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Estimating Ebola Treatment Needs, United States

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To the Editor: By December 31, 2014, the Ebola epidemic in West Africa had resulted in treatment of 10 Ebola case-patients in the United States; a maximum of 4 patients received treatment at any one time (1). Four of these 10 persons became clinically ill in the United States (2 infected outside the United States and 2 infected in the United States), and 6 were clinically ill persons medically evacuated from West Africa (online Technical Appendix 1 Table 6, <http://wwwnc.cdc.gov/EID/article/21/7/15-0286-Techapp1.pdf>).

To plan for possible future cases in the United States, policy makers requested we produce a tool to estimate future numbers of Ebola case-patients needing treatment at

any one time in the United States. Gomes et al. previously estimated the potential size of outbreaks in the United States and other countries for 2 different dates in September 2014 (2). Another study considered the overall risk for exportation of Ebola from West Africa but did not estimate the number of potential cases in the United States at any one time (3).

We provide for practicing public health officials a spreadsheet-based tool, Beds for Ebola Disease (BED) (online Technical Appendix 2, <http://wwwnc.cdc.gov/EID/article/21/7/15-0286-Techapp2.xlsx>) that can be used to estimate the number of Ebola patients expected to be treated simultaneously in the United States at any point in time. Users of BED can update estimates for changing conditions and improved quality of input data, such as incidence of disease. The BED tool extends the work of prior studies by dividing persons arriving from Liberia, Sierra Leone, and Guinea into the following 3 categories: 1) travelers who are not health care workers (HCWs), 2) HCWs, and 3) medical evacuees. This categorization helps public health officials assess the potential risk for Ebola virus infection in individual travelers and the subsequent need for post-arrival monitoring (4).

We used the BED tool to calculate the estimated number of Ebola cases at any one time in the United States by multiplying the rate of new infections in the United States by length of stay (LOS) in hospital (Table). The rate of new infections is the sum of the rate of infected persons in the 3 listed categories who enter the United States from Liberia, Sierra Leone, or Guinea. For the first 2 categories of travelers, low and high estimates of Ebola-infected persons arriving in the United States are calculated by using low and high estimates of both the incidence of disease in the 3 countries and the number of arrivals per month (Table). Calculating the incidence among arriving HCWs required estimating the number of HCWs treating Ebola patients in West Africa (online Technical Appendix 1, Tables 2–4). For medical evacuations of persons already ill from Ebola, we calculated low and high estimates using unpublished data of such evacuations through the end of December 2014.

Although only 1 Ebola case has caused additional cases in the United States (7), we included the possibility that each Ebola case-patient who traveled into the United States would cause either 0 secondary cases (low estimate) or 2 secondary cases (high estimate) (Table). Such transmission might occur before a clinically ill traveler is hospitalized or between a patient and HCWs treating the patient (7). To account for the possibility that infected travelers may arrive in clusters, we assumed that persons requiring treatment would be distributed according to a Poisson probability distribution. Using this distribution enables us to calculate, using the BED tool, 95% CIs

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Table. Calculated monthly rates of Ebola disease among persons arriving in the United States and additional secondary cases, 2014

Arriving persons		Input 1: infections/mo*	Input 2: at-risk population	Input 3: US arrival rate/mo†	Output 1: importations/mo‡	Output 4: additional secondary cases§	Output 2: total cases/mo‡
Non-HCW	Low	1	10,000	2,000	0.2	0	0.2
	High	3	10,000	3,000	0.9	2	2.7
HCW	Low	1	100	30	0.3	0	0.3
	High	5	100	60	3.0	2	9.0
Medical evacuations¶	Low	NA	NA	1	1.0	0	1
	High	NA	NA	3	3.0	0	3

*Infections in travelers who are not HCWs were based on the monthly incidence identified in World Health Organization situation reports during June–October 2014 (online Technical Appendix 1 Table 1) (5). The high value was the highest monthly incidence [September] rounded to the nearest whole number; the low value was set at 30% of the high value. Infections in HCWs were based on estimates of the number of HCWs in West Africa with and without Ebola virus infection at different times in the epidemic [online Technical Appendix 1 and Appendix 1 Tables 2–4]. HCW, health care worker; NA, not applicable.

†The low estimate of US arrival rates for travelers who are not HCWs and both the low and high rates for HCWs were based on the count of screened airline passengers originating in Liberia, Sierra Leone, and Guinea in the month from mid-October through mid-November 2014 (Centers for Disease Control and Prevention [CDC], unpub. data). For the high US arrival rate for travelers who are not HCWs, we assumed a 50% increase over the low value [$3,000 = 2,000 \times 1.5$] to approximate the arrival rate in 2013, before the epidemic (3). Rates of HCW arrivals were based on travelers who identified themselves as having worked in a health care facility during the previous 21 d during screenings at their airport of entry to the United States during November 5–December 1, 2014, and the exposure risk category assigned to them according to CDC's Interim US Guidance for Monitoring and Movement of Persons with Potential Ebola Virus Exposure (4,6). The low estimate value of arrivals of HCWs (30 arriving HCWs) was approximately the lowest rate of high-risk and some-risk HCWs entering the United States. The high estimate value (60 arriving HCWs) was approximately the highest rate of high-, some-, and low-risk HCWs entering the United States (CDC, unpub. data).

‡Output 1 = (Input 1 / Input 2) × Input 3; Output 2 = Output 1 + (Output 1 × Input 4). See online Technical Appendix 1 for further details.

§Assumed number of additional secondary transmissions occurring in the United States per primary case based on the range of experience from the outbreak: 1 imported case to the United States resulted in 2 secondary infections, and several case-patients have been treated without any secondary infections (7).

¶Number of medical evacuations was obtained from unpublished Medical Evacuation Missions Reports (US Department of Health and Human Services, unpub. data).

around the average estimate of arriving case-patients. The treatment length used in both the low and high estimate calculations was 14.8 days, calculated as a weighted average of the LOS of hospitalized case-patients treated in West Africa through September 2014 (online Technical Appendix 1 Table 5) (8). We conducted a sensitivity analysis using LOS and reduced case-fatality rate of patients treated in the United States (online Technical Appendix 1 Table 6).

For late 2014, the low estimate of the average number of beds needed to treat patients with Ebola at any point in time was 1 (95% CI 0–3). The high estimate was 7 (95% CI 2–13).

In late 2014, the United States had to plan and prepare to treat additional Ebola case-patients. By mid-January 2015, the capacity of Ebola treatment centers in the United States (49 hospitals with 71 total beds [9]) was sufficient to care for our highest estimated number of Ebola patients. Policymakers already have used the BED model to evaluate responses to the risk for arrival of Ebola virus–infected travelers, and it can be used in future infectious disease outbreaks of international origin to plan for persons requiring treatment within the United States.

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Highly Pathogenic Avian Influenza A(H5N1) Virus in Poultry, Nigeria, 2015

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To the Editor: In Nigeria, from February 2006 through July 2008, outbreaks of highly pathogenic avian influenza (HPAI) subtype H5N1 virus infection in poultry negatively affected animal and public health as well as the agricultural sector and trade. These outbreaks were caused by viruses belonging to genetic clades 2.2 and 2.2.1 (1). In January 2015, seven years after disappearance of the virus, clinical signs of HPAI (swollen head and wattles, hemorrhagic shank and feet) and increased mortality rates were observed among backyard poultry in Kano and in a live bird market in Lagos State, Nigeria. The virus was isolated from 2 samples independently collected from the poultry farm (parenchymatous tissues) and the market (tracheal swab), and H5 subtype virus was identified by reverse transcription PCR. The samples were adsorbed onto 2 Flinders Technology Associates cards (GE Healthcare Life Sciences, Little Chalfont, UK), which were sent to the World Organisation for Animal Health/Food and Agriculture Organization of the United Nations Reference Laboratory for Avian Influenza in Italy for subtype confirmation and genetic characterization. Influenza A(H5N1) virus was detected in both samples, and sequencing of the hemagglutinin (HA) gene showed that the viruses possessed the molecular markers for HPAI viruses with a multibasic amino acid cleavage site motif (PQRERRRKR*G).

The complete genome of the virus from backyard poultry was successfully sequenced from the genetic material

extracted from the Flinders Technology Associates cards by using an Illumina MiSeq platform (2) and was submitted to the Global Initiative on Sharing All Influenza Data database (<http://platform.gisaid.org/>) under accession nos. EPI556504 and EPI567299–EPI567305. Maximum-likelihood trees were estimated for all 8 gene segments by using the best-fit general time reversible plus invariant sites plus gamma 4 model of nucleotide substitution with PhyML (3). The topology of the phylogenetic tree of the HA gene demonstrated that the H5N1 virus from Nigeria (A/chicken/Nigeria/15VIR339-2/2015) falls within genetic clade 2.3.2.1c (Figure, panel A). In particular, the HA gene sequence clustered with H5 viruses collected in China in 2013 and with an H5N1 virus (A/Alberta/01/2014) isolated from a Canada resident who had returned from China (similarity 99.3%–99.5%) (4).

The remaining 7 genes were closely related to genes of A/Alberta/01/2014(H5N1), although the 2 viruses differed by 32 aa (online Technical Appendix, <http://wwwnc.cdc.gov/EID/article/21/7/15-0421-Techapp1.pdf>). Just as for the virus from Canada (4), 7 of 8 gene segments of the virus from Nigeria clustered with HPAI A(H5N1) virus circulating in Vietnam and China, while the polymerase basic 2 gene segment (Figure, panel B) resulted from reassortment with viruses circulating in the same Asian countries but belonged to the H9N2 subtype. Differing from the strain from Canada (only 2 aa mutations compared with the 2.3.2.1c candidate vaccine strain; 5), the strain from Nigeria possesses 6 aa differences: 3 in HA1 and 3 in HA2 (online Technical Appendix). The effect of these mutations on the antigenic relatedness of these strains should be further explored.

Molecular characterization demonstrated that the polymerase basic 2 sequence contains glutamic acid at position 627, establishing the lack of a well-known mammalian adaptation motif (6). Mutations associated with increased virulence in mice have been observed in the nonstructural protein 1 (P42S, D87E, L98F, I101M, and the 80–84 deletion) and in the matrix 1 proteins (N30D, T215A). In addition, the substitutions D94N, S133A, S155N (H5 numbering) associated with increased binding to α -2,6 sialic acid have been identified in the HA protein. However, most of these substitutions are present in the H5N1 virus sequences from Asia included in our phylogenetic analyses, suggesting that they may be common among the HPAI H5 virus subtype. Mutations associated with resistance to antiviral drugs have not been detected (7).

The results obtained from whole-genome analysis provide evidence that a novel clade of the A(H5N1) virus, specifically clade 2.3.2.1c, has reached Nigeria. Although ascertaining how and exactly when this has happened is difficult, it seems most likely that the virus entered the country in December 2014, as evidenced by unverified

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