Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

similar to the rates reported for *B microti* infection, there were no acute complications and no deaths.[1,10] These data suggest that "*B venatorum*" disease is milder than *B microti* disease in immunocompetent individuals. Reasons for milder disease might include lower microbial virulence, as suggested by low "*B venatorum*" parasitemia in SCID mice, and a younger patient population because two-thirds of the confirmed cases were younger than 50 years.

Circulating concentrations of several proinflammatory cytokines (tumour necrosis factor α, interferon γ, and interleukin 6) and one adhesion molecule (vascular cell adhesion molecule 1) were increased in confirmed cases, lending support to the idea that excessive production of proinflammatory cytokines and activated vascular endothelium contribute to the pathogenesis of the disease. Cure of "*B venatorum*" infection previously was achieved with quinine plus clindamycin or atovaquone plus azithromycin.[2,6,9] In the current case series, none of the seven patients admitted to hospital received standard regimens; four were given clindamycin without quinine. All patients recovered, however, follow-up to detect possible sequelae was not done.

Cases of babesiosis have been reported in mainland China and Taiwan for more than three decades, but there is still much to be learned.[4] Co-infections with *B microti* and *Plasmodium falciparum* have been reported in areas of Yunnan province that border Burma.[12] *B microti*, *B divergens,* and "*B venatorum*" can all infect *I persulcatus* and human co-infection with several of these pathogens is an intriguing possibility.[13] As cases continue to emerge in mainland China and elsewhere in Asia, it is imperative that we improve our understanding of the health burden of human babesiosis in this densely populated region of the globe. This report should provide further impetus and direction toward that goal.

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1 Jiang JF, Zheng YC, Jiang RR, et al. Epidemiological, clinical, and laboratory characteristics of 48 cases with "*Babesia venatorum*" infection in China: a descriptive study. *Lancet Infect Dis* 2014; published Dec 22. http://dx.doi.org/10.1016/S1473-3099(14)71046-1.
2 Sun YS, Li SG, Jiang JF, et al. *Babesia venatorum* infection in child, China. *Emerg Infect Dis* 2014; **20:** 896–97.
3 Vannier E, Krause PJ. Human babesiosis. *N Engl J Med* 2012; **366:** 2397–407.
4 Zhou X, Li S, Wang J, et al. Human babesiosis, an emerging tick-borne disease in the People's Republic of China. *Parasit Vectors* 2014; **7:** 509.
5 Qi C, Zhou D, Liu J, et al. Detection of *Babesia divergens* using molecular methods in anemic patients in Shandong Province, China. *Parasitol Res* 2011; **109:** 241–45.
6 Hunfeld KP, Hildebrandt A, Gray JS. Babesiosis: recent insights into an ancient disease. *Int J Parasitol* 2008; **38:** 1219–37.
7 Prevention CDC. Babesiosis surveillance—18 states, 2011. *Morb Mortal Wkly Rep* 2012; **61:** 505–09.
8 Herwaldt BL, Linden JV, Bosserman E, et al. Transfusion-associated babesiosis in the United States: a description of cases. *Ann Intern Med* 2011; **155:** 509–19.
9 Blum S, Gattringer R, Haschke E, et al. The case: hemolysis and acute renal failure. *Kidney Int* 2011; **80:** 681–83.
10 Krause PJ, McKay K, Gadbaw J, et al. Increasing health burden of human babesiosis in endemic sites. *Am J Trop Med Hyg* 2003; **68:** 431–06.
11 Joseph JT, Roy SS, Shams N, et al. Babesiosis in Lower Hudson Valley, New York, USA. *Emerg Infect Dis* 2011; **17:** 843–47.
12 Zhou X, Li S, Chen S, et al. Co-infections with *Babesia microti* and plasmodium parasites along the China—Myanmar border. *Infect Dis Poverty* 2013; **2:** 24.
13 Rar VA, Epikhina TI, Livanova NN et al. Genetic diversity of babesia in *Ixodes persulcatus* and small mammals from North Ural and West Siberia, Russia. *Parasitol* 2011; **138:** 175–82.

Controlling Ebola: key role of Ebola treatment centres

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What initially was perceived to be a self-limited outbreak of Ebola virus disease in a forested area of Guinea has become an unprecedented epidemic of international concern that continues to spread unabated in parts of west Africa.[1,2] A lack of public health infrastructure together with delays in virus detection and implementation of control interventions have contributed to the widespread transmission of Ebola virus disease in a region inexperienced with this disease.[3]

As in previous international health crises, such as the severe acute respiratory syndrome epidemic and the 2009 influenza pandemic, mathematical models are proving instrumental to guide the public health response against Ebola virus disease and monitor the effectiveness of control interventions.[4,5] Whereas earlier modelling efforts have relied on compartmental homogeneous-mixing models,[6–8] the study by Stefano Merler and colleagues,[9] reported in *The Lancet Infectious Diseases*, uses a microsimulation model to capture spatial heterogeneity in the transmission dynamics of

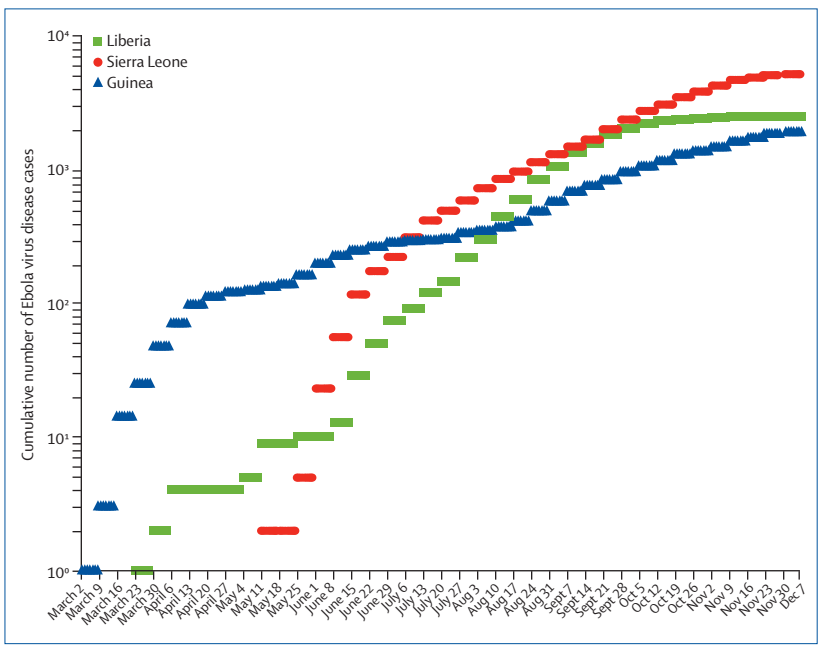

***Figure*: Cumulative number of Ebola virus disease cases (log scale) in Guinea, Sierra Leone, and Liberia**
As of Dec 10, 2014, 27 Ebola treatment centres were open in Liberia (1079 beds), 12 in Sierra Leone (565 beds), and four in Guinea (200 beds).[12]

Ebola virus disease in Liberia. Indeed, local epidemics of Ebola virus disease seem to be asynchronous and show slower than expected growth, a pattern probably driven by the geometry of the contact network or social behaviour changes.[10]

The model of Merler and colleagues incorporates fine details of Liberia's population structure and geography, including location of households, hospitals, and Ebola treatment units. Infectiousness is assumed to intensify in the later and more severe stages of Ebola virus disease, when infectious individuals are confined at home or in the health-care setting, and exposed to a restricted number of caregivers. The resulting contact network is highly clustered, giving rise to a slow and local mode of dissemination,[9] a pattern that homogeneous-mixing models have been unable to capture. Long-distance transmission events (eg, during unsafe funerals) are predicted to be uncommon; instead, the slow geographic spread of Ebola virus disease is best explained by distance travelled to reach a hospital.[9] This point is interesting, because several long-distance transmission events were key in the dissemination of the infection to neighbouring countries (Mali, Nigeria, Senegal) and other continents (Europe [Spain], North America [USA]).[2]

For more on **flowminder** see http://www.flowminder.org/

One important aspect of the model by Merler and colleagues is to assess the effectiveness of intervention measures put in place in Liberia since mid-August, 2014.[9] In the pre-intervention period from June to mid-August, 2014, most of the Ebola infections were estimated to occur in hospitals (38%), followed by households (31%), the community (22%), and at funerals (9%). The rapid establishment of new Ebola treatment units was a key step to curb the epidemic in Liberia, although the model assumes near perfect isolation of infectious individuals in Ebola treatment units, which could be overly optimistic. Distribution of household protection kits and implementation of safe burial procedures were also associated with significant reduction in Ebola virus disease transmission. Of note, other interventions not explicitly modelled could have played a part, including use of rapid diagnostic kits in Ebola treatment units, which reduces the delay from presentation to isolation, and changes in population behaviour in response to mass education campaigns and accumulation of Ebola virus disease cases.[11] Some of these effects could have been absorbed in the model by Merler and colleagues[9] through the estimated effect of household protection kits.

The model by Merler and colleagues provides a substantial improvement compared with earlier homogeneous mixing models[6–8] and in turn their more optimistic predictions align better with the observed trajectory of the epidemic in Liberia.[9] However, the model tends to underestimate Ebola treatment unit admissions and predicts an earlier peak than reported, suggesting that further improvements could be useful. Ideally, future models should integrate more realistic population mobility patterns derived from cellphone usage data (eg, flowminder), proxies of social behaviour, and differences in reporting and hospitalisation rates between rural and urban areas. However, these important data are lacking for the region.

The outlook for Liberia has substantially improved over the past few weeks with news of an epidemic slowdown[2] (figure). By contrast, incidence has remained relatively stable in Guinea, whereas the epidemic continues to ascend quickly in Sierra Leone (figure). Difficulties in building and staffing Ebola treatment units could explain the worrisome turn of the outbreak in Sierra Leone. A key test of the robustness of the model by Merler and colleagues will be whether it can reproduce the highly distinct dynamics of Ebola virus disease in different countries. In the longer run,

microsimulations and other modelling approaches could prove instrumental to optimise interventions to curb and ultimately eliminate Ebola virus disease in the region, especially as an Ebola vaccine might materialise in the near future.

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1 Baden LR, Kanapathipillai R, Campion EW, Morrissey S, Rubin EJ, Drazen JM. Ebola—an ongoing crisis. *N Engl J Med* 2014; **371:** 1458–59.
2 WHO. Ebola response roadmap update. http://www.who.int/csr/disease/ebola/situation-reports/archive/en/ (accessed Dec 10, 2014).
3 Baize S, Pannetier D, Oestereich L, et al. Emergence of Zaire Ebola virus disease in Guinea—preliminary report. *N Engl J Med* 2014; **371:** 1418–25.
4 Lipsitch M, Cohen T, Cooper B, et al. Transmission dynamics and control of severe acute respiratory syndrome. *Science* 2003; **300:** 1966–70.
5 Fraser C, Donnelly CA, Cauchemez S, et al. Pandemic potential of a strain of influenza A (H1N1): early findings. *Science* 2009; **324:** 1557–61.
6 Lewnard JA, Ndeffo Mbah ML, Alfaro-Murillo JA, et al. Dynamics and control of Ebola virus transmission in Montserrado, Liberia: a mathematical modelling analysis. *Lancet Infect Dis* 2014; **14:** 1189–95.
7 Pandey A, Atkins KE, Medlock J, et al. Strategies for containing Ebola in west Africa. *Science* 2014; **346:** 991–95.
8 Chowell G, Nishiura H. Transmission dynamics and control of Ebola virus disease (EVD): a review. *BMC Med* 2014; **12:** 196.
9 Merler S, Ajelli M, Fumanelli L, et al. Spatiotemporal spread of the 2014 outbreak of Ebola virus disease in Liberia and the effectiveness of non-pharmaceutical interventions: a computational modelling analysis. *Lancet Infect Dis* 2015; published online Jan 7. http://dx.doi.org/10.1016/S1473-3099(14)71074-6
10 Chowell G, Viboud C, Hyman JM, Simonsen L. The western Africa Ebola virus disease epidemic exhibits both global exponential and local polynomial growth rates. *PLoS Curr* 2014; published online Nov 30. http://lanl.arxiv.org/abs/1411.7364.
11 Chowell G, Simonsen L, Viboud C, Kuang Y. Is West Africa approaching a catastrophic phase or is the 2014 Ebola epidemic slowing down? Different models yield different answers for Liberia. *PLoS Curr* 2014; published online Nov 20. DOI: 0.1371/currents.outbreaks.b4690859d91684da963dc40e00f3da81.
12 UN Office for the Coordination of Humanitarian Affairs. The humanitarian data exchange—Ebola treatment centers or units (ETCs or ETUs). 2014. https://data.hdx.rwlabs.org/dataset/ebola-treatment-centers (accessed Dec 14, 2014).

Shortening treatment of tuberculosis: lessons from fluoroquinolone trials

In clinical trial settings the standard 6-month treatment regimen for drug-sensitive pulmonary tuberculosis can achieve relapse-free cure in more than 95% of people. However, poor adherence might increase the risk of relapse and lead to drug resistance. Shortening the duration of treatment has become a major priority for global control of tuberculosis—it will benefit patients and reduce the selection pressures that lead to the evolution of new drug-resistant strains.[1,2]

Attempts to use shorter courses of standard regimen drugs have not been successful except for smear-negative disease,[3,4] and recent research has focused on fluoroquinolones. The authors of a Cochrane review of five studies assessing 6-month fluoroquinolone-containing regimens to treat drug-sensitive disease concluded that the available evidence was of low quality: the only consistently reported clinical outcome was all-cause mortality.[5] However, data from studies of mice and phase 2 trials suggested that use of fluoroquinolones could shorten treatment for drug-sensitive tuberculosis from 6 months to 4 months.[6] This possibility has now been assessed in human beings in four large phase 3 randomised controlled trials.[7–10] Although fluoroquinolone-containing regimens led to more negative culture results at 2 months, this did not translate into improved clinical outcomes when treatment was shortened (figure).

The RIFAQUIN,[7] OFLOTUB,[8] and REMoxTB[9] trials benefitted from large numbers of patients, more than 18 months of follow-up, and robust methods (such as the ability to differentiate relapse from reinfection by strain typing). A trial done by the Indian National Institute for Research in Tuberculosis was discontinued early on account of an unacceptable number of relapses.[10] The non-inferior result of the RIFAQUIN 6-month group, in which high-dose rifapentine and moxifloxacin were given once weekly in the continuation phase, seems consistent with findings from previous trials of 6-months' treatment with fluoroquinolones, suggesting that they are broadly equivalent to the standard regimen. Apart from the 6-month RIFAQUN once-weekly regimen, which could be useful in some settings, it is disappointing that, despite these large trials—each costing several million dollars and lasting up to 10 years—we remain with the same 6-month regimen used in the 1970s. Since fluoroquinolones alone do not seem to allow treatment to be shortened, it is