on HEV pathogenesis in rabbits are in part controversial, occurrence of HEV in apparently healthy laboratory rabbits suggests that rabbits frequently survive HEV infection (10). Whether the apparently low seroprevalence in hares compared with rabbits is thus due to infrequent infection, differential antibody responses, or other host- or virus-associated factors remains to determined.

We detected no statistically significant differences in seroprevalence rates, either between sexes (χ^2 0.01; p = 0.92) or across the 8 sampling years (Yates χ^2 0.6; p = 0.96) and the 5 individual sampling regions (Yates χ^2 1.945; p = 0.96). These findings suggested constant low levels of HEV transmission in hares irrespective of sex and geographic region.

The infection of hares with HEV strains that are closely related to raHEV strains suggests that hares may act as sporadic sources of zoonotic HEV infections. Although the low RNA detection rate and seroprevalence speak against a prominent role of hares in the epidemiology of zoonotic HEV, hunters and persons handling hare-derived products could represent risk groups. Awareness about hare-derived HEV infections may be particularly relevant for immunocompromised persons, in whom chronic HEV infections are most common.

About the Author

Dr. Corman is a physician and virologist at the Institute of Virology, Charité-Universitätsmedizin Berlin. His current research is dedicated to characterization of novel human and zoonotic viruses and development of diagnostic tools.

References

1. Aggarwal R. The global prevalence of hepatitis E virus infection and susceptibility: a systematic review. Geneva: World Health Organization; 2010.
2. Abravanel F, Lhomme S, El Costa H, Schvartz B, Peron JM, Kamar N, et al. Rabbit hepatitis E virus infections in humans, France. Emerg Infect Dis. 2017;23:1191–3. http://dx.doi.org/10.3201/eid2307.170318
3. Izopet J, Dubois M, Bertagnoli S, Lhomme S, Marchandeau S, Boucher S, et al. Hepatitis E virus strains in rabbits and evidence of a closely related strain in humans, France. Emerg Infect Dis. 2012;18:1274–81. http://dx.doi.org/10.3201/eid1808.120057
4. Chapman JA, Flux JEC; International Union for Conservation of Nature and Natural Resources. Lagomorph Specialist Group. Rabbits, hares, and pikas: status survey and conservation action plan. Gland (Switzerland): International Union for Conservation of Nature and Natural Resources; 1990.
5. Hammerschmidt F, Schwaiger K, Dähnert L, Vina-Rodriguez A, Höper D, Gareis M, et al. Hepatitis E virus in wild rabbits and European brown hares in Germany. Zoonoses Public Health. 2017;64:612–22. http://dx.doi.org/10.1111/zph.12355
6. Hewitt PE, Ijaz S, Brailsford SR, Brett R, Dicks S, Haywood B, et al. Hepatitis E virus in blood components: a prevalence and transmission study in southeast England. Lancet. 2014;384: 1766–73. http://dx.doi.org/10.1016/S0140-6736(14)61034-5
7. Smith DB, Simmonds P, Izopet J, Oliveira-Filho EF, Ulrich RG, Johne R, et al. Proposed reference sequences for hepatitis E virus subtypes. J Gen Virol. 2016;97:537–42. http://dx.doi.org/10.1099/jgv.0.000393
8. Krumbholz A, Joel S, Neubert A, Dremsek P, Dürrwald R, Johne R, et al. Age-related and regional differences in the prevalence of hepatitis E virus-specific antibodies in pigs in Germany. Vet Microbiol. 2013;167:394–402. http://dx.doi.org/10.1016/j.vetmic.2013.10.001
9. Faber MS, Wenzel JJ, Jilg W, Thamm M, Höhle M, Stark K. Hepatitis E virus seroprevalence among adults, Germany. Emerg Infect Dis. 2012;18:1654–7. http://dx.doi.org/10.3201/eid1810.111756
10. Han SH, Park BJ, Ahn HS, Kim YH, Go HJ, Kim DH, et al. Evidence of hepatitis E virus infection in specific pathogen-free rabbits in Korea. Virus Genes. 2018;54:587–90. http://dx.doi.org/10.1007/s11262-018-1562-3

Sarcoptic Mange of Fox Origin in Multiple Farm Animals and Scabies in Humans, Switzerland, 2018

Simone R.R. Pisano, Marie-Pierre Ryser-Degiorgis, Luca Rossi, Andrea Peano, Karin Keckeis, Petra Roosje

Author affiliations: University of Bern, Bern, Switzerland (S.R.R. Pisano, M.-P. Ryser-Degiorgis, P. Roosje); University of Turin, Grugliasco, Italy (L. Rossi, A. Peano); consulting veterinarian, Wabern, Switzerland (K. Keckeis)

Fox-derived *Sarcoptes scabiei* mites caused an outbreak of mange on a farm in Switzerland in 2018. Pruritic skin lesions suggestive of *S. scabiei* mite infestation developed in 4 humans who had direct contact with affected farm animals but not foxes. Sarcoptic mange is continuously spreading; such outbreaks affecting humans could start occurring more frequently.

The *Sarcoptes scabiei* mite is the causative agent of scabies in humans and sarcoptic mange in animals (*1*). Scabies is considered a neglected reemerging disease of public health concern (*2*). Sarcoptic mange causes distress in livestock, economic loss in the livestock industry, and disease and death in wildlife (*3*). The degrees of host specificity and cross-infectivity of *S. scabiei* mites are still debated (*3*).

In January 2018, sarcoptic mange was suspected on a farm in the Jura Mountains, Switzerland. The outdoor loose housing system of this farm hosting 2 oxen (*Bos taurus*), 2 horses (*Equus caballus*), 5 goats (*Capra hircus*), 4 alpacas (*Vicugna pacos*), 8 fallow deer (*Dama dama*), and 15 sheep (*Ovis aries*) was separated from a stable housing 3 pigs (*Sus scrofa domesticus*). Six dogs (*Canis lupus familiaris*) and 17 cats (*Felis catus*) had access to all stables. Pruritic skin lesions developed in several species 2–3 weeks after repeated episodes of mangy red foxes (*Vulpes vulpes*) sleeping in the stables and making partial body contact with the livestock (Figure, panels A, B). Pruritic skin lesions also developed in 4 persons who had direct contact with the domestic animals but not the foxes. A fox with mange was found dead nearby and a necropsy was performed. Oxen, dogs, and pigs were treated with avermectins before diagnostic investigations were carried out.

Clinical examination revealed papules, erythema, excoriations, hyperkeratosis, and hypotrichosis with variable severity in 2 pigs, 2 goats, 2 dogs, all horses, and all oxen (Figure, panels C, D). The 3 sheep and 1 cat examined did not have lesions suggestive of mange. Close examination of the fallow deer and alpacas was impracticable. Humans had pruritic erythematous papules and excoriations on their neck, legs, or arms (Figure, panel E). Health authorities temporarily prohibited 1 affected person (a teenager) from attending school because of suspected scabies. Pruritus and skin lesions disappeared in the affected animals and humans within 6 weeks after ≥2 treatments with avermectins, topical neem oil, or both.

We identified *S. scabiei* mites by light microscopy in the skin scrapings from 2 pigs, 1 horse, 1 ox, 1 goat, and 1 fox but none of the scrapings from 3 sheep, 5 dogs, and 1 cat sampled. A few mites but no eggs, eggshells, or gravid females were observed on livestock, whereas all stages were present and numerous on the fox. Skin scrapings were not obtained from the affected humans. We confirmed *S. scabiei* mite mitochondrial 16S rDNA by TaqMan real-time PCR (*4*) in the sampled horse, ox, goat, and fox but not in the sampled sheep, cat, dogs, or pigs. Analyses with a panel of 9 microsatellites (sarms 33, 35–38, 40, 41, 44, and 45) (*5*) confirmed that foxes were the source of the mites (Figure, panel F); the mites on the outbreak farm were similar to each other and to mites previously collected from foxes in Switzerland (*6*) but different from those collected from wild ungulates in Spain, Switzerland, France, and Italy (*5,7,8*).

Genetic investigations suggest that multiple *S. scabiei* mite subpopulations can infect the same host and that mite subpopulations can differ from host to host. Different subpopulations undergo varying degrees of gene flow depending on the geographic distances among infested hosts and cluster in animals that share a taxonomic classification above the species level (*1,9*). In Europe, wildlife herbivore-, carnivore- and omnivore-derived *S. scabiei* mites have been described as distinct groups, and intraspecies and interspecies transmission have been proposed to occur among hosts of the same taxon but not among different taxa under natural conditions (*8*). However, prey-to-predator transmission was demonstrated in Africa (*10*). Thus, direct contact between affected hosts or fomites and susceptible hosts (*1*) rather than mite host specificity might determine whether *S. scabiei* mites are transmitted to different taxonomic groups.

Our investigation unambiguously identified wild carnivore–derived *S. scabiei* mites as the cause of a point-like outbreak involving different domestic herbivores and omnivores. However, we found no evidence of mite reproduction, which suggests that the mites that transmitted from foxes to other species were not able to actively replicate. Yet, persistence of clinical signs despite treatment and suspected subsequent transmission from domestic animals to humans is not fully consistent with the self-limiting pattern described for zoonotic scabies, although reinfection of domestic animals by other foxes with mange could have occurred.

Increased fox abundance, reemergence, and continuous spread of sarcoptic mange in foxes could lead to its emergence in other wild and domestic animal species. Although mites or their DNA could not be demonstrated in the affected humans, their clinical signs were highly suggestive of scabies, highlighting the zoonotic potential of *S. scabiei* mites. The propensity of foxes with mange to live close to human settlements, the increase in green farming, and increased density and size of domestic animal populations augment the risk for contacts between foxes, domestic animals, and humans. Therefore, such outbreaks might become more frequent in the future.

About the Author

Mr. Pisano is a veterinary resident in the Wildlife Population Health specialty of the European College of Zoological Medicine at the Centre for Fish and Wildlife Health, University of Bern, Bern, Switzerland. He has a special interest in infectious diseases in free-ranging wildlife and researches various aspects of sarcoptic mange in Swiss wildlife.
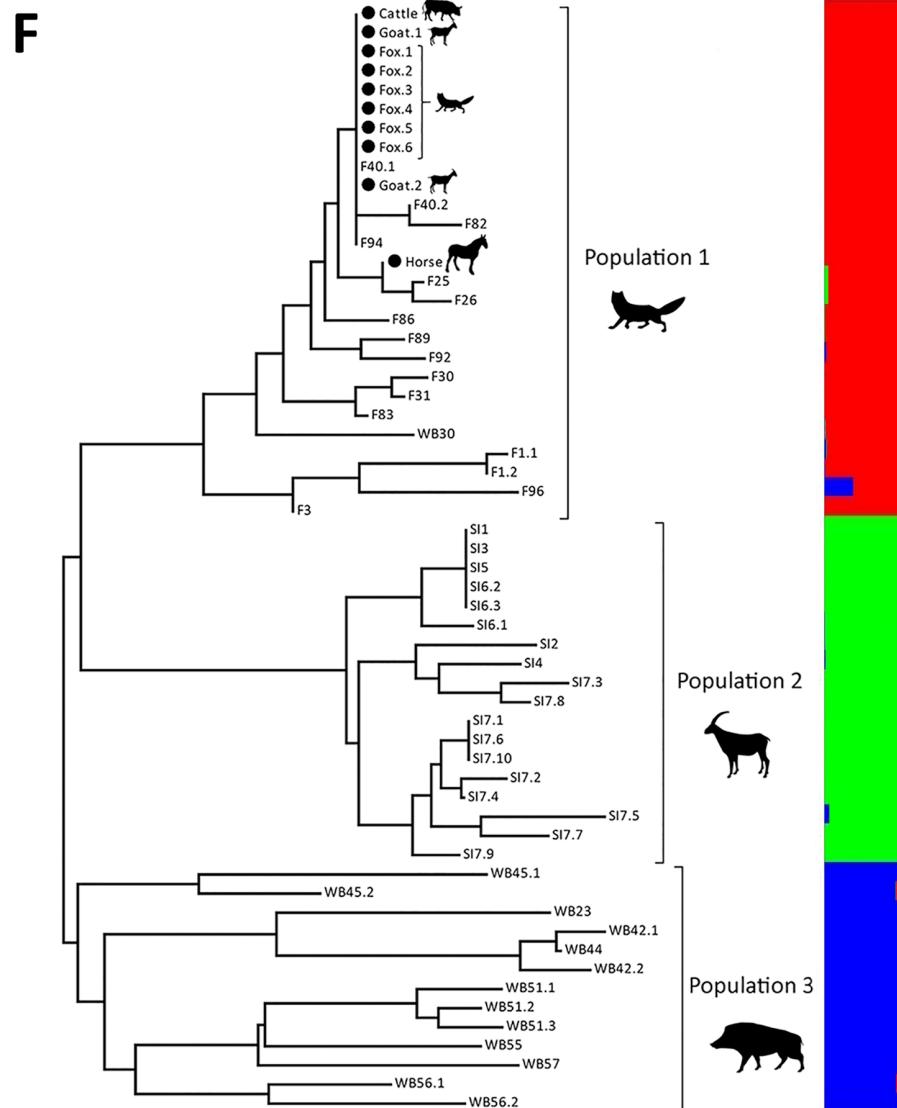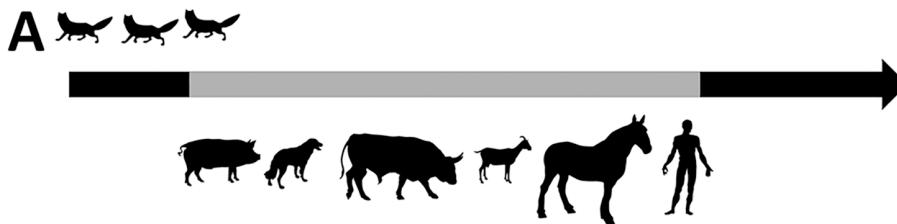
Figure. Clinical and molecular characterization of an outbreak of fox-derived *Sarcoptes scabiei* mites in multiple mammal species on a farm in Switzerland, 2018. A) Outbreak timeline displaying animal species (pigs [*Sus scrofa domesticus*], oxen [*Bos taurus*], dogs [*Canis lupus familiaris*], goats [*Capra hircus*], horses [*Equus caballus*], and red foxes [*Vulpes vulpes*]) showing clinical signs compatible with sarcoptic mange and humans with signs of zoonotic scabies, in order of appearance. Gray portion of arrow indicates the period during which clinical signs were observed in domestic animals and humans. Foxes with mange were observed in stables up to 3 weeks before the beginning of clinical signs in livestock. B–E) Clinical signs observed in a red fox (B; lethargy, severe hyperkeratosis), a pig (C; erythematous papules on shoulder and thorax), an ox (D; alopecia and erythema in the perineal region), and a teenage girl (E; erythematous papules on an arm). F) Multilocus microsatellite analysis demonstrating the genetic relationship of 10 individual mites isolated from a horse, an ox, a goat, and a fox at the farm where the outbreak occurred (black dots) and 48 additional mites from red foxes from the same region of Switzerland (population 1); Iberian ibex (*Capra pyrenaica*) from southern Spain (population 2); and wild boars (*Sus scrofa*) from Switzerland, nearby areas of France, and northern Italy (population 3). Neighbor-joining tree (left) constructed by using distance matrices with Populations version 1.2.28 (http://bioinformatics.org/populations) and displayed by using MEGA4 (http://www.megasoftware.net). Tree branch lengths are proportional to the percent genetic distance. Bar plot (right) obtained with Structure 2.3.4 (https://web.stanford.edu/group/pritchardlab/structure.html) represents the cluster membership according to the analyses of 9 markers for K = 3 with the probability (0%–100%) for each mite to belong to a different population. Medium gray indicates population 1, light gray indicates population 2, and dark gray indicates population 3. The 3 populations are the same as those in the distance tree. F, red fox; SI, Iberian ibex; WB, wild boar.

References

1. Arlian LG, Morgan MS. A review of *Sarcoptes scabiei*: past, present and future. Parasit Vectors. 2017;10:297. http://dx.doi.org/10.1186/s13071-017-2234-1
2. Karimkhani C, Colombara DV, Drucker AM, Norton SA, Hay R, Engelman D, et al. The global burden of scabies: a cross-sectional analysis from the Global Burden of Disease Study 2015. Lancet Infect Dis. 2017;17:1247–54. http://dx.doi.org/10.1016/S1473-3099(17)30483-8
3. Fraser TA, Charleston M, Martin A, Polkinghorne A, Carver S. The emergence of sarcoptic mange in Australian wildlife: an unresolved debate. Parasit Vectors. 2016;9:316. http://dx.doi.org/10.1186/s13071-016-1578-2
4. Angelone-Alasaad S, Molinar Min A, Pasquetti M, Alagaili AN, D'Amelio S, Berrilli F, et al. Universal conventional and real-time PCR diagnosis tools for *Sarcoptes scabiei* [published erratum in Parasit Vectors. 2015;8:622]. Parasit Vectors. 2015;8:587. http://dx.doi.org/10.1186/s13071-015-1204-8
5. Alasaad S, Oleaga Á, Casais R, Rossi L, Min AM, Soriguer RC, et al. Temporal stability in the genetic structure of *Sarcoptes scabiei* under the host-taxon law: empirical evidences from wildlife-derived *Sarcoptes* mite in Asturias, Spain. Parasit Vectors. 2011;4:151. http://dx.doi.org/10.1186/1756-3305-4-151
6. Nimmervoll H, Hoby S, Robert N, Lommano E, Welle M, Ryser-Degiorgis M-P. Pathology of sarcoptic mange in red foxes (*Vulpes vulpes*): macroscopic and histologic characterization of three disease stages. J Wildl Dis. 2013;49:91–102. http://dx.doi.org/10.7589/2010-11-316
7. Haas C, Origgi FC, Rossi S, López-Olvera JR, Rossi L, Castillo-Contreras R, et al. Serological survey in wild boar (*Sus scrofa*) in Switzerland and other European countries: *Sarcoptes scabiei* may be more widely distributed than previously thought. BMC Vet Res. 2018;14:117. http://dx.doi.org/10.1186/s12917-018-1430-3
8. Rasero R, Rossi L, Soglia D, Maione S, Sacchi P, Rambozzi L, et al. Host taxon-derived *Sarcoptes* mite in European wild animals revealed by microsatellite markers. Biol Conserv. 2010;143:1269–77. http://dx.doi.org/10.1016/j.biocon.2010.03.001
9. Andriantsoanirina V, Ariey F, Izri A, Bernigaud C, Fang F, Charrel R, et al. *Sarcoptes scabiei* mites in humans are distributed into three genetically distinct clades. Clin Microbiol Infect. 2015;21:1107–14. http://dx.doi.org/10.1016/j.cmi.2015.08.002
10. Gakuya F, Rossi L, Ombui J, Maingi N, Muchemi G, Ogara W, et al. The curse of the prey: *Sarcoptes* mite molecular analysis reveals potential prey-to-predator parasitic infestation in wild animals from Masai Mara, Kenya. Parasit Vectors. 2011;4:193. http://dx.doi.org/10.1186/1756-3305-4-193

Address for correspondence: Petra Roosje, Department of Clinical Veterinary Medicine, Division of Clinical Dermatology, Vetsuisse Faculty, University of Bern, Laenggassstrasse 128, PO Box 8466, 3001 Bern, Switzerland; email: petra.roosje@vetsuisse.unibe.ch

Suboptimal Handling of Piccolo Samples or Reagent Discs for Consideration in Ebola Response

Jessica R. Spengler, Stephen R. Welch, Sarah C. Genzer, JoAnn Coleman-McCray, Jessica R. Harmon, Stuart T. Nichol, Christina F. Spiropoulou

Author affiliation: Centers for Disease Control and Prevention, Atlanta, Georgia, USA

Operating clinical analyzers within recommended parameters can be challenging during outbreak response. Using the Piccolo Xpress point-of-care blood chemistry analyzer on guinea pig blood, we found that values of many analytes are still readily comparable when samples and reagent discs are handled at various conditions outside of manufacturers recommendations.

Blood chemistry analyses are useful for guiding patient care. However, following manufacturer-recommended handling and storage conditions can be challenging in areas with underdeveloped infrastructure, as experienced in past and ongoing Ebola outbreak response (*1*). To investigate the utility of data from samples or reagent discs handled under suboptimal conditions, we evaluated 14 conditions outside of manufacturers recommendations by using Strain 13/N guinea pig blood and plasma samples. Animal procedures were approved by the Centers for Disease Control and Prevention Institutional Animal Care and Use Committee and conducted at an AAALAC-International–accredited facility.

Samples were run on the Abaxis Piccolo Xpress Chemistry Analyzer (https://www.abaxis.com; quality control with Abbot General Chemistry controls and verification sample, https://www.fishersci.com/shop/products/piclpd-pls-gen-chm-ct-2x6x1ml/07p0401a). This platform is a compact and portable Clinical Laboratory Improvement Amendments–approved automated point-of-care system for whole blood, serum, and plasma (*2*). This platform, together with the General Chemistry 13 reagent disc used here, is widely used in past and ongoing Ebola outbreak responses (*3–6*) and in laboratory research on viral pathogenesis, therapeutics, and vaccine efficacy (*7–9*). All samples were collected in the recommended lithium heparin (LiH) tubes, except as indicated.

We determined intrinsic variation of each analyte under recommended conditions by running 31 samples on 2