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Ebola Virus-A Review Rogo, L.D.<sup>1</sup>, Auwal, I.K.<sup>2,3\*</sup>

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#### **Summary**

Ebola virus (EBOV) is a single stranded zoonotic RNA virus of positive sense polarity under Filoviridae family, with no geographic, socioeconomic, ethnic, gender or age boundaries, introduced to humans via contact with body fluids and products of wild animals. Direct human-to human transmission is equally important as it results to high transmission and mortality rates. EBOV primarily attack macrophages and dendritic cells with suppression of type-I interferon response with early systemic spread following release of large progeny particles into the extracellular fluid. Due to the complex genetic evolution, strange properties and functional profile, researchers are still struggling to comprehend the pathogenic capacity of this virus and its interaction with the host cellular machineries. This comprehensive review is an overview of what is known about Ebola virus and encompasses biology of the virus including its interaction with the host, epidemiology, disease presentation, diagnosis, therapeutics and progress in vaccine development.

Keywords: Ebola; Haemorrhagic fever; Ebola virus disease; Pathogenesis; Therapeutics.

### **Introduction**

Ebola virus (EBOV) is a linear, single stranded, negative-sense RNA virus (ssRNA) of the order Mononegavirale and Filoviridae family, with five (5) species under the genus Ebola virus. These includes, Sudan ebolavirus (SUDV), Zaire ebolavirus (EBOV), Tai Forest (Ivory Coast) ebolavirus (TAFV), Reston ebolavirus

(RESTV) and *Bundibugyo ebolavirus* (BDBV) (Feldmann et al., 2005; Mayo, 2002). These viruses together cause the severe and often fatal haemorrhagic fever in both humans and nonhuman primates known as Ebola Virus Disease (EVD). Zaire ebolavirus is the most ancient and was first discovered in Ebola River - Zaire (currently Democratic Republic of Congo) following the 1976 outbreak, hence the name "Ebola virus"(Kuhn et al., 2010).

Zaire ebolavirus is associated with high transmission and very high case fatality rate. This was further testified by the fatal outbreak between 2013 and 2015 that reported 28,603 cases and  $40\%$  mortality (Liu et al., 2015). Mucosal surfaces or skin abrasions are the main porta of entry; however, most of human infection occurs after direct contact with infected patients or cadavers. In addition, eating contaminated meat of wild animal sources have been found to be associated with the disease (Chowell and Nishiura, 2015).

The symptoms of high fever, chills and myalgia occur following an incubation period of 2-21 days, followed by the multisystem presentation involving gastrointestinal tract, respiratory, central nervous system, clotting and tegumentary systems, resulting in the classical disease with bleeding diathesis (Baize et al.,  $2014$ ). Infected individuals develop strong immune response during the first stage of the infection as evidenced by the high level of specific immunoglobulin G (IgG). Following virus clearance from the circulation, there is consistent immune activation with persistently



activated CD8 T cells (McElroy et al., 2015). Management is mainly supportive and aimed at maintaining adequate circulation; however, specific symptoms management is associated with increased chance of survival. There is no available chemotherapeutic agent or vaccine against EBOV yet, hence other public health measures like contact tracing, good surveillance system, state of the act laboratory services, careful burials of the deceased and good social

mobilization programs, remained the main stay of prevention and control.

#### **Virion structure**

A particle of EBOV is made up of seven structural proteins locked together, giving a strand of cooked spaghetti-like appearance. It measures 80nm by 1000nm with approximate nucleotide size of 19 kb (Fig. 1) (Nanbo et al., 2013).



Figure 1. Cylindrical/tubular structure of Ebola virus. Nucleoprotein (NP), polymerase co-factor (VP35), (VP40), GP, transcription activator (VP30), VP24, and RNA-dependent RNA polymerase (L).

The virion is cylindrical or somehow tubular with envelope, matrix, and nucleocapsid components. A complete cylinder is roughly 80 nm in diameter with viral encoded glycoprotein (GP) protruding as 7-10 nm long spikes from its lipid bilayer surface (Tran *et al.*, 2014). The cylinders are of variable length, typically 800 nm, but sometimes up to 1000 nm long. The outer most viral envelope is obtained through budding from domains of host cell membrane into which the GP spikes have been fitted at the time of their biogenesis (Nanbo et al., 2013). Individual GP molecule appear with spacing of about 10 nm (Erin et al., 2014). Viral proteins VP40 and VP24 are stationed in the *matrix space*, in between the envelope and the nucleocapsid. The nucleocapsid is made up of series of viral proteins joined to an 18–19 kb linear, negativesense RNA without 3'-polyadenylation or 5'capping (Fig. 2) (Fieldmann, 1993). The viral RNA is helically wound in complex with NP, VP35, VP30, and L proteins; this helix has a diameter of 80 nm and contains a central channel of 20–30 nm in diameter (Nanbo et al., 2013). It is important to note that NP, VP35 and L gene sections from filoviruses have been realized as endogenous in the genomes of many groups of small mammals as seen in the figure 2 above (Taylor et al., 2014; Hulo et al., 2011).



Figure 2: Genome structure of Ebola virus. The gene order is 3'-leader-NP-VP35-VP40-GP/sGP-VP30-VP24-L-trailer-5'; with the leader and trailer being non-transcribed regions, which contains vital signals for transcription, replication, and packaging of the viral genomes into progeny virions.



## **Functional genomics of EBOV**

The seven EBOV genes are split by variable gene borders, including short (4- or 5-nucleotide) intergenic regions (IRs), a single long (144nucleotide) IR, and gene overlaps, where the adjacent gene end and start signals share five conserved nucleotides (Castilletti et al., 2015). Each gene encodes for one protein, except for the GP gene that encode three glycoproteins.

The nucleoprotein (NP) is connected to the viral genome and assembles into a helical nucleocapsid (NC) together with the polymerase co-factor (VP35), the transcription activator (VP30), and RNA-dependent RNA polymerase (L) (Brauburger et al., 2014). Together encapsidate and protect the genome from the endonucleases. The encapsidated genomic RNA produce the nucleocapsid and serve as a template for both transcription and replication.

Vp35 of EBOV is a multifunctional dsRNA binding protein (d-RBP) that play significant role in viral replication, innate immune evasion and pathogenesis. It is also cofactor of viral RNA polymerase complex and together with NP and VP24 take part in nucleocapsid biosynthesis. VP35 communicate with helical NP-RNA complexes via C-terminus of NP and their coexpression decrease production of NP-RNA complexes. Consequently, represses the emergence of NP-induced inclusion bodies that usually form in EBOV-infected cells. Muhlberger et al. (1999) have also established significant correlation between the NP: VP35 ratio and viral replication.

Vp40 is situated straight under the viral lipid bilayer and thus provide structural support. It is the most prolific protein in the virus particle and is considered inevitable for assembly and budding of new virus particles. VP40 is equally important in the movement of NCs to the cell surface and its incorporation into virions. The interaction between nucleoprotein and the matrix protein VP40 is probably vital for these processes (Noda et al., 2011). EBOV replicate in the cytoplasm, while assembly of new virus particles and budding occur at the plasma membrane. At this stage, VP40 connect with cellular membranes and are brought together via interactions with the C-terminal ends of viral glycoproteins (Noda et al., 2011). It has been shown that VP40 in solution forms an octameric ring with a central pore. The two farthest N and C end tail regions have been shown to stabilize the monomeric state via a direct connection. The tails seem to be functioning as a latch, released upon a particular molecular stimulation such as RNA ligation. The stimulated release of the tails allows coordination of late-stage activities in the viral life cycle at the inner membrane of the host cell. The N-tail release in particular, exposes the L-domain motifs PTAP/PPEY to the transport and budding complexes while stimulated C-tail release enhance connection with the site of budding (Dessen et al., 2000).

Glycoprotein (GP) of EBOV, the only viral protein expressed on the virion surface play an important role for binding and enhances membrane fusion. The GP gene encodes seven consecutive adenosine nucleotides within a predicted hairpin loop (Silva et al., 2012). Initial pre-GP is cleaved by furin at a multi-basic motif into two subunits, GP1 and GP2, which remain connected via a disulfide linkage between Cys53 of GP1 and Cys609 of GP2 (Sanchez et al., 1996). The virion-bonded GP is important in the EBOV life cycle as it is exclusively important for binding, fusion and entry into the target cells. GP is also important for main in pathogenicity and specie differentiation. GP1 subunit is important for cellular binding and contains supposed receptor-binding regions as well as an excessively glycosylated region, named the mucin-like domain (Jeffers et al., 2002). GP2 subunit play a key role in viral-host membrane fusion. It bears the hydrophobic internal fusion loop, two heptad repeats (HR1 and HR2), a CX6CC disulfide bond motif, a membrane proximal external region and a transmembrane anchor (Lee and Saphire, 2009). In addition to its surface glycoprotein (GP 1 and 2), EBOV manipulate the production of large amount of a truncated glycoprotein isoform (sGP) which is released into the extracellular space. Generation and secretion of antigens was studied in many viruses and was found to be a means of host immune evasion by removing antibodies and meddling with antibody-mediated clearance. It has been found that sGP easily subvert a



previously immunized host's anti-GP 1 and 2 responses resulting in strong cross-reactivity with sGP (Gallaher, 1996).

Vp30 is known to be a transcription activation factor necessary for the viral life cycle. Although the mechanism is not completely understood, it is proposed that this protein is connected with initiation of transcription because VP30dependent transcription is controlled by RNA of the first transcription start signal. The starting 23 nucleotides of this NP mRNA are concerned in stem-loop structure formation that might meddle with the progression of transcription by physically interfering with polymerase movement (Mohan et al., 2012). In addition, the N-terminal of VP30 contains a  $Zn^{2}$  binding Cys-His motif (Weik et al., 2002) and high amount of basic amino acids, allowing it to straight ahead interact with RNA (Modrof et al., 2003). Consequently, VP30 could either resolve or cover this secondary structure and permit transcription to continue. Many works also reported that VP30 is vital in transcription reinitiation and may attach to stem-loops generated by the promoter of each Ebola virus gene (John et al., 2008). It has been shown that phosphorylation of VP30 prevents viral transcription but viral replication is enhanced at the same time. Phosphorylation of VP30 in return controls a recently explained interaction of VP30 with VP35 and fortifies the interaction with NP. VP30 phosphorylation was reported to be critical for viral transcription and replication, implying a means by which VP30 phosphorylation regulate the composition of the viral polymerase complex, thereby probably forming a transcriptase in the existence of nonphosphorylated VP30 or a replicase with phosphorylated VP30 (Martinez et al., 2008).

Another important protein is VP24, this works to prevent transcription and replication of the EBOV genome. Though the exact means is still not yet clarified, it may be that VP24 attaches to NP and interfere with the function of VP35, VP30 or L. This interference may be vital in converting the viral genome from a transcription or replication competent form to one that is ready for virion assembly and exit (Biedenkopf et al., 2013). It has been shown that VP24 is essential for the accurate assembly of a functional nucleocapsid, as lack of VP24 leads to decreased transcription/translation of VP30 (Watanabe et  $al., 2007.$ 

It was found that 472 nucleotides from the 3' end and 731 nucleotides from the 5' end are enough for a viral "mini-genome" replication, although not enough for infection (Hoenen et al., 2006). In accordance with the stop-start model describing NNS RNA virus transcription, the viral polymerase complex attaches to a single transcription promoter at the 3' end of the genome and moves toward the 5' end, sequentially synthesizing mostly mono-cistronic mRNAs (Klenk et al., 2004).

An L gene and 5' trailer region nucleotide sequence of Ebola virus has been resolved, as such finalized the sequence of the Ebola virus genome. The L gene carries a single ORF encoding a polypeptide of 2212 amino acid. Messenger RNAs are capped and polyadenylated by the L protein at the time of biogenesis. The 5'-trailer sequence of the genomic RNA is made up of 676 nucleotides and discloses self-complementary sequence at the farthest end, and may play a vital part in virus replication (Whelan et al., 2004). The functions of these genes are summarized in table I.



Gene	<b>Function/role</b>
Nuclear protein (NP)	Connect with the viral genome and assemble into a helical nucleocapsid (NC), the genome from nuclease also protect activities.
Viral protein-35 (VP35)	Serve as a polymerase co -factor. As a multifunctional dsRNA binding protein, it plays important role in viral replication, innate immune evasion and pathogenesis.
Viral protein-40 (VP40)	A membrane connected protein considered inevitable for assembly and budding of new virus particles.
Glycoprotein GP/sGP	Plays important role for binding to host cells and for fusion. Is responsible for pathogenic differences among the viral species.
Viral protein-30 (VP30)	n factor A known transcription activatio necessary for viral life cycle.
Viral protein-24 (VP24)	Prevent transcription and replication of the Ebola virus genome. Essential for accurate assembly of functional nucleocapsid.
L gene	Carries a single ORF encoding polypeptide of 2212 aa. Res ponsible for capping and polyadenylation of mRNAs at the time of biogenesis.

**Table I: Ebola virus proteins and their functions**

(Castelletti et al., 2015; Nanbo et al., 2013; Noda et al., 2011; Jeffers et al., 2002; Fieldman et al., 1993)

### Ebola virus receptor and internalization

Two proteins have been reported as candidates for host cell entry. First, is a cholesterol transporter protein, the host-encoded Niemann-Pick C1 (NPC1), that appears to be vital for entry of Ebola virions into the host cell and for its final replication (Carette et al., 2011; Volchkov et al., 1999) and the second candidate is TIM-1 (Côté et al., 2011). Report shows that NPC1 play vital role in entry of Ebola virus due to the fact that it interfere in the infection by attaching directly to viral GP and TIM-1 was shown to attach to the receptor binding domain of the EBOV glycoprotein, to enhance the receptivity of vero cells (Hofmann-Winkler et al., 2015; Kondratowicz et al., 2011; Saeed et al., 2010). Mechanism of cell entry between the Ebola Virus from Zaire, 1976 and Sierra Leone, 2014, where reported to be the same (Noda et al., 2006). The virus attach to the host cell surface via glycoprotein (GP) surface peplomer and enter by endocytosis in macropinosomes. To penetrate the cell, the viral membrane fuses with vesicle membrane to release the nucleocapsid into the



cytoplasm. Encapsidated, negative-sense genomic ssRNA is used as a template for the biogenesis (3'-5') of polyadenylated, monocistronic mRNAs, and using the host cell's ribosomes, tRNA molecules, the mRNA is translated into respective viral proteins. These proteins are deal with: a glycoprotein precursor (GP0) is split to GP1 and GP2, which are then greatly glycosylated by cellular enzymes and substrates. These two molecules join, first into heterodimers, and then into trimers to produce the surface peplomers. Released glycoprotein (sGP) precursor split to sGP and delta peptide, both of which are released from the cell (Cox et al., 1983). More so, as viral protein levels increase, a switch occurs from translation to replication. Using the negative-sense genomic RNA as a template, a complementary  $(+)$  ssRNA is produced; which is then used as a template for biogenesis of new genomic (-) ssRNA, which is immediately encapsidated. Examination of virus-infected cells revealed virions carrying NCs to appear horizontally from the cell surface, whereas empty virions usually bud vertically, indicating that horizontal budding is the main form of Ebola virus budding (Muyembe-Tamfumet et al., 2012).

### Epidemiology

The first outbreak of EVD occurred in small villages close to Ebola River - Zaire (currently Democratic Republic of Congo) in 1976 located in tropical rainforests (Feldmann and Geisbert, 2011). This partly explained why first outbreak of EVD was due to EBOV and SUDV and remained restricted to a limited area (Goeiienbier et al., 2014). Since then, there was no another outbreak until in 1994, but after 1994 the number increases, leading to the discovery of two new Ebola virus species (BDBV and TAFV) (Kreuels et al., 2014). This was attributed to increased bush meat consumption and movements to previously inaccessible areas (Baize et al., 2014). There is no certainty on how the index case became infected in the 2013 outbreak that took place in Guinea (Park et al., 2015). Animals implicated in introduction of EBOV into the human population are chimpanzee, gorillas, duikers and specific species of fruit bats, all found to be infected with EBOV during the targeted studies (Folarin et al., 2016). Recent outbreak was the largest ever-documented epidemic of EVD in terms of numbers and geographical spread throughout EVD history with case fatality rate of 90%. EBOV is capable of actively circulating worldwide without ethnic or geographical boundaries, albeit with some regional differences (Folarin et al., 2016).

A seven-month epidemiological study of EBOV Makona genome showed both host-to-host transmission and recurrent emergence of intrahost genetic variants and increasing impact of purifying selection in suppressing accumulation of nonsynonymous mutations over time (Varkey et al., 2015). A report by Christie et al. (2015) confirmed a single source for the Nigerian cases indicating that the Nigerian EBOV lineage nests within the previously but genetically distinct form seen in Liberia and supports the notion that transmission from Nigeria to other places did not occur. By May 2016, 28, 657 clinically suspected or confirmed cases were reported including 11.325 mortalities. Over 870 of infected individuals were healthcare workers and a significant number have lost their lives in three most prevalent (Guinea, Liberia and Sierra Leone) and other affected countries (Mali, Nigeria, Senegal, Spain and USA) (Christie et  $al., 2015).$ 

### Pathogenesis and immune response

Ebola virus enters the host primarily through mucosal surfaces or skin abrasions, with most human infections occurring after direct contact with infected humans. The virus is shed in body fluids such as urine, semen, saliva, aqueous humor, breast milk, tears and sweat (Osterholm et al., 2015; Bray and Geisbert, 2005). Several cases were attributed to ingestion of meats from infected wild animals with hunters being the most affected. Airborne transmission between monkeys was demonstrated during the outbreak in Virginia, but there is limited evidence to support this in humans (Baize et al., 2014). Ebola virus can fit in as an opportunistic pathogen transmitted via aerosols under certain conditions, since infectious aerosols (either large or small droplet), could be generated and emitted during the course of disease (Basler, 2005).

Due to the problem of conducting clinical studies at the time of outbreak situations, virtually all information concerning the pathogenesis of Ebola virus disease was derived from laboratory



experiments using non-human primates, guinea pigs and mice. However, observational studies/case reports involving large-scale patients in recent outbreaks shed more lights regarding the pathogenesis in humans (Basler,  $2005$ ).

Following viral entry, many different cell types including Macrophages and dendritic cells are mostly affected. Filoviruses replicate easily within these omnipresent "sentinel" cells, resulting in their necrosis and freeing large numbers of progeny particles into extracellular fluid (Hensley et al., 2002). Type I interferon response suppression result in an early systemic spread (Hutchinson and Rollin, 2007). Spread to regional lymph nodes result in another round of replication, with secondary haematogenuous extension to dendritic cells and mobile/fixed macrophages located in some reticuloendothelial organs such as liver, spleen and thymus gland. Further studies have also established the involvement of other cell types, including endothelial cells, fibroblasts, adrenal cortical and epithelial cells. In fatal infection, there is multifocal necrosis involving hepatic and splenic tissues (Geisbert et al., 2003). Gastrointestinal symptoms such as diarrhoea and vomiting may result in severe dehydration and consequently hypovolaemic shock (Geisbert et al., 2000). However, there is dilemma as to whether this is because of direct involvement of the gastrointestinal tract, induced by cytokines or both (Geisbert et al., 2003). The virus also induces systemic inflammatory response with release of inflammatory cells as well as proinflammatory mediators from macrophages and other cells (Baize et al., 2000). Tumor necrosis factor (TNF- $\alpha$ ), interleukin (IL)-1 $\beta$ , IL-6, macrophage chemotactic protein (MCP)-1, and nitric oxide (NO) among others were recovered in blood samples of Ebola-infected macaques and severely infected humans in Africa (Bradfute et al., 2007). Breakdown products of necrotic cells also trigger the release of the same mediators (Parrino et al., 2007).

Ebola virus appears to be involved indirectly in inducing coagulation defect because of host inflammatory response. Infected macrophages synthesize cell-surface tissue factor (TF), stimulating the extrinsic coagulation pathway: pro-inflammatory cytokines also trigger macrophages to release TF (Bradfute et al., 2008). These simultaneous phenomena explain the rapid development and severity of platelet dysfunction in Ebola virus infection. Furthermore, there are other supporting evidences that explained coagulopathy in Ebola virus disease. For examples, D-dimers were recovered in blood samples of infected monkeys within 24 hours of virus challenge. This was also demonstrated in plasma of infected humans. Activated protein C was found to decrease on the 2nd day of infection in infected macaque, but with a sustainable level of platelets count until after the 3rd or 4th day of virus challenge. implying that activated platelets remained attached to the endothelial cells. With disease progression, hepatic injury has also been associated with decrease plasma levels of certain coagulation factors (Geisbert et al., 2003). Flaviviruses were frequently associated with severe fatal disease due to failure of host adaptive immunity because of incapacitated dendritic cells and lymphatic apoptosis. Furthermore, with decrease levels of lymphocytes, adaptive immunity tends to be impaired (Fowler et al., 2014; Crary et al., 2003). Although these cells appear to remain uninfected, they undergo "bystander" apoptosis, presumably induced by inflammatory mediators and/or loss of support signals from dendritic cells. This was similarly observed in septic shock (Kibadi et al., 1999). Report shows that virusspecific lymphocyte proliferation occurs despite the surrounding massive apoptosis in infected mice, but arrives too late to stop fatal outcome (Kibadi et al., 1999). The pathogenesis of EBOV has been summarized in figure 3 and 4 below.

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Figure 3: Schematic representation of pathogenesis of Ebola virus (Vingolo et al., 2015).



Figure 4: Immune response and inhibition pathways in Ebola virus infection (Vingolo et al., 2015).



### **Clinical manifestation and complications**

The spectrum of clinical disorders that are connected with EBV infection ranges from mild to life threatening. Initial symptoms of fever, chills, malaise and myalgia occur 8-12 days after exposure (Vingolo et al., 2015). These nonspecific symptoms often may be confused with other more common infectious diseases such as malaria, typhoid fever, meningococcemia among others most especially in the early course of the disease. Individuals can advance (in five days) to more specific presentations like terrible diarrhoea, nausea, vomiting and abdominal pain. Other systemic symptoms such as angina, dyspnea, cephalalgia or perplexity can also begin. Conjunctival injection, hiccups, seizures and cerebral edema have been reported too (Vingolo et al., 2015). Bleeding is not universally present but can manifest late in due course as purpura, ecchymosis/bruises, mucosal haemorrhages or oozing from venipuncture sites and. Frank haemorrhage is less common, but unexplained bleeding has been reported in 18% and bloody stool in 6% of affected individuals in the 2015 outbreak in Sierra Leon (Park et al., 2015). Patients may develop diffuse erythematous maculopapular rash by day 5 to 7 (usually around the neck, trunk, and arms) which may desquamate.

Analysis of symptoms in the 2014 outbreak from onset to full-blown disease revealed the following; fever  $(87\%)$ , fatigue  $(76\%)$ , vomiting  $(68\%)$ , diarrhoea  $(66\%)$ , and loss of appetite  $(65\%)$ . Fatal disease cases usually develop more severe clinical signs immediately and die typically of multiple organ failure and shock within 6 to 16 days (average 7.5 days) (CDC, 2015; Baize et al., 2014; WHO, 2014). A constellation of symptoms including unexplained bleeding; and many more other signs and symptoms example diarrhoea, chest pain, cough, dyspnoea, dysphasia, conjunctivitis, sore throat, confusion, hiccups and coma were associated with fatal outcomes, especially in those above the age of 45 years in West Africa (Chua et al., 2015; Martin et al., 2015). Ocular complications were reported in three  $(15\%)$  of 20 survivors of the 1995 outbreak in the DRC. Ocular pain, photophobia, increased lacrimation, decreased visual acuity and uveitis were among the ocular presentations (Martins et al., 2015). Survivors have also reported longterm sequelae including myalgia, asymmetric and migratory arthralgia, headache, fatigue, bulimia, amenorrhea, hearing loss, tinnitus, unilateral orchitis and suppurative parotitis (Basler, 2005).

## **Diagnosis**

In early stage of the disease, diagnosis is often strenuous due to non-specific features that mimic common illnesses in the endemic zones (Towner et al., 2004). Suspected individual, especially with strong history of contact should be quarantine and reported to the appropriate public health authorities for immediate prompt action. Emphasis should be giving to people who come in contact with: blood or body fluids from a suspected individual or died from Ebola, fomites that have been contaminated with blood or body fluids of suspects or someone who died of Ebola. infected fruit bats and primates (apes and monkeys), or semen from recovered patients (Beeching et al., 2014; Rollin et al., 2007). Presumptive diagnosis can be made in the appropriate clinical context based on history of exposure, symptomatology, and/or laboratory findings in keeping with the disease (Kortepeter) et al., 2011). Laboratory parameters that are paramount in the diagnosis of EVD are summarized in table II and III. Low platelet count with significant lymphopenia, even though is not diagnostic can be observed in the early phase. Often followed by neutrophil leukocytosis in patients who eventually recovered along with normalization of thrombocytopenia. However, leukocytosis may persist and show immature cells. Progressive decrease in platelet count in patients with severe disease could suggest disseminated intravascular coagulation (DIC). Low haemoglobin concentration indicates significant blood loss (Bishop, 2014; McElroy et al., 2014; Kortepeter et al., 2011). Prolonged prothrombin time or activated partial thromboplastin time is associated with more severe infection and bleeding manifestation such as DIC. The value of D-dimers may rise four times higher on day 6-8 of infection as evidenced by post-mortem results in comparison with that of the survivors (Oswald et al., 2007). A raise in serum creatinine, urea or



derange electrolytes may indicate acute kidney injury and may be seen at the end of first week of infection (King et al., 2015). Hypokalaemia, Haematuria and proteinuria indicate fatal disease. Elevated serum lactate is in keeping with tissue hypoperfusion and shock. Derange liver enzymes such as AST and ALT with marked AST: ALT ratio up to 15:1 was observed on day 6-8 in fatal cases as compared with 5:1 in nonfatal (King et al., 2015). Bilirubin, y-glutamyl transferase, and alkaline phosphatase are often slightly raised. Higher concentrations of serum amylase may indicate pancreatitis, also suggestive of fatal infection (King et al., 2015;

Bray et al., 2000). Negative blood culture is helpful and rule out other non-viral infectious causes such as sepsis or enteric fever (Kortepeter et al., 2011).

Detection of viral genome in peripheral blood or other tissue fluid is considered more direct and appropriate diagnostic approach (King et al., 2015). As a progress towards rapid and accurate molecular diagnosis, a wide array of molecular hybridization and nucleic acid amplification techniques are continuously being developed (table II and III) (Goodman, 2014; Bray et al., 2000).





(Beeching et al., 2014; McElroy et al., 2014; Kortepeter et al., 2011; Rolling et al., 2007) Key: PCR-polymerase chain reaction, IgM-immunoglobulin M, IgG-immunoglobulin G.

### Table III: Other supportive diagnostic approaches





(King et al., 2015; Oswald et al., 2007; Bray et al., 2000)



## **Therapeutics**

Specific antiviral therapy is not available to treat EBV infection. The treatment approach depends on clinical presentation, host immune status and other underlying conditions (Zhang et al., 2014). Previous study shows that EBOV has a mechanism of infection propagation in vivo in macaques that is distinctively insensitive even to increased concentration of neutralizing antibody (McCarthy, 2014; Oiu et al., 2014). Postexposure protection with rNAPc2 in primates provides a new foundation for therapeutic regimens that target the disease process rather than viral replication (Qiu et al., 2014). Evidence from past outbreaks shows that transfusion of blood from recovering patients might be beneficial in the acute phase of infection and was associated with decreased mortality; now at the stage of clinical trials (Choi and Croyle, 2013). Adenosine analogues were found to inhibit in vitro, probably by blocking the cellular enzyme. S-adenosyl-L-homocysteine hydrolase, thereby indirectly limiting methylation of 5' cap of the viral messenger RNA (Thi et al., 2014; Choi and Croyle, 2013). ZMapp, a mixture of three humanized monoclonal antibodies targeted against three of the virus glycoprotein epitopes was engineered for expression in tobacco plant, currently may be the best option for treatment (WHO, 2014). Before the 2014 outbreak, ZMapp had established its protective role when given to non-human primates 24-48 hours after infection. Another study reported that the drug could save non-human primates if treatment is extended up to five days post infection (Furuta et al., 2009). Even though its safety or efficacy is not yet proven in humans, very small quantity (seven doses) was made available to infected individuals and only one of them died. Regardless of its potential, numbers are very little to make any inferences on the drug's safety and efficacy. However, additional doses are being developed with support from the US government (Warren et al., 2014).

TKM-Ebola is another drug, consisting of a mixture of small interfering RNAs targeted against EBOV RNA polymerase L and is produced using lipid nanoparticle technology. This is also shown to be promising in non-human primates and is equally effective against Marburg virus in guinea pigs and monkeys (Turone, 2014; Iversen et al., 2012). Brincidofovir, previously known as CMX-001, presently at phase III trial for the treatment of cytomegalovirus and adenovirus, is reported to be active against Ebola virus in vitro. Has been used in individuals with EVD in US under Emergency Investigational New Drug applications approved by the FDA, trials are underway in West Africa (Towner et al., 2004). Favipiravir (T-705), a potent antiviral, selectively inhibits viral RNA dependent RNA polymerase of many viruses including influenza viruses, West Nile virus, yellow fever virus, foot and mouth disease virus, other flaviviruses, arenaviruses, bunya viruses, and alphaviruses. The drug was approved in Japan for influenza pandemics and show potency against EBOV in mouse models (Fletcher et al., 2014). Another adenosine analogue (BCX-4430), shown to be active against Ebola virus in rodents, and thought to work by inhibiting viral RNA-dependent RNA polymerase. Is also active against flaviviruses, bunya viruses, arenaviruses, and paramyxoviruses. The drug has been shown to be protective in non-human primates and rodents, even when given 48 hours after infection with filoviruses; however, no study was carried out on humans (Xu et al., 1998). AVI-7537 is another antiviral agent consisting of antisense phosphorodiamidate morpholino oligomers (PMOs) that target Ebola virus VP24 gene and provide survival advantage to Ebola virus infected non-human primates (Ye and Yang, 2015). AVI-6002 consists of two PMOs (AV-7537 and AV-7539) and targets both VP24 and VP35 genes. AV-6002 have also undergone phase I clinical studies (Ledgerwood et al., 2017). Therapeutic agents used for other diseases, such as amiodarone, clomiphene, and chloroquine inhibit Ebola virus interactions with human cells in models and amiodarone will shortly be trialed in West Africa (Ledgerwood et  $al., 2017.$ 

### **Prevention and vaccine development**

Currently, no any vaccine is licensed against EBOV in humans; however, two experimental vaccines are at various stages of clinical trial. cAd3-ZEBOV, a chimpanzee derived adenovirus vector with an Ebola virus gene



inserted (Ledgerwood et al., 2017) is undergoing further evaluation in the United Kingdom. United States, Switzerland, and some African countries. rVSV-ZEBOV is attenuated form of vesicular stomatitis virus and has one of its genes replaced by an Ebola virus gene, is being evaluated on humans in the US. Another vaccine candidate, which uses a prime-boost protocol to increase immunogenicity with two distinct viral vectors administered at different doses (Ad26-EBOV and MVA-EBOV) is also available (Marzi et al., 2011). Report showed addition of Matrix-M adjuvant to the EBOV/Mak GP nanoparticles enhanced both B and T-cell immune stimulation, which may be critical for an Ebola subunit vaccine with broad and long lasting protective immunity (Bengtsson et al., 2017).

Considering high pathogenicity and rapid spread of EBOV and lack of appropriate vaccine. quarantine measures should be the first line of action and continued until an individual is tested negative (Marzi et al., 2011). Careful hygiene practices should be employed, hand washing with soap and water or an alcohol-based hand sanitizer is necessary. Always avoid contact with blood Sand body fluids (urine, feces, saliva, sweat, urine, vomit, breast milk, semen or vaginal secretions from suspected or established case (Ledgerwood et al., 2014). Handling of items that may have encountered infected person's blood or body fluids (clothes, bedding, needles, and medical equipment) should be avoided. Avoid contact with bats and nonhuman primates or blood, fluids, and raw meat prepared from these animals. Health care workers should wear appropriate personal protective equipment (Marzi et al., 2011). Report show good correlation between protection with antibody titer and antigen-specific T-cell responses to sGP or GP.

## **Conclusions**

Infection with EBOV is connected with broad spectrum of clinical diseases of which majority lack pathogenetic explanations. The form of its genetic evolution, strange properties and functional profile coupled with poorly understood complicated connection with the host are all subjects far from absolute

comprehension. Extended awareness and definition of the actual pathogenetic role of EBOV in human diseases, development of better diagnostic methods and algorithms including prophylaxis and drug development are crucial issues worth of efforts by the scientific community.

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