needle (*12*). Alignment shows amino acid identity at 95.9% and similarity at 98.4%.



Technical Appendix Figure 3. A bootstrap consensus phylogenetic tree of the hantavirus genomic L segment constructed by using the maximum likelihood method based on the Tamura 3-parameter (G+I) model. Tree shows relationships among Tatenale virus-like lineages and other relevant lineages. Molecular analysis and model prediction were conducted using MEGA7 (*11*) with a bootstrap consensus inferred from 10,000 replicates. Node values represent the bootstrap values. Sequences are represented by the taxonomic names, strain (if >1 is included), and GenBank accession numbers. Kielder Hantavirus (in bold) represents the 145>A variant found in this study. ADLV, Adler virus; CATV, Catacamas virus; HOKV, Hokkaido virus; KBRV, Khabarovsk virus; LNV, Laguna Negra virus; PHV, Prospect Hill virus; PUUV, Puumala virus; TULV, Tula virus.

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