Ebola returns to its Congo Basin heartland

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On 8 May 2018, the Ministry of Health of the Democratic Republic of Congo (DRC, formerly Zaire) notified the World Health Organization of an outbreak of Ebola virus disease (EVD) in Bikoro Health Zone, Équateur Province. This is the ninth outbreak of EVD in DRC since 1976 (Table 1, Fig. 1), and the eighth caused by Zaire ebolavirus (EBOV; order Mononegavirales; family Filoviridae; genus Ebola virus).

The Congo Basin is the heartland of Ebola virus disease. Why this should be the case, is still obscure. The most accepted theory, that viruses of the genus Ebolavirus spill over as zoonoses from fruit bats, is consonant with previous findings of EBOV sequences in three fruit bat species, and the overlap of their geographical ranges with outbreak areas in central and western Africa. However, efforts to pinpoint the source of the outbreak that began in Guéckédou, Guinea, in December 2013 have only provided circumstantial evidence relating to insectivorous bats [1]. Whatever EBOV’s mammalian reservoir, the handling of uncooked bushmeat is widely believed to be a contributory factor for outbreaks in humans.

One of the successes of the fight against EVD in west Africa in 2013–2016 was the use of deep sequencing techniques to produce large numbers of EBOV genomes. Nearly 1400 of these have been deposited in GenBank, representing 5% of the official case total in that outbreak. Viral genome sequencing and phylogenetic analysis played a crucial role in both outbreak tracking and the identification of potential super-spreading factors, such as funerals or infected healthcare workers [2]. In the much smaller 2014 EVD outbreak in Boende, DRC, five complete genomes were also obtained. However, no sequence is so far available from the 2017 outbreak in Bas-Uele province. Filling this gap in our knowledge by recourse to sequencing from any samples remaining from the 2017 outbreak and ensuring that we prioritize sequencing in the current outbreak is essential.

EVD outbreaks in the same geographical locality are not necessarily related. For instance, in Gabon, the 1994–1996 cluster of outbreaks and the 2001–2002 outbreak are found on separate branches of the EBOV phylogenetic tree (Fig. 2). Given the geographical proximity of the 2014, 2017 and 2018 outbreaks in north-western DRC, a phylogenetic analysis of their relatedness might help to determine if a wavefront model of spread is applicable, following the analysis of the cluster of outbreaks in neighbouring Republic of Congo and Gabon around the turn of the millennium [3]. Our inability to predict outbreaks is due to our scant knowledge of what happens to EBOV between outbreaks. Progress towards this goal requires accurate reconstruction of how individual outbreaks are genetically related, and epizootically connected, which in turn requires genome sequencing from all outbreaks.

Regardless of its origins, the current outbreak has the potential for rapid expansion in numbers. The 2014 and 2017 outbreaks in DRC were in relatively isolated rural areas, with low population density and limited opportunities for wider transmission. The similarly poorly connected area of Ikoko-Impenge, 40 km inland from the town of Bikoro, was the site of the first 21 identified cases in early April 2018. However, the transfer of two cases to Bikoro General Hospital with a subsequent funeral in that town gave rise to infections in two mourners who then travelled on to the Wangata district of Mbandaka, 130 km by road to the north. Such long-range seeding of new foci by small numbers of travellers, and the involvement of funerals as transmission events, is reminiscent of the events of March and April 2014 in west Africa [4].

Estimates of the true population of African shanty cities are necessarily approximate, but Mbandaka, with a population of around 1.2 million, is comparable in size to Freetown and Monrovia, two of the three west African capital cities most affected in 2014. Mbandaka is a port on the River Congo, the main arterial transport link from DRC’s capital Kinshasa to inland cities, including Bangui, capital of the Central African Republic. With poor to non-existent provision of running water, sewage and electricity, the similarities with the urban situation in Monrovia, Conakry and Freetown during the west African outbreak are obvious. The risk of transmission to Kinshasa – central Africa’s main megacity with >12 million estimated inhabitants – either by river
Table 1. Ebola virus disease (EVD) outbreaks in the Democratic Republic of Congo (DRC, formerly Zaire) since 1976.
Case numbers as of 24 May 2018. See Fig. 1 for map.

<table>
<thead>
<tr>
<th>Year</th>
<th>Locality</th>
<th>Province</th>
<th>Latitude, longitude</th>
<th>Ebolavirus species</th>
<th>Cases</th>
<th>Deaths</th>
<th>Case fatality</th>
</tr>
</thead>
<tbody>
<tr>
<td>2018</td>
<td>Bikoro</td>
<td>Equateur</td>
<td>0.73° S, 18.14° E</td>
<td>Zaire</td>
<td>58</td>
<td>22</td>
<td>38 %</td>
</tr>
<tr>
<td>2017</td>
<td>Likati</td>
<td>Bas-Uele</td>
<td>3.35° N, 23.88° E</td>
<td>Zaire</td>
<td>8</td>
<td>4</td>
<td>50 %</td>
</tr>
<tr>
<td>2014</td>
<td>Boende</td>
<td>Tshuapa</td>
<td>0.28° S, 20.89° E</td>
<td>Zaire</td>
<td>66</td>
<td>49</td>
<td>74 %</td>
</tr>
<tr>
<td>2012</td>
<td>Isiro</td>
<td>Haut-Uele</td>
<td>2.77° N, 27.61° E</td>
<td>Bundibugyo</td>
<td>57</td>
<td>29</td>
<td>51 %</td>
</tr>
<tr>
<td>2008</td>
<td>Luebo</td>
<td>Kasai-Occidentale</td>
<td>5.35° S, 21.42° E</td>
<td>Zaire</td>
<td>32</td>
<td>15</td>
<td>47 %</td>
</tr>
<tr>
<td>2007</td>
<td>Kampungu</td>
<td>Kasai-Occidentale</td>
<td>5.20° S, 21.42° E</td>
<td>Zaire</td>
<td>264</td>
<td>187</td>
<td>71 %</td>
</tr>
<tr>
<td>1995</td>
<td>Kikwit</td>
<td>Kwilu</td>
<td>5.05° S, 18.78° E</td>
<td>Zaire</td>
<td>315</td>
<td>250</td>
<td>79 %</td>
</tr>
<tr>
<td>1977</td>
<td>Tandala</td>
<td>Equateur</td>
<td>2.97° N, 19.35° E</td>
<td>Zaire</td>
<td>1</td>
<td>1</td>
<td>100 %</td>
</tr>
<tr>
<td>1976</td>
<td>Yambuku</td>
<td>Mongala</td>
<td>2.82° N, 22.22° E</td>
<td>Zaire</td>
<td>318</td>
<td>280</td>
<td>88 %</td>
</tr>
</tbody>
</table>

or by air from Mbandaka’s regional airport, is a major concern. Ring vaccination, effective during the latter stages of the west African outbreak [5], is being tested for the first time in the early stages of an EVD emergency. Traditional methods of containment, including testing for signs of fever in passengers embarking onto Congo riverboats at Mbandaka or flying out of Mbandaka airport, may prevent wider dissemination.
Whatever the trajectory of the present outbreak over the coming months, the question of how to prevent future EVD outbreaks remains depressingly open.

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Conflicts of interest
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References

Fig. 2. Maximum-likelihood tree of selected Zaire ebolavirus genomes from DRC (Boende, Kikwit, Luebo and Yambuku) and elsewhere. The numbers on nodes are bootstrap confidence values, where >70. The scale is substitutions per site.

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