The 2 patients from Slovakia lived in the Czech Republic for 5 (*5*) and 14 years, respectively, before the diagnosis of AE. Considering the long incubation period of the disease, these patients were likely infected in Slovakia, where occurrence of AE is also reported (*1*).

In summary, we report 20 cases of human AE in the Czech Republic during 1998–2014. However, because asymptomatic patients with only mild liver involvement are unlikely to seek clinical investigation, the actual number of patients in the Czech Republic who have AE is expected to be even higher than that reported here.

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L.K. conceived and wrote the paper. J.M., J.H., H.K., L.H., V.Z., H.A., and F.S. participated in the design of the analysis, commented on the first draft of the paper, and approved the final version.

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Address for correspondence: Libuše Kolářová, National Reference Laboratory for Tissue Helminthoses, Studničkova 7, CZ-128 00 Prague 2, Czech Republic; email: libuse.kolarova@lf1.cuni.cz

Use of Capture–Recapture to Estimate Underreporting of Ebola Virus Disease, Montserrado County, Liberia

Etienne Gignoux, Rachel Idowu, Luke Bawo, Lindis Hurum, Armand Sprecher, Mathieu Bastard, Klaudia Porten

Author affiliations: Epicentre, Paris, France (E. Gignoux, M. Bastard, K. Porten); Centers for Disease Control and Prevention, Atlanta, Georgia, USA (R. Idowu); Ministry of Health and Social Welfare, Monrovia, Liberia (L. Bawo); Médecins Sans Frontières, Brussels, Belgium (L. Hurum, A. Sprecher)

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To the Editor: Underreporting of cases during a large outbreak of disease is not without precedent (*1–5*). Health systems in West Africa were ill-prepared for the arrival of Ebola virus disease (Ebola) (*6*). The Ebola outbreak in Liberia was declared on March 31, 2014, and peaked in September 2014. However, by mid-June, the outbreak had reached Montserrado County, where the capital, Monrovia, is located. In response, the Liberia Ministry of Health and Social Welfare (MOHSW) created a National Ebola Hotline: upon receipt of a call, a MOHSW case investigation team was dispatched to the site of the possible case. Additionally, persons could seek care at an Ebola Treatment Unit (ETU) or be referred to an ETU by another health care facility. During June 1–August 14, 2014, MOHSW, Médecins Sans Frontières, and the US nongovernment organization Samaritan's Purse managed 3 ETUs in Montserrado County, including 2 in Monrovia operated by Eternal Love Winning Africa (ELWA).

In August 2014, to assess the extent of underreporting in the midst of the Ebola outbreak, we analyzed 2 sources of data collected during June 1–August 14. The first comprised data collected by MOHSW case investigation teams. These data were collected on MOHSW case forms and entered into a database emulating these forms using Epi Info version 7 software (Centers for Disease Control and Prevention, Atlanta, GA, USA). The second data source

(designed on Excel 2003; Microsoft, Redmond, WA, USA) comprised data on all patients admitted to the 2 ELWA ETUs (ELWA1 and ELWA2). We used a capture–recapture (CRC) approach.

CRC can evaluate the completeness of reporting and thereby be used to correct for underreporting (*7*). CRC methods use data from overlapping databases to estimate the number of unreported cases and thus more closely derive the true number of Ebola cases. Both databases were populated and managed separately, although the included Ebola cases are assumed to reflect the same patient population in Montserrado County. These 2 databases enabled us to use CRC to estimate the true number of Ebola cases in Montserrado County.

To be included in either database, a case must have been classified as suspected, probable, or confirmed Ebola. The case definitions, following the official MOHSW definition for Ebola, were identical in both databases. Eventually, after laboratory confirmation, cases could be reclassified as "not a case" and thus be excluded from the analysis.

To estimate the total number of Ebola cases during the study period, we used Chapman's 2-sample CRC population estimate (*7*); we calculated the 95% CI as proposed by Wittes et al. (*8*). We performed a sensitivity analysis measuring impact of error in matching cases during record linkage.

A total of 227 Ebola cases were recorded in the MOHSW database and 99 Ebola cases in the Montserrado County ETUs database (Table). Of these, 25 were found in both databases, 202 in the MOHSW database only, and 74 in the Montserrado County ETU database only. We estimated that the cumulative number of Ebola cases for Montserrado County during the study period was 876 (95% CI 608–1,143).

A sensitivity analysis performed with ±5 cases showed that, with 5 additional cases in common between databases, the cumulative number of cases would decrease to 734 (95% CI 537–931); with 5 additional discordant cases, the estimate would increase to 1,085 (95% CI 700–1,469). Our analysis shows that the number of cases in Montserrado Country was at least 3-fold higher than that reported during the study period.

Our study had several limitations. According to the doctor in charge of data collection up to August 4, some forms (<10) completed at the beginning of June 2014 might have been misplaced. Additionally, some patients who entered the ETU were not recorded in the registry book (<5). CRC assumes a closed population. In Montserrado County, persons can move freely. In both databases, we included only cases that occurred in or were reported in Montserrado County.

CRC assumes that links between the 2 sources based on identifying case information are error free. The sensitivity analysis suggested that even if up to 5 case matches were not detected, our conclusion was relatively robust.

CRC assumes homogeneity in the likelihood of being captured and recaptured and that data sources are independent. In our analysis, homogeneity is unlikely. For example, the MOHSW database was more likely to capture cases in persons more likely to seek care; the ETU database was more likely to detect cases in persons referred by health workers. Similar behaviors might have resulted in positive dependency in each data source. Both heterogeneity and positive dependency with data sources leads to underestimation.

Despite these limitations, we estimated more Ebola cases than were reported through official channels during the beginning of the outbreak in Montserrado County. Routine studies similar to ours can rapidly provide public health officials managing the outbreak response with estimates of underreporting and enable timely mobilization of appropriate resources. However, we believe that further exploration of this technique to better understand the possible difference of capture preference of each source may help improve the technique and benefit future outbreaks.

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Address for correspondence: Etienne Gignoux, Médecins Sans Frontières,78 Rue de Lausanne, CP 116, 1211 Geneva 21, Switzerland; email: etienne.gignoux@geneva.msf.org

Malformations Caused by Shuni Virus in Ruminants, Israel, 2014–2015

Natalia Golender,[1] Jacob Brenner,[1] Motti Valdman, Yevgeny Khinich, Velizar Bumbarov, Alexander Panshin, Nir Edery, Shimon Pismanik, Adi Behar

Author affiliations: Kimron Veterinary Institute, Bet Dagan, Israel (N. Golender, J. Brenner, Y. Khinich, V. Bumbarov, A. Panshin, N. Edery, A. Behar); Hachaklait, Caesarea, Israel (M. Valdman); Israeli Veterinary Field Services, Gilboa, Israel (S. Pismsanik)

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To the Editor: Viruses in the Simbu serogroup are arboviruses that cause abortion, stillbirth, and congenital abnormalities in domestic ruminants. Akabane virus (AKAV), Aino virus (AINV), and Schmallenberg virus are the most studied in this serogroup; Shuni, Sabo, Shamonda, and Sango viruses (*1*,*2*) are examined less frequently. Until 2012, only AKAV had been associated with congenital abnormalities in Israel, although AINV had been identified serologically in dairy cow herds with no clinical signs in 2003 (*3*). Moreover, of 15 brain samples collected during February–October 2012 from adult cows with central nervous system manifestations, 6 were positive for AKAV by PCR.

In late December 2014, the Israeli Veterinary Field Services was notified of the appearance of arthrogryposis-hydranencephaly syndrome (*1*) in 2 herds of sheep in the villages of Yokneam and Sde Ya'akov, respectively; both villages are located in the Izre'el Valley, in Israel's northern valleys (online Technical Appendix Figure 1, http://wwwnc.cdc.gov/EID/article/21/12/15-0804-Techapp.pdf), where several arboviral infections have occurred in recent decades. From our past experience (*3*), ≥1 virus of the Simbu serogroup was suspected to have infected the ruminants, probably during August–October 2014.

We collected 27 samples of brain, placenta, spleen, lung, and blood (mixed with EDTA to prevent coagulation) from 15 sheep, goats, and cattle. Most samples were from the 2 affected flocks in the northern valley; a few were from ruminants in additional locations: Avadon, near Israel's border with Lebanon; Ein Hachoresh, near central Israel; and Hura, close to the Negev desert (online Technical Appendix Figure 1).

Of the 27 samples, 23 (85%) were positive for Shuni virus (SHUV) by PCR (Table). SHUV, which had not been reported in Israel, was isolated from the brain and placenta of 1 malformed lamb (strain 2504/3/14; sample 11 in the Table). Moreover, partial nucleotide sequences of the small, medium, and large DNA segments (580/850, 4,320/4,326, and 285/6,880 bp, respectively) were identified from 3 samples (strains Yokneam 2417/2/14 and 2504/3/14 and Hura 273/14 from samples 2, 11, and 9, respectively, in the Table; online Technical Appendix Figure 2). Sequence data obtained by conventional PCR in this study have been deposited into GenBank (accession nos. KP900863–5, KP900873–5, KP900879–80, and KP900884). Phylogenetic analysis of the samples showed that they were isolates of SHUV (online Technical Appendix Figure 2). Additional SHUV RNA-specific fragments were detected in pathologic samples from kids, lambs, and calves (Table). Full-genome sequences were not performed, although sequencing should be done when possible to determine precise origin of isolates.

For further testing, we inoculated homogenate material from 7 distinct malformations (samples 1, 2, 6, 8, 11, 12, and 15 in the Table) into baby mice; only 1 family of baby mice inoculated intracerebrally with the SHUV isolate (sample 11 in the Table) exhibited characteristic neurologic signs of nervousness. PCR confirmed that SHUV caused the cerebral infections in these mice. The isolate was also suitable for further propagation in the Vero cell line (Table).

Our results showed the presence of SHUV in sheep in Israel during the winter of 2014–15 and suggest a northward expansion of SHUV from sub-Saharan Africa. Although SHUV was first isolated in the 1960s (*2*), its role as a pathogen has been shown only recently in its involvement in encephalitis in horses (*4*). We isolated SHUV from the pathologic fetal brain of a malformed lamb, an unusual laboratory finding because, although Simbu viruses are readily isolable from vectors or exposed animals during the 3 or 4 days of viremia, they are seldom isolable from pathologic specimens collected for study of congenital malformations. We deduce from the clinical evidence that malformations appear up to 6 months after infection with SHUV and after the virus has been eliminated from the host after immune

[1]These authors contributed equally to this article.