

This is an author produced version of a paper published in Epidemiology & Infection.

This paper has been peer-reviewed but may not include the final publisher proof-corrections or pagination.

Citation for the published paper:

O. Borg, M. Wille, P. Kjellander, U. A. Bergvall, P.-E. Lindgren, J. Chirico & Å. Lundkvist. (2017) Expansion of spatial and host range of Puumala virus in Sweden: an increasing threat for humans?. *Epidemiology & Infection*. Volume: 145, Number: 8, pp 1642–1648. http://dx.doi.org/10.1017/S0950268817000346.

Access to the published version may require journal subscription. Published with permission from: Cambridge University Press.

Standard set statement from the publisher:

This article has been published in a revised form in Epidemiology & Infection [http://doi.org/ 10.1017/S0950268817000346]. This version is free to view and download for private research and study only. Not for re-distribution, re-sale or use in derivative works.

Epsilon Open Archive http://epsilon.slu.se

1	Expansion of spatial and host range of Puumala virus in Sweden: an increasing threat
2	for humans?
3	
4	O. Borg ¹ , M. Wille ^{1,*} , P. Kjellander ² , U. A. Bergvall ^{2, 3} , PE. Lindgren ^{4,5} , J. Chirico ⁶ , Å.
5	Lundkvist ^{1,7,*}
6	
7	¹ Zoonosis Science Center, Department of Medical Biochemistry and Microbiology, Uppsala
8	University, Uppsala, Sweden

- 9 ² Grimsö Wildlife Research Station, Department of Ecology, Swedish University of
- 10 Agricultural Sciences, SLU, Riddarhyttan, Sweden
- ³ Department of Zoology, Stockholm University, Stockholm, Sweden
- ⁴ Medical Microbiology, Department of Clinical and Experimental Medicine, Linköping
- 13 University, Linköping, Sweden
- ⁵ Microbiological Laboratory, Medical Services, County Hospital Ryhov, Jönköping, Sweden
- ⁶ National Veterinary Institute, SVA, Uppsala, Sweden
- ⁷ Laboratory of Clinical Microbiology, Uppsala University Hospital, Uppsala, Sweden

- 18 * Co-corresponding author: Åke Lundkvist; Zoonosis Science Center, Department of Medical
- 19 Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden; Email:
- 20 Åke.Lundkvist@imbim.uu.se
- 21 *Co-corresponding author: Michelle Wille; Zoonosis Science Center, Department of Medical
- 22 Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden; Email:
- 23 Michelle.Wille@imbim.uu.se
- 24
- 25 Running Head: Puumala hantavirus in Sweden

26 Summary

27 Hantaviruses are globally distributed and cause severe human disease. Puumala hantavirus 28 (PUUV) is the most common species in Northern Europe, and the only hantavirus confirmed 29 to circulate in Sweden, restricted to the northern regions of the country. In this study, we 30 aimed to further add to the natural ecology of PUUV in Sweden by investigating prevalence, 31 and spatial and host species infection patterns. Specifically, we wanted to ascertain whether 32 PUUV was present in the natural reservoir, the bank vole (*Myodes glareolus*) further south 33 than Dalälven river, in south-central Sweden, and whether PUUV, in addition, can be 34 detected in other rodent species in addition to the natural reservoir. In total, 559 animals were 35 collected at Grimsö (59°43'N; 15°28'E), Sala (59°55'N; 16°36'E) and Bogesund (59°24'N; 36 18°14'E) in south central Sweden between May 2013 and November 2014. PUUV ELISA-37 reactive antibodies were found both in 2013 (22/295) and in 2014 (18/264), and 9 samples 38 were confirmed as PUUV-specific by focus reaction neutralization test. Most of the PUUV-39 specific samples were from the natural host, the bank vole, but also from other rodent hosts, 40 indicating viral spill-over. Finally, we showed that PUUV is present in more highly populated 41 central Sweden.

42

43 **Keywords**: Bank vole; *Bunyaviridae*; Disease emergence; Hantavirus; *Myodes glareolus*;

44 Puumala virus; Sweden; Zoonosis

45 Introduction

Hantaviruses are single-stranded, negative-sense RNA viruses belonging to the family 46 47 Bunyaviridae [1]. These constitute a widespread group of viruses, several are zoonotic agents 48 with great impact on public health [2]. Hantaviruses are the major causative agents of two 49 severe human diseases: hemorrhagic fever with renal syndrome (HFRS) and hantavirus 50 cardiopulmonary syndrome (HCPS) [3, 4]. Geographically, HFRS is mainly limited to 51 Eurasia while HCPS is restricted to the Americas. Approximately, 10 000 cases of human 52 HFRS are diagnosed annually in Europe [4, 5], about 150,000 to 200,000 cases throughout 53 the world, although there are likely thousands of cases that are never reported [6-8]. Further, 54 the number of HFRS cases are increasing, although the drivers of this phenomenon are 55 unclear. Factors may range from increased surveillance to climatic factors [9, 10], including a 56 shift in host distribution and behaviour as a result of climate change [5]. The clinical 57 manifestation differs between hantaviruses, where Puumala virus (PUUV) causes less severe 58 human diseases compared to other more pathogenic hantavirus species [11]. However, all 59 pathogenic hantavirus infections have a similar initial clinical presentation; mainly influenza-60 like illness, with symptoms including myalgia, malaise and high fever [12]. Virus 61 transmission to humans occurs through inhalation of virus-contaminated aerosol from rodent 62 excreta. Humans are most likely exposed to virus-contaminated aerosol through dust or 63 handling hay/timber that has been in close contact with the hosts. Furthermore, there is a 64 strong correlation between human infections and the number of infected rodents circulating 65 in the same area [13, 14]. Rodent-to-rodent transmission occurs through both indirect 66 (aerosol) and direct (contact) transmission [13-15]. 67 Hantaviruses constitute a large group of viruses with global distribution, reflecting the distribution of host reservoirs. There has been an increased focus on wild rodents as 68

69 reservoirs for hantaviruses in Europe due to recent detections of Seoul virus (SEOV) in wild

70 rats combined with severe SEOV-caused human HFRS cases. Specifically, SEOV has 71 recently been detected in England [16], France [17], and the Netherlands [18]. Furthermore, 72 SEOV was found in Swedish pet rats that originated from England [16]. Globally, more than 73 20 distinct species of hantaviruses have been described, and each virus species is spread by 74 one specific mammalian host as a result of of long term co-evolution [19-21]. This hypothesis 75 is supported by phylogenetic studies, whereby the genetic relationship between host and virus 76 diversification is mirrored [22-24]. Although rodents constitute the majority of hosts, 77 hantaviruses might have first appeared in *Chiroptera* (bats) or *Soricomorpha* (moles and 78 shrews), before emerging in rodent species [25]. 79 The natural reservoir host for PUUV, the most common hantavirus circulating in central and 80 northern Europe, is the bank vole Myodes glareolus. PUUV is currently the only hantavirus 81 known to circulate in Sweden, and is endemic in the northern parts of the country [13, 26]. 82 The current hypothesis is that PUUV is endemic only north of the river Dalälven, located 83 north of the most urbanised regions of Sweden [26, 27]. This is reflected by the lack of 84 human cases of south of the river Dalälven, however, recent sampling of rodents has 85 suggested this may no longer be correct [13, 28]. In this study, we aimed to further add to the 86 ecology of PUUV in Sweden by investigating prevalence, spatial, and host species infection 87 patterns. Specifically, we wanted to ascertain the prevalence and distribution of hantaviruses 88 in Swedish rodents south of the river Dalälven, and assess the host range of PUUV in rodent 89 species in addition to the natural reservoir in this region.

90

91 Materials and Methods

92 Sampling strategy and ethics statement

All trapping and sampling was carried out in accordance with Swedish and European law and
regulations provided by the Swedish Board of Agriculture. The capture and sampling

protocols were approved by an ethical permission from the Animal Experiments Ethical
Committee, Umeå, (Reference: A13-14). All trapping and sampling was conducted by trained
biologists.

98 Study sites and sample collection

99 Rodents were captured between May 2013 – November 2014 from three geographical 100 locations south of the river Dalälven: Sala (59°55'N, 16°36'E), Grimsö (59°43'N, 15°28'E), and Bogesund (59°24'N, 18°14'E) (Figure 1). These geographic locations represent three 101 102 different ecotypes. Both Sala and Grimsö are inland, however where Grimsö is more 103 forested, the area around Sala is mostly agricultural. Furthermore, at the time of sampling the 104 area around Sala had been heavily affected by a large fire, resulting in a disturbed landscape. 105 Bogesund is in close proximity to the Baltic Sea and has a more rocky terrain. Rodents were 106 captured using commercially available snap-traps. Following capture, carcasses were frozen 107 to \leq -20 °C within 2 hours of collection. In the laboratory, the rodents were defrosted and 108 were dissected. Partial spleen and heart tissues were collected and frozen in -80 °C until 109 required for analysis. Other tissues were collected from the rodents for a number of other 110 studies, and the carcasses were appropriately disposed following dissections.

111 Serological screening

112 Enzyme Linked Immunosorbant Assay

113 Tissues were subdivided into smaller pieces of approximately 25 g, and homogenized in PBS

114 (using a beater for 3 minutes in PBS). The homogenate was initially assayed using a

115 hantavirus IgG ELISA, based on baculovirus-expressed PUUV nucleocapsid protein antigen

- 116 [29], as previously described for use in sera [30]. This method has been validated and
- successfully used previously with organ homogenates [eg. 16, 18].

118 Focus reaction neutralization test

119 To confirm hantavirus-specificity, the ELISA positive samples were further evaluated by

120 focus reaction neutralisation test (FRNT), the gold standard for hantavirus serology [31].

121 Briefly, a new subsection of tissue was homogenised as described above, initially extracted in

122 PBS (1:25). The homogenate was further diluted (1:2) in 1x Hanks balanced serum solution

123 (Corning, New York, USA), mixed with diluted virus (PUUV strain Kazaan-E6) [31] and

added to confluent Vero E6 cell monolayers in six-well tissue culture plates. After 7 days, a

solution of monkey anti-PUUV polyclonal serum in 5% Fetal Calf Serum (Gibco,

126 ThermoFisher, Boston, USA) and wash buffer (0,15% Tween- 20 in PBS) was added and

127 incubated. Virus-infected cells were visualized by addition of peroxidase-labelled goat anti-

128 human IgG (BioRad Laboratories, Hercules, CA), followed by terminative 3, 3', 5, 5'-

129 tetramethylbenzidine substrate (Sigma, Stockholm, Sweden). The FRNT-positive samples

130 from 2014 were further titrated (1:50 to 1:800) to ascertain the minimal dilution of rodent

tissues to avoid non-specific inhibition. FRNT results are presented in percentages,

132 representing the percentage reduction of the number of foci. A dilution series of infected

133 Vero E6 cells were used as a positive control, and, 80% reduction of the number of foci was

134 selected as the cut-off for the virus neutralization titre.

135

136 **Results**

137 A total of 559 animals were screened for PUUV reactive antibodies across three locations,

south of the putative PUUV geographical boarder. Roughly similar numbers of organs were

screened in 2013 and 2014, however in 2013 all 295 samples were homogenates from

spleens, as compared to 187 hearts and 77 spleens in 2014. More than 50% of samples

141 collected were from bank vole (n= 342), and PUUV reactive antibody prevalence in bank

142 vole was 7.6% with no significant difference in prevalence between 2013 and 2014 (Fisher

143 Exact Test; X^2 =1.237, df=1, p=0.266). However, a number of other species were also positive 144 including pygmy shrew (Sorex minutus, 25%), common shrew (S. araneus, 3.1%), yellow-145 necked mouse (Apodemus flavicollis, 11.6%), wood mouse (A. sylvaticus; 16.7%) and a 146 neonate roe deer (*Capreolus capreolus*, 9%). While antibody prevalence appeared higher in 147 yellow-necked mouse and pygmy shrew as compared to bank vole, sample size for these 148 species was much smaller. Species tested but not positive included Eurasian water shrew 149 (Neomys fodiens), field vole (Microtus agrestis), wood lemming (Myopus schisticolor), and 150 three avian species. Different locations appeared to have different importance for different 151 species, however sampling bias did not allow for comparisons except for bank voles and 152 yellow-necked mouse. For bank vole, PUUV antibody prevalence was higher in Bogesund 153 (Fisher Exact Test; X^2 =8.787, df=1, p=0.003) and Grimsö (Fisher Exact Test; X^2 =4.26, df=1, 154 p=0.04) than Sala. In contrast, yellow-necked mice in Sala had a higher prevalence (18.2%) 155 than Bogesund (0.5%), however due to small sample sizes this is not significant (Fisher Exact 156 Test; X^2 =3.634, df=1, p=0.056) (Table 1). 157 Subsequently, all ELISA positives were assayed by FRNT to confirm hantavirus-specificity. 158 Diluting homogenates prior to FRNT analysis proved crucial; homogenates from 2014 were

160 sample type (antibodies extracted from rodent spleens and hearts). The dilution 1:50, used in

serially diluted and revealed that a minimal dilution for a reliable result was 1:100 for this

159

161 2013, was insufficient to avoid the possibility of non-specific inhibition, which would result

162 in false positive outcomes. Thus, FRNT confirmation from the 2013 samples is tentative,

163 however we infer that 5 of the 22 ELISA positives in 2013 reacted at 1:50 by FRNT dilution;

164 roe deer (n=1), common shrew (n=1) and bank voles (n=3). In 2014, 9 ELISA positives were

165 confirmed by FRNT, limited to bank voles from Bogesund (5/56 tested), a wood mouse in

166 Bogesund (1/2 tested) and yellow-necked mice in Sala (3/22 tested). Interestingly, one

167 yellow-necked mouse (Sample 134, 2014) had an end-point titre of >= 1:800 (Table 2)

168

169 **Discussion**

170 Emerging and re-emerging pathogens are among the greatest challenges of the twenty-first 171 century, and present a large economic burden to society. Further, most emerging and 172 remerging pathogens are zoonotic viruses; viruses with natural hosts in the animal reservoir 173 [32-34]. European studies indicate that hantaviruses are not only spreading to new areas [17, 174 18], but also to new hosts [35]. In this study, we aimed to assess the dynamics of hantaviruses 175 in Sweden, by assessing virus diversity and prevalence, spatial distribution, and host species 176 fidelity through antibodies. Spatially, the current working hypothesis is that PUUV in 177 Sweden is endemic north of the river Dalälven [26, 27], however both this study and Lõhmus 178 et al (2016) clearly demonstrated PUUV infections in bank voles south of this boarder. We 179 found positive rodents from Grimsö, Sala and Bogesund, captured in both 2013 and 2014, 180 however, different areas were more important for different species. Reactive antibody 181 prevalence was highest in Grimsö and Bogesund in bank vole; the Sala landscape, which is 182 mostly agricultural was devastated by a large fire during the sampling period of this study. 183 How this affects PUUV antibody prevalence is uncertain. In contrast, Sala was more 184 important for yellow-necked mouse. The role of habitat for disease risk is complex, but a 185 recent review suggests that there is a strong correlation between habitat and disease 186 prevalence. Specifically, factors such as forest cover, fires, fragmentation and barrow space 187 influence the dispersal of voles (and in this case mice), consequently affecting the 188 epidemiology of PUUV [4, 19, 36, 37]. The Bogesund site is particularly interesting as it is 189 the southern most location of both this study, where PUUV prevalence in bank voles was 190 high. At this southern location Lõhmus et al 2016 detected PUUV in a more southern 191 location, but in yellow-necked mice [28]. This range expansion of PUUV in wildlife 192 reservoirs has yet to result in numerous human causes. A similar trend is evident in France,

where PUUV has been detected in voles in populated regions with no human cases of HFRS,
however in this case it is suggested to be driven by specific animo acid differences in the
viruses [38]. Regardless, expansion of PUUV into areas with a higher human population is
concerning in context of public health.

197 Not only did we detect an expansion in the known PUUV geographic range, we also illustrate 198 an increase in host range following detection of PUUV reactive antibodies in a number of 199 permissive species. Yellow-necked mouse, wood mouse, common shrew and pygmy shrew 200 were found among the ELISA positive samples; in total 37% of ELISA reactive samples 201 were from species other than bank vole, indicating PUUV spill-over to other rodent and 202 shrew species, or the presence of to date unknown hantaviruses causing cross-reacting 203 antibodies detected by ELISA. Yellow-necked mouse has previously been shown to be a 204 permissive host for PUUV in Sweden [28], but we found ELISA reactive antibodies in most 205 species tested (given a large enough sample size), with the exception of field vole. While 206 rodents, specifically mice are plausible spill over hosts, detection of PUUV reactive 207 antibodied from a roe deer is unusual. The actual hantavirus species infecting Swedish 208 shrews awaits further investigations. Given the numerous shrew-carried hantaviruses 209 discovered during the last decade [6, 8], it is likely that one or several of these species are 210 circulating also in Sweden, although also PUUV spill-over events can not be excluded at this 211 stage. Given the deviation from known hantavirus host range, a more in depth analysis of 212 shrews and ungulates ranging from sampling to virus sequencing is warranted. Indeed, Ahlm 213 et al. (2000), described hantavirus-infected moose from northern Sweden [39], thus ungulates 214 appear permissive to PUUV infection, but whether they are dead-end hosts or not is 215 unknown. Hantaviruses are considered to be host-specific [21], however, this study revealed 216 unexpected spill-over to a spectrum of different rodents, corroborating the hypothesis that 217 PUUV epidemiology may be more complex [30, 40, 41].

218 Based upon our results, and emerging evidence [30, 40, 41], strict host fidelity in this system 219 seems unlikely. The role that these spill-over hosts play in the epidemiology is, however 220 unclear; they are indeed permissive to infection, and given the detection levels in this study, 221 these spill over events are not rare. In order to reveal the role of putative spill over hosts play 222 in the epidemiology of PUUV we need to ascertain whether they are dead-end hosts, spill 223 over hosts, or are able to transmit infection. Regardless, it is likely that PUUV potentially has 224 lower fitness in species other than bank voles, which may in turn limit frequency of 225 infections. This potentially expanded model of PUUV (and hantavirus) epidemiology has 226 large implications for the mitigation of human hantavirus-derived disease cases, as more 227 hosts increase the risk for human transmission. This is further compounded with range 228 expansion into more populated regions of Sweden. If these phenomena result in endemicity 229 in new hosts or geographic regions, the health burden caused by hantaviruses will certainly 230 increase.

231 Conclusions

232 Studies such as these are imperative in ascertaining PUUV prevalence in wildlife hosts to 233 better inform risk areas for human infections. Given an expansion of PUUV range in the 234 wildlife host, surveillance in humans is prudent. Hantavirus is an emerging virus in Sweden, 235 with detections of antibodies against PUUV in both the reservoir and other small mammals 236 farther south than previously described. Specifically, PUUV is now detected in more densely 237 populated, as described here, in close proximity to large cities such as Uppsala and 238 Stockholm. Moreover, rodents such as yellow-necked mouse utilize anthropogenic buildings 239 ten times more frequently than bank voles [28]. These two factors rapidly decrease distance, 240 and thus increase interactions, between humans and the wildlife reservoir. This may have 241 large implications, as it increases the probability of human contact with infected rodent

excreta, creating a large reservoir for potential hantavirus infections in humans.

243 Acknowledgements

- 244 We would like to acknowledge Madeleine Christensson organizing all fieldwork and
- 245 personnel collecting various mammals used in this study. Additionally, Torsten Berg and
- 246 Jonas Nordström for important contribution to fieldwork.

247 Financial Support

- 248 This study was partially funded by EU grant FP7-261504 EDENext and is cataloged by the
- EDENext Steering Committee as (<u>http://www.edenext.eu</u>). This work was supported by the
- 250 Swedish Environmental Protection Agency project (PK), the Swedish hunters organization
- 251 (PK) and the foundation Marie-Claire Cronstedt stiftelse (PK) and by EU Interreg -
- 252 ScandTick Innovation (PK, PEL). The funding sources had no role in study design,
- 253 collection, analysis, interpretation of data, writing of the report, or in the decision to submit
- the paper for publication.

255 Conflict of interest

256 The authors declare no conflict of interest

257 Ethical standards

- 258 The authors assert that all procedures contributing to this work comply with the ethical
- standards of the relevant national and institutional committees on human experimentation and
- with the Helsinki Declaration of 1975, as revised in 2008. The authors assert that all
- 261 procedures contributing to this work comply with the ethical standards of the relevant
- and institutional guides on the care and use of laboratory animals.

263 **References**

- 264 (1) Plyusnin A, et al. Family Bunyaviridae. In: King AMQ, et al., eds. Virus Taxonomy-
- 265 Ninth Report of the International Committee on Taxonomy of Viruses. London, UK:
- Elsevier/Academic Press, 2011: pp. 725-741.
- 267 (2) Kahlon S. Viral Hemorrahagic Fever: Bunyaviridae. *Current Treatment Options in*
- 268 Infectious Diseases 2015; **7**(3): 240-247.
- 269 (3) Lee HW, van der Groen G. Hemorrhagic fever with renal syndrome. *Progress in*270 *Medical Virology* 1989; 36: 62-102.
- 271 (4) Jonsson CB, Figueiredo LT, Vapalahti O. A global perspective on hantavirus
- ecology, epidemiology, and disease. *Clinical Microbiology Reviews* 2010; 23: 412-441.
- 273 (5) Heyman P, et al. Hemorrhagic fever with renal syndrome. In: *Viral Hemorrhagic*
- 274 *Fevers*: CDC Press, 2014: pp. 415–425.
- 275 (6) **Kruger DH, et al.** Hantaviruses--globally emerging pathogens. *Journal of Clinical*
- 276 *Virology* 2015; **64**: 128-136.
- 277 (7) Avsic-Zupanc T, Saksida A, Korva M. Hantavirus infections. *Clinical Microbiology* 278 and Infection 2015.
- 279 (8) Vaheri A, et al. Hantavirus infections in Europe and their impact on public health.
- 280 *Reviews in Medical Virology* 2013; **23**(1): 35-49.
- 281 (9) Heyman P, Vaheri A, Members E. Situation of hantavirus infections and
- haemorrhagic fever with renal syndrome in European countries as of December 2006.
- *Eurosurveillance* 2008; **13**.
- 284 (10) Schwarz AC, et al. Risk factors for human infection with Puumala virus,
- southwestern Germany. *Emerging Infectious Diseases* 2009; **15**: 1032-1039.
- 286 (11) **Bi Z, Formenty PB, Roth CE.** Hantavirus infection: a review and global update.
- 287 Journal of Infection in Developing Countries 2008; 2: 3-23.

- 288 (12) Vaheri A, et al. Uncovering the mysteries of hantavirus infections. *Nature Reviews*
- 289 *Microbiology* 2013; **11**: 539-550.
- 290 (13) Olsson GE, et al. Predicting high risk for human hantavirus infections, Sweden.
- *Emerging Infectious Diseases* 2009; **15**: 104-106.
- 292 (14) **Pettersson L**, Transmission and pathogenesis of hantavirus. Umeå University
- 293 Dissertation Series. ISBN: 978-91-7601-225-3; 2015.
- 294 (15) Voutilainen L, et al. Life-long shedding of Puumala hantavirus in wild bank voles
- 295 (Myodes glareolus). *Journal of General Virology* 2015; **96**: 1238-1247.
- 296 (16) Lundkvist A, et al. Pet rat harbouring Seoul hantavirus in Sweden, June 2013.
- *Eurosurveillance* 2013; **18**.
- 298 (17) Heyman P, et al. Seoul hantavirus in Europe: first demonstration of the virus genome
- 299 in wild Rattus norvegicus captured in France. European Journal of Clinical Microbiology
- 300 *and Infectious Disease* 2004; **23**: 711-717.
- 301 (18) Verner-Carlsson J, et al. First evidence of Seoul hantavirus in the wild rat
- 302 population in the Netherlands. *Infection, Ecology and Epidemiology* 2015; **5**: 27215.
- 303 (19) Dearing MD, Dizney L. Ecology of hantavirus in a changing world. Annals of the
- 304 *New York Academy of Sciences* 2010; **1195**: 99-112.
- 305 (20) Henttonen H, et al. Recent discoveries of new hantaviruses widen their range and
- 306 question their origins. *Annals of the New York Academy of Sciences* 2008; **1149**: 84-89.
- 307 (21) Vapalahti O, et al. Hantavirus infections in Europe. *Lancet Infect Disease* 2003; 3:
 308 653-661.
- 309 (22) Morzunov SP, et al. Genetic analysis of the diversity and origin of hantaviruses in
- 310 Peromyscus leucopus mice in North America. Journal of Virology 1998; 72: 57-64.
- 311 (23) Plyusnin A, Morzunov SP. Virus evolution and genetic diversity of hantaviruses and
- their rodent hosts. *Current Topics in Microbiology and Immunology* 2001; **256**: 47-75.

- 313 (24) **Plyusnin A, Sironen T.** Evolution of hantaviruses: Co-speciation with reservoir hosts
- 314 for more than 100 MYR. *Virus Research* 2014; **187**: 22-26.
- 315 (25) Zhang YZ. Discovery of hantaviruses in bats and insectivores and the evolution of
- the genus Hantavirus. *Virus Research* 2014; **187**: 15-21.
- 317 (26) Olsson GE, et al. Human hantavirus infections, Sweden. *Emerging Infectious*
- 318 *Diseases* 2003; **9**: 1395-1401.
- 319 (27) Olsson GE, Leirs H, Henttonen H. Hantaviruses and Their Hosts in Europe:
- 320 Reservoirs Here and There, But Not Everywhere? *Vector-Borne Zoonotic Disease* 2010;
- **10**(6): 549-561.
- 322 (28) Lohmus M, et al. Hantavirus in new geographic regions, Sweden. *Infection, Ecology*323 and Epidemiology 2016; 6: 31465.
- 324 (29) Vapalahti O, et al. Antigenic properties and diagnostic potential of puumala virus
 325 nucleocapsid protein expressed in insect cells. *Journal of Clinical Microbiology* 1996; 34:
 326 119-125.
- 327 (30) Sjolander KB, et al. Evaluation of serological methods for diagnosis of Puumala
 328 hantavirus infection (nephropathia epidemica). *Journal of Clinical Microbiology* 1997; 35:
 329 3264-3268.
- 330 (31) Lundkvist A, et al. Puumala and Dobrava viruses cause hemorrhagic fever with renal
 331 syndrome in Bosnia-Herzegovina: evidence of highly cross-neutralizing antibody responses
 332 in early patient sera. *Journal of Medical Virology* 1997; 53: 51-59.
- 333 (32) Jones KE, et al. Global trends in emerging infectious diseases. *Nature* 2008; 451:
 334 990-993.
- 335 (33) Woolhouse ME. Population biology of emerging and re-emerging pathogens. *Trends*336 *in Microbiology* 2002; 10: S3-7.

- 337 (34) Woolhouse ME, Gowtage-Sequeria S. Host range and emerging and reemerging
- pathogens. *Emerging Infectious Diseases* 2005; **11**: 1842-1847.

339 (35) Eckerle I, Lenk M, Ulrich RG. More novel hantaviruses and diversifying reservoir

- hosts--time for development of reservoir-derived cell culture models? Viruses 2014; 6: 951-
- 341 967.
- 342 (36) Khalil H, et al. Dynamics and Drivers of Hantavirus Prevalence in Rodent
- 343 Populations. *Vector-Borne Zoonotic Disease* 2014; **14**(8): 537-551.
- 344 (37) Salvador AR, et al. Concomitant influence of helminth infection and landscape on
- 345 the distribution of Puumala hantavirus in its reservoir, Myodes glareolus. BMC Microbiology
- **346** 2011; **11**.
- 347 (38) Castel G, et al. Complete Genome and Phylogeny of Puumala Hantavirus Isolates
- 348 Circulating in France. *Viruses* 2015; **7**(10): 5476-5488.
- 349 (39) Ahlm C, et al. Serologic evidence of Puumala virus infection in wild moose in
- ason northern Sweden. American Journal of Tropical Medicine and Hygiene 2000; 62: 106-111.
- 351 (40) Klingstrom J, et al. Rodent host specificity of European hantaviruses: evidence of
- 352 Puumala virus interspecific spillover. *Journal of Medical Virology* 2002; **68**: 581-588.
- 353 (41) Schmidt-Chanasit J, et al. Extensive host sharing of central European Tula virus.
- 354 *Journal of Virology* 2010; **84**: 459-474.
- 355

356 Table Legends

357 Table 1: ELISA prevalence and number of samples collected from locations south of the river

358 Dalälven in 2013-2014 in Sweden.

Species	Prevalence (# ELISA positive/# samples collecte					
	Ye	ar		Total		
		-				
	2013	2014	d	Grimsö	Sala	
				8.1%		7.6%
Bank vole (Myodes	9.3%	6.1%	13.4%	(13/160	2.0%	(26/342)
glareolus	(15/162)	(11/180)	(11/82))	(2/100)	
				< 0.001		<0.001%
Field vole (Microtus	<0.001%	< 0.001%	< 0.001%	%	< 0.001	(0/26)
agrestis)	(0/17)	(0/9)	(0/1)	(0/19)	% (0/6)	
Common shrew (Sorex	3.4%	< 0.001%	< 0.001%	3.4%	< 0.001	3.1%
araneus)	(3/89)	(0/7)	(0/3)	(3/89)	% (0/4)	(3/96)
Eurasian Pygmy shrew				25%		25%
(Sorex minutus)	25% (2/8)	NT	NT	(2/8)	NT	(2/8)
Eurasian Water shrew	<0.001%			< 0.001		< 0.001%
(Neomys fodiens)	(0/1)	NT	NT	% (0/1)	NT	(0/1)
Wood lemming		<0.001%		< 0.001		< 0.001%
(Myopus schisticolor)	NT	(0/1)	NT	% (0/1)	NT	(0/1)
Wood mouse		16.7%	50%		12.5%	16.7%
(Apodemus sylvaticus)	NT	(3/18)	(1/2)	NT	(2/16)	(3/18)
Yellow-necked mouse	25%%	10.2%	0.5%	< 0.001	18.2%	11.6%
(Apodemus flavicollis)	(1/4)	(4/39)	(1/20)	% (0/1)	(4/22)	(5/43)
Unknown mouse		< 0.001%	< 0.001%		< 0.001	< 0.001%
species	NT	(0/8)	(0/7)	NT	% (0/1)	(0/8)
Roe deer (Capreolus			12.5%	< 0.001		9%
capreolus)	9% (1/11)	NT	(1/8)	% (0/3)	NT	(1/11)
	< 0.001%	< 0.001%		< 0.001	< 0.001	< 0.001%
Great tit (Parus major)	(0/1)	(0/2)	NT	% (0/1)	% (0/2)	(0/3)
Eurasian nuthatch	< 0.001%					< 0.001%
(Sitta europaea)	(0/1)	NT	NT	NT	NT	(0/1)
European robin	< 0.001%			< 0.001		< 0.001%
(Erithacus rubecula)	(0/1)	NT	NT	% (0/1)	NT	(0/1)
Total	295	264	123	285	151	559

359

361 Table 2: FRNT neutralization of ELISA positive samples from small mammals collected in

362 2014.

Samp le ID	Year	Organ	Area	Species	FRNT ^{a,b}				
					Interp retatio n	(1:50)	(1:100)	(1:200)	(1:800)
2	2014	Heart	Bogesund	Bank vole	POS	3%	1,70%	10%	53%
11	2014	Heart	Bogesund	Bank vole	POS	8%	0%	17.5%	92,50%
22	2014	Heart	Bogesund	Bank vole	POS	5%	1,70%	18%	56,70%
28	2014	Heart	Bogesund	Bank vole	POS	1,70%	3%	25%	51,70%
40	2014	Heart	Bogesund	Bank vole	NEG	10%	32%	85%	110%
43	2014	Heart	Bogesund	Bank vole	NEG	5%	30%	52,50%	70%
47	2014	Heart	Bogesund	Wood mouse	POS	0%	1,70%	6,70%	45%
51	2014	Heart	Bogesund	Bank vole	POS	8%	20%	77,50%	117,50%
72	2014	Heart	Sala	Yellow- necked mouse	NEG	10%	30%	47,50%	135%
129	2014	Heart	Sala	Bank vole	NEG	8%	35%	67,50%	110%
130	2014	Heart	Sala	Wood mouse	NEG	10%	62,50%	112,50%	137,50%
132	2014	Heart	Sala	Wood mouse Yellow-	NEG	31%	\mathbf{NT}^{c}	NT	NT
134	2014	Heart	Sala	necked	POS	11,70%	12,50%	2,50%	15%
135	2014	Heart	Sala	mouse Bank vole	NEG	13%	62.5%	52,50%	60%
142	2014	Spleen	Sala	Yellow- necked	POS	5%	5%	25%	90%
145	2014	Spleen	Sala	mouse Yellow- necked mouse	POS	10%	10%	22,50%	55%
249	2014	Heart	Grimsö	Bank vole	NEG	5%	50%	75%	90%
252	2014	Spleen	Bogesund	Bank vole	NEG	48%	52.5%	80%	90%

363

a. FRNT result at 1:100 dilution of less than 20% indicates a positive result

b. Percentage of foci as compared to virus control

365 c. Not tested

367 Figure Legend

- 368 Figure1: Locations from which small mammals were collected in this study. Sample sites are
- indicated in black. Stockholm, the largest city in Sweden, and Uppsala, Sweden's fifth largest
- 370 city are indicated with a grey marker have been included for reference. The river Dalälven,
- the assumed Swedish PUUV border, is indicated.