PRINT: ISSN 0970-9274 ONLINE: ISSN 2456-6608
J Hum Ecol, 51(3): 257-263 (2015)
DOI: 10.31901/24566608.2015/51.03.04

A Note on Ebola's Outbreak and Human Migration Dynamic

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KEYWORDS Ebola Mathematical Model. Population Traveling. Ebola Haemorrhagic Fever. Ebola Virus Spread. Outbreak 2014

ABSTRACT In the present research, a multi-country system modelling people travelling between four countries touched by ebola-virus and a multi-compartmental model of ebola dynamic are analysed. The travel model showed how total population present in a country is affected by other infected residents or visitors. Numerical simulations are performed for a sample population of 1000 people and clearly, they reveal that, even a small amount of infected visitors may cause, within a short period of time, the extermination of an entire human population in a region if nothing is done to stop the disease. This result is pertinent since it corresponds to the ongoing situation in West Africa. Further, it agrees with countries closing their borders to limit individuals' flux coming in. Thus, the urgency of educating people about the disease process, ways to stop its spread and finding its cure is huge and looks like a race against time for the world.

INTRODUCTION

Ebola fever disease which is caused by ebola virus, a virus belonging to the family of filoviridae is a severe viral and fatal hemorrhagic disease characterized by initial fever and malaise followed by gastrointestinal symptoms, bleeding, shock, and multi-organ system failure. The genus Ebola virus is one of three members of the *Filoviridae* family (filo virus), together with the genus Marburg virus and the genus Cueva virus. Genus Ebolavirus is itself divided into five distinct species: Bundibugyo ebola virus (BDBV), Zaire ebola virus (EBOV), Sudan ebola virus (SUDV), Reston ebola virus (RESTV) and Taï Forest ebola virus (TAFV) (Atangana et al. 2014; Baize et al. 2014; Doungmo Goufo et al. 2015; Grady et al. 2014; Geisbert et al. 2003; Hoenen et al. 2006; Leffel et al. 2004; Liberia Ebola SitRep 2015; WHO Media Centre 2014; World Health Organization 2015). The first three have been largely associated with the ebola hemorrhagic fever outbreaks in Africa, for instance, the actual 2014 fatal outbreak seen in West Africa. Ebola hemorrhagic fever is generally recognized only when there are outbreaks, usually of less than 100 cases, which are almost invariably fueled by nosocomial transmission in hospitals located in resource-poor areas where proper infection control practices are not maintained.

Transmission through Contact and People Movements

Roughly speaking, ebola is introduced in the human population through close contact with blood, body fluids, organs or other bodily fluids of infected animals. In Africa, the infection was documented by the handling of infected chimpanzees, gorillas, fruit bats, monkeys, forest antelope and porcupines found dead or sick in the forest. Figure 1 shows one of the most common ebola virus transmission modes.

Ebola virus spreads in the community through human-to-human transmission, with infection resulting from direct contact (through broken skin or mucous membranes) with the blood, secretions, organs or other bodily fluids of infected people. The virus is also spread by indirect contact with environments contaminated with such fluids (Doungmo Goufo et al. 2015; Grady et al. 2014; Gonzalez et al. 2007; Kuhn et al. 2010; WHO Media Centre 2014; World Health Organization 2015). Burial ceremonies in which mourners usually have direct contact with the body of a deceased person can also play a role in the transmission of Ebola. Men who have recovered from the disease can still transmit the virus through their semen for up to 7 weeks after recovery from illness.

A huge amount of infected people also catch the disease by traveling into an infected zone or by contacting someone who has travelled from an infected environment. As a proof, it is believed (Baize et al. 2014; Grady et al. 2014) that the first human case of the Ebola hemorrhagic fever leading to the current outbreak was a two-year-old boy who died on 6 December 2013 in the village of Meliandou in Guinea. Further, the close members of his family became ill with symptoms consistent with ebola infection and also died. People around those victims also got in-

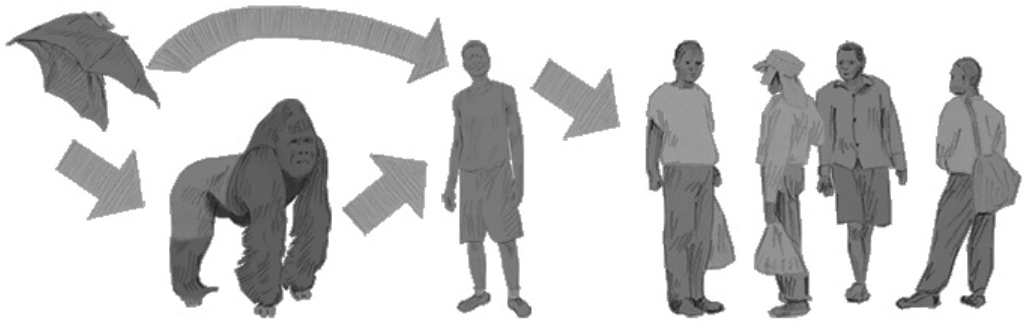

Fig.1. Ebola virus transmission
Source : <http://www.abc.net.au/news/2014-07-30/ebola-virus-explainer/5635028> (Retrieved on 20 August 2014).

fected and spread the disease to other villages, cities and countries by moving or traveling. A concrete example is the case of Patrick Sawyer (Wesse 2014), a Liberian official working at the Ministry of Finance who flew from Liberia to Nigeria after exposure to the virus, and died at Lagos soon after his arrival. In a very short period of time, the virus was widespread in four West African countries, namely Guinea Nigeria, Sierra Leone, and Liberia. Today it is reported that nine countries in three continents (Africa, Europe and America) have so far (January 2015) experienced the virus, leading to a total of about 20750 recorded cases in the world. There might still be suspected or non-transmissible cases of infections in other countries of the region, but the four countries mentioned above were believed to have an active local transmission and high contamination rates (Doungmo Goufo et al. 2015; Liberia Ebola SitRep 2015; World Health organization 2015) . Fortunately, Nigeria was declared ebola-free after five weeks without any reported case of ebola.

Further, it is clear that people cannot speak about Ebola virus dynamic and spreading without taking into account the impact of travelling and migration from one place to another. In the following section a multi-country system modelling people migration dynamic is provided and analysed.

METHODOLOGY

Migration Dynamic From a Country *i* to Another Country *j*

Since, one of the main causes of the fever transmission is the displacement of people from an infected country to another, the researchers established in this section the migration dynamics between the four major outbreak zones: Nigeria, Sierra Leone, Guinea and Liberia.

Following the same approach as in (Arino et al. 2003; Sattenspiel et al. 1995), the researchers name *residents* of a country *i* people who were born in country *i* and live in the same country. As visitors, we mean people who are not physically present in their country of residence at the time they are considered. The researchers denoted by $V_{ij}(t)$ the number of residents of country *i* who are visiting the country *j* at time t. Then, $V_{ij}(t)$ is the number of residents of a country *i* present in at the time (t) and when we add its residents who are outside visiting one of the three other countries, the researchers obtained the total number of residents of country *i* at time *t* given as

$$N_i^r(t) = \sum_{j=1}^{4} V_{ij}(t)$$

In addition, when the researchers add to $V_{ii}(t)$ all the people visiting the country *i* from one of the three other countries, the researchers get the population of country *i* at time *t* , that is, the number of people who are physically present in country *i* at time and expressed as

$$N_i^p(t) = \sum_{j=1}^{4} V_{ji}(t)$$

The researchers assume that residents of country *i* leave the country at a per capita rate $hi \geq 0$ per unit time and a fraction $q_{ji} \geq 0$ of them go to country *j*. Then, it followed that $q_{ii}=0$ and $\Sigma_{j=1}^{4} q_{ji}=1$ if $h_i>0$. Further, $h_i q_{ji}$ is the travel rate from *i* country to country *j*. Residents of country *i* who are in country *j* return to *i* with a per capita rate of $b_{ij} \geq 0$, with $b_{ii}=0$. Hence, these assumptions impose that a person resident in a country, let us say *i* and who is present in anoth-

er country *j*, is assumed to first return to country *i* before leaving for a third country, say *m*, distinct from *i* and *j*. The travel dynamics between two countries *i* and *j* is represented in Figure 2.

With the above assumptions, the evolution of the number of residents $V_{ii}(t)$ of country present in that country and the evolution of the number of residents $V_{ij}(t)$ of country *i* who are outside visiting a country j(j≠i) are respectively expressed by differential equations:

$$\begin{cases} \dot{V}_{ii}(t) = d\left(N_i^r(t) - V_{ii}(t)\right) + \sum_{j=1}^{4} b_{ij} V_{ii}(t) - h_i V_{ii}(t) \\ \dot{V}_{ij}(t) = h_i q_{ji} V_{ii}(t) - b_{ij} V_{ij}(t) - dV_{ij}(t), \qquad i \neq j \end{cases} \quad (1)$$

With this model, we can easily prove (see Arino et al. 2003; Sattenspiel et al. 1995) that the total number $N^r_\varepsilon(t)$ of residents of country is all the time constant, that is

Indeed,

$$\dot{N}_i^r(t) = \frac{dN_i^r(t)}{dt}$$
$$= \frac{d}{dt}\left(\sum_{j=1}^{4} V_{ij}(t)\right)$$
$$= \frac{d}{dt}V_{ii}(t) + \frac{d}{dt}\left(\sum_{\substack{j=1 \\ j\neq i}}^{4} V_{ij}(t)\right)$$
$$= 0,$$

Where the relations (1) have been used, in the same way, it is shown that the number $N_i^p(t)$ of people who are physically present in country *i* is in general a variable quantity, but the total population in the four West-African countries considered here is a fixed quantity expressed by

$$T = \sum_{i=1}^{4} N_i^r(t) = \sum_{i=1}^{4} N_i^p(t) = \sum_{i=1}^{4}\sum_{j=1}^{4} V_{ij}(t) = \text{constant}$$

Ebola Fever Model Description and Settings

Let us consider a West African country *i* with a constant overall number of individuals, $N^r_t = N^r_t$ (t) at a given time *t*. The researchers assume that everyone is susceptible to catch Ebola fever and that an overall fraction βN^r_i of the total resident population dies by natural death and other diseases, with β constant. The researchers denoted by κ, τ and *d* the rate of infection by Ebola, the recovery rate from the disease and the rate of death due to the fever respectively. At the time *t* in country country *i*, $S^r_i(t)$ is the number representing resident individuals susceptible to Ebola, $I^r_i(t)$ is the number of individuals infected with Ebola, $R^r_i(t)$ is the number representing people that recover from Ebola $D^r_i(t)$, is the number of death due to Ebola. Due to the virulence of the fever and its highly contagious state, people from recovery compartment turn out to be vulnerable again, and go back to the susceptible compartment at the rate constants. The transfer diagram describing the

$N_i^r(t) = \text{constant}.$

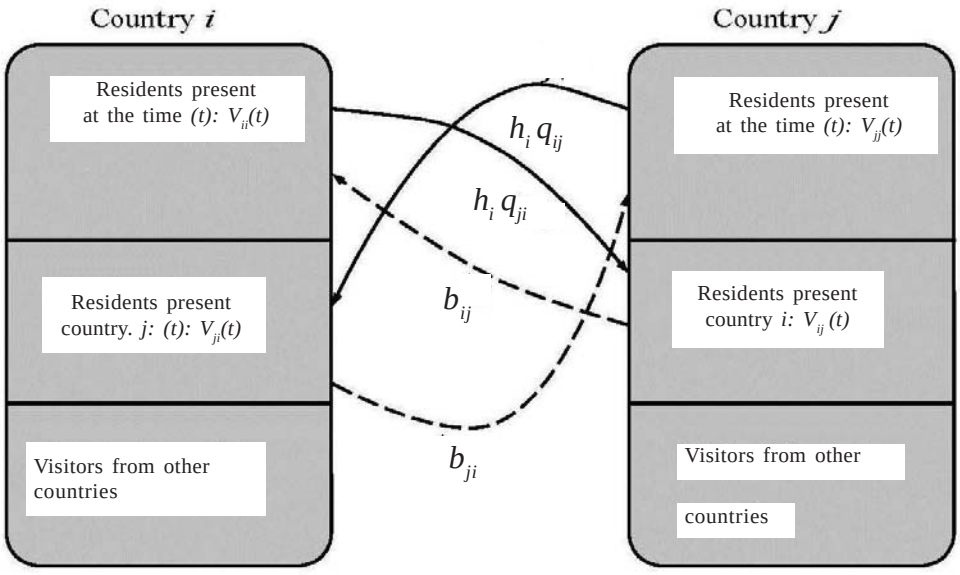

Fig. 2. Travel dynamics between two countries *i* and *j*

above dynamics for Ebola fever is given in Figure 3 and expressed by the system

$$\begin{cases} \dot{S}_i^r(t) &= -\kappa S_i^r(t) I_i^r(t) + sR_i^r(t) - \beta N_i^r(t) \\ \dot{I}_i^r(t) &= \kappa S_i^r(t) I_i^r(t) - (\tau + d) I_i^r(t) \\ \dot{R}_i^r(t) &= \tau I_i^r(t) - sR_i^r(t) \\ \dot{D}_i^r(t) &= dI_i^r(t) + \beta N_i^r(t), \end{cases} \quad (2)$$

The model (3) is well posed and every non negative initial solution ($S^r_i(0)$, $I^r_i(0)$, $R^r_i(0)$, $D^r_i(0)$) of (3) generates a corresponding solution ($S^r_i(t)$, $I^r_i(t)$, $R^r_i(t)$, $D^r_i(t)$) that is non-negative for all . For more details about well-posedness of epidemic models see (Atangana et al. 2014; Ball et al. 2002; Doungmo Goufo et al. 2014; Van den Driessche et al. 2002) and the references therein.

Since, the researchers are concerned only about the impact of Ebola fever outbreak and migration on the whole human resources and eco-system, the researchers don't need to deeply study, in this paper, the well posed-ness of the model (3). The researchers main concern is the disease free and endemic equilibrium points.

Equilibrium Points

Let a country *i*,the number of dead people D^r_ican be derived as

$$D_i^r = N_i^r - S_i^r - I_i^r - R_i^r$$

Thus, we will use only the first three compartments of the population to find the equilibrium points. The disease free equilibrium point is obtained by putting $I^r_i=R^r_i=0$ and is given by

$$P_i^o = (S_i^r(0) = N_i^r(0), 0, 0).$$

The endemic equilibrium point is obtained by solving the system

$$\begin{aligned} 0 &= -\kappa S_i^r I_i^r + sR_i^r - \beta N_i^r \\ 0 &= \kappa S_i^r I_i^r - (\tau + d) I_i^r \\ 0 &= \tau I_i^r - sR_i^r, \end{aligned}$$

Which yields the endemic equilibrium point for the model (2)

$$P_i^* = (S_i^*, I_i^*, R_i^*),$$

Where

$$S_i^* = \frac{\tau + d}{\kappa}$$

$$I_i^* = \frac{-\beta N_i^r}{d}$$

$$R_i^* = \frac{-\tau\beta N_i^r}{sd}.$$

Hence, there is a non-trivial solution to the system (3) and since I^*_i and R^*_i are non-negative, then, there is no positive endemic equilibrium associated to the model (2). For discussion about the stability of these equilibrium point, the reader can refers to (Atangana et al. 2014; Ball et al. 2002; Doungmo Goufo et al. 2014; Van den Driessche et al. 2002) and the references therein.

Numerical Simulations

Let us consider a country *i*. To provide a prediction about the disease evolution and see what will really happen if no interventions are done on time, the researchers make use of the following realistic parameter according to reported data (Atangana et al. 2014; Gonzalez et al. 2007; Grady 2014). The parameters are listed in the Table 1.

Table 1: The estimated parameters for Ebola model

β	d	κ	τ	s	$N^r_i = N$
0.01	06	0.01	0.4	0.02	1000

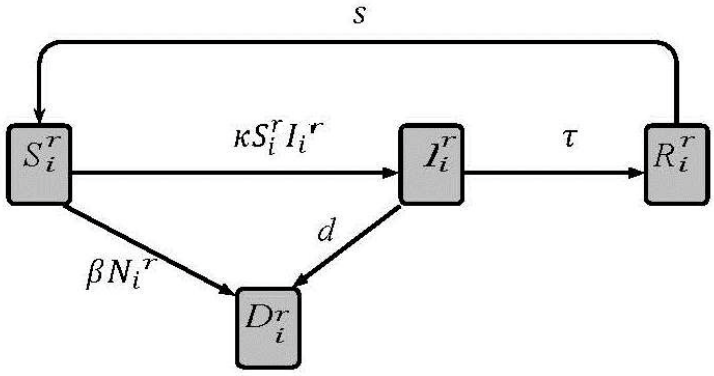

Fig. 3. Transfer diagram for the dynamics of Ebola fever transmission in an African country *i*

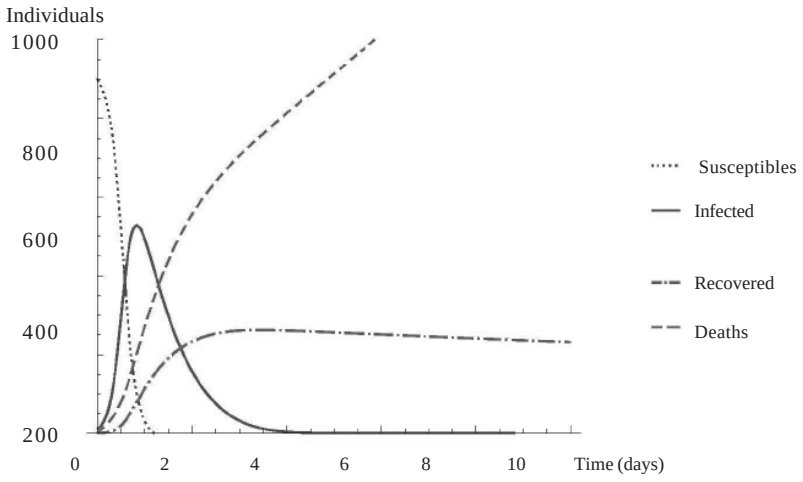

Fig. 4. The approximate evolution of Ebola fever in a West African country *i*

The researchers make use of the following the initial conditions for graphical representations

$S_i^r(0) = 900\,, \quad I_i^r(0) = 10\,, \quad R_i^r(0) = 0, \quad D_i^r(0) = 0.$

The implementation code of the predictor-corrector PECE method of Adams-Bash forth-Moulton type described in (Diethelm et al. 2005) is used, which yields the Figure 4. This figure shows the global evolution the Ebola epidemic in the given country *i* for the four compartments. Note that the remaining population is understood to be people dying from any other causes.

FINDINGS AND DISCUSSION

The models and simulations clearly show how the total population present in a certain region can be substantiallyhit by ebola infected residents or infected people coming in. The fact that the number N^p_i of people who are physically present in country i is a variable quantity is very significant in the dynamic and transmission of a virus like ebola virus. People travel from a zone where they have been exposed to the virus to another zone where they transmit the virus to people around them. The case of Patrick Sawyer mentioned in the introduction is a very good illustration of ebola spread via traveling. Indeed, it is reported (Wesse 2014) that the doctor and the nurse who treated him also passed away. Clearly, the researchers have proven, as shown in Figure 4, that a small number (about 1%)of a population) who are ebola infected visitors (or residents) may cause, in a short period of time, the total extermination of an entire human population in a country if nothing is done to halt the spread of the disease. The simulations show that the 1000 people will die in less than a week. Recall that the incubation period is about 8 days (range 3-21 days) and infectious patients typically present abrupt onset of non-specific signs and symptoms. This includes fever, malaise, headache, chest pain, and myalgia/arthralgia, followed rapidly by gastrointestinal symptoms (vomiting, diarrhea, abdominal pain) and, in some cases, a maculopapular skin rash. Severe cases develop bleeding (sub-conjunctival hemorrhage, epistaxis, bleeding from the mouth and rectum, oozing from venipuncture sites), neurologic involvement (disorientation, convulsions, coma), shock, and multi-organ system failure, leading to the death. Obviously, a small fraction of people dying from any other causes has been included in the model and are supposed to be counted among the 1000 people dying.

CONCLUSION

A multi-country system modelling the travelling of people between four West-African

countries touched by the ebola disease has been provided and analysed together with a model of the Ebola haemorrhagic fever dynamic. Numerical simulations have been done for a total population of 1000 people, revealing how the total population physically present in a country can be deeply affected by a small number of ebola infected individuals residing or coming in from outside. The work and results presented in this study are pertinent and current since they correspond the actual situation in West-Africa. Indeed, by August 2015, almost 27984 people have been infected in countries like Guinea, Liberia, Sierra Leone, Mali, Nigeria, Senegal, Spain, United Kingdom, United States of America with about 11298 deaths from the ongoing 2014 Ebola outbreak.

However, not everyone who has contracted the disease dies and with no confirmed cure or vaccine, it is still a mystery the fact that some people die, but some survive. However, some of the drugs are being experimented with promising results. This brings out the severity of the situation and the urgency of educating people and discovering a real and reliable cure or a vaccine.

RECOMMENDATIONS

Since complete literature on ebola, in terms of curing and species' variety, is not yet largely known and diffused around the world, it is urgent and necessary to educate people about the real dynamic of ebola-virus, its transmission's mode and ways to avoid or reduce its spreading. The study presented in this research has been conducted only for a small amount of individuals between four countries. It can be extended in a larger scale to many more cities and countries. This will provide a bigger picture of the situation, and therefore, closer to the reality. However, the model used here and the results suggest that if there are no interventions, the ebola virus may decimate everybody in a region where only few individuals were initially infected.

No known confirmed cure to the disease exists and then, it is urgent to quickly put in place adequate steps to prevent the spread of the virus. The first one is to avoid travelling to infect-

Fig. 5. Preventing Ebola virus from spreading
Source: <http://www.oaupeeps.com/2014/07/ebola-outbreak-causes-transmission.html> (Retrieved on 20 August 2014).

ed or suspected zones. As a matter of fact, the analysis of this paper gives right to many West-African neighbouring countries that have closed their borders to limit the number of people travelling in. Others steps are stated as follows: Avoid physical contact with people showing signs and symptoms such as continuous high fever, red eyes, vomiting and stomach aches, wash one's hands regularly with soap and clean water, avoid shaking hands of suspicious people showing signs and symptoms of the fever, stay away from animals like macaques or bats and suspicious meats, especially, bush meat that one does not know the origin. Figure 5 shows more details steps to prevent the spread of Ebola virus.

REFERENCES

Arino J, van den Driessche P 2003. A Multi-city Epidemic Model, Mathematical Population Studies: An International Journal of Mathematical Demography, 10(3): 175-193.From < http://DOI: 10.1080/08898480306720> (Retrieved on 20 August 2014).

Atangana A, Doungmo Goufo EF 2014. Computational Analysis of the Model Describing HIV Infection of CD4+T Cells. BioMed Research International, 2014, Paper ID 618404, 7 pages. From <http://dx.doi.org/10.1155/2014/618404> (Retrieved on 20 August 2014).

Atangana A, Doungmo Goufo EF 2014. On the Mathematical Analysis of Ebola Hemorrhagic Fever: Deathly Infection Disease in West African Countries, BioMed Research International, Volume 2014, Paper ID 261383. From <http://dx.doi.org/10.1155/2014/261383> (Retrieved on 20 August 2014).

Ball FG, Lyne OD 2002. Epidemics among a population of households. In: C, Castillo-Chavez S, Blower P van D, Driessche D, Kirschner D, Yakubu (Eds.): *Mathematical Approaches for Emerging and Reemerging Infectious Diseases Part II: Models, Methods and Theory, IMA Vol. 126,* New York: Springer-Verlag New York, pp. 115-142.

Baize S, Pannetier D, Oestereich L, Rieger T 2014. Emergence of Zaire Ebola Virus Disease in Guinea - Preliminary Report. New England Journal of Medicine From <http://doi:10.1056/NEJMoa 1404505> (Retrieved on 20 August 2014).

Diethelm K, Ford NJ, Freed AD, Luchko Yu 2005. Algorithms for the fractional calculus: A selection of numerical methods. *Comput Methods Appl Mech Engrg,* 194: 743-773.

Doungmo Goufo EF, Atangana A, Mugisha S 2015. Epidemic models of ebola hemorrhagic fever with non-linear transmission. A*pplied Mathematics and Computation,* (in press).

Doungmo Goufo EF, Oukouomi Noutchie SC, Mugisha S 2014. A Fractional SEIR Epidemic Model for Spatial and Temporal Spread of Measles in Metapopulations. Abstract and Applied Analysis, 2014, Paper ID 781028, 6 pages. From <http://dx.doi.org/10.1155/2014/781028> (Retrieved on 20 August 2014).

Geisbert TW, Hensley LE, Larsen T, Young HA, Reed DS, Geisbert JB, Scott DP, Kagan E, Jahrling PB, Davis KJ 2003. Pathogenesis of ebola hemorrhagic fever in Cynomolgus Macaques. *American Journal of Pathology,* 163(6): 2347-2370

Grady D, Fink S 2014. Tracing Ebola's Breakout to an African 2-Year-Old.The New York Times. ISSN 0362-4331. From <http://www.nytimes.com/2014/08/10/world/africa/tracing-ebolas-breakout-to-an-african-2-year-old.html> (Retrieved on 14 August 2014).

Gonzalez JP, Pourrut X, Leroy E 2007. Ebolavirus and other filoviruses: Current topicsin microbiology and immunology. *Current Topics in Microbiology and Immunology,* 315: 363–387.

Hoenen T, Groseth A, Falzarano D, Feldmann H 2006. Ebola virus: Unravelling pathogenesis to combat a deadly disease. *Trends in Molecular Medicine,* 12(5): 206–215.

Kuhn JH, Becker S, Ebihara H, Geisbert TW, Johnson KM, Kawaoka Y, Lipkin WI, Negredo AI, Netesov SV, Nichol ST, Palacios G, Peters CJ, Tenorio A, Volchkov VE, Jahrling PB 2010. Proposal for a revised taxonomy of the family Filoviridae: Classification, names of taxa and viruses, and virus abbreviations. *Archives of Virology,* 155(12): 2083–2103.

Leffel EK, Reed DS 2004. Marburg and Ebola viruses as aerosol threats. *Biosecurity and Bioterrorism: Biodefense Strategy, Practice, and Science,* 2(3): 186–191.

Liberia Ebola SitRep 2015. No. 236. 8 January 2015. From <http://www.mohsw.gov.lr/documents/Sitrep-20236-20Jan-206th-202014.pdf> (Retrieved 9 January 2015).

Sattenspiel L, Dietz K 1995. A structured epidemic model incorporating geographic mobility among regions. *Math Biosci,* 128: 71-91.

Van den Driessche P, Watmough J 2002. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Math Biosci,* 180: 29-48.

Wesee BP 2014. I'm Ok - Nigerian Ambassador Assures Public. The New Dawn, Monrovia. From <http://www. thenewdawnliberia.com/index. php?view=paper&id= 12289> (Retrieved on 19 August 2014).

WHO Media Centre 2014. Ebola Virus Disease. Fact Sheet N°103. From <http://www.who.int/mediacentre/factsheets/fs103/en/> (Retrieved on 20 August 2014).

World Health Organization 7 January 2015. Ebola Situation Report on 7 January 2015. From <http://apps.who.int/iris/bitstream/10665/147112/1/roadmap sitrep7Jan2015eng.pdf> (Retrieved on 8 January 2015).