Ebola virus

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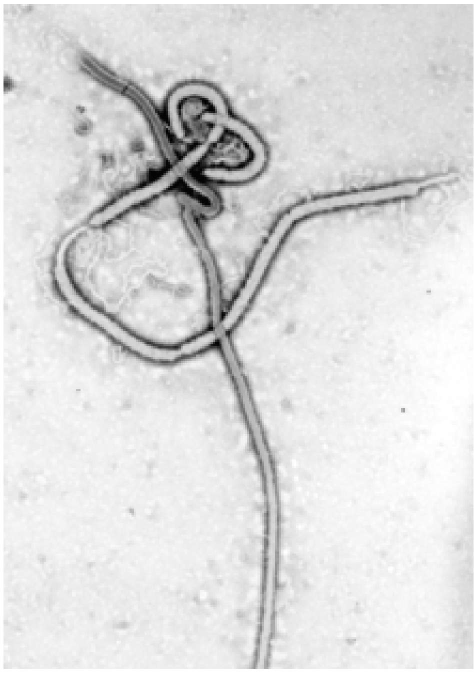
Ebola virus (**EBOV**, formerly designated **Zaire ebolavirus**) is one of five known viruses within the genus *Ebolavirus*.[1] Four of the five known ebolaviruses, including EBOV, cause a severe and often fatal hemorrhagic fever in humans and other mammals, known as Ebola virus disease (EVD). Ebola virus has caused the majority of human deaths from EVD, and is the cause of the 2013–2014 Ebola virus epidemic in West Africa, which has resulted in at least 13,567 suspected cases and 4,951 confirmed deaths.

Ebola virus and its genus were both originally named for Zaire (now the Democratic Republic of Congo), the country where it was first described,[1] and was at first suspected to be a new "strain" of the closely related Marburg virus.[2][3] The virus was renamed "Ebola virus" in 2010 to avoid confusion. Ebola virus is the single member of the species *Zaire ebolavirus*, which is the type species for the genus *Ebolavirus*, family *Filoviridae*, order *Mononegavirales*.[4][1] The natural reservoir of Ebola virus is believed to be bats, particularly fruit bats, and it is primarily transmitted between humans and from animals to humans through body fluids.[5]

The EBOV genome is a single-stranded RNA approximately 19,000 nucleotides long. It encodes seven structural proteins: nucleoprotein (NP), polymerase cofactor (VP35), (VP40), GP, transcription activator (VP30), VP24, and RNA polymerase (L).[6]

Because of its high mortality rate, EBOV is also listed as a select agent, World Health Organization Risk Group 4 Pathogen (requiring Biosafety Level 4-equivalent containment), a U.S. National Institutes of Health/National Institute of Allergy and Infectious Diseases Category A Priority Pathogen, U.S. CDC Centers for Disease Control and Prevention Category A Bioterrorism Agent, and listed as a Biological Agent for Export Control by the Australia Group.

Ebola virus (EBOV)

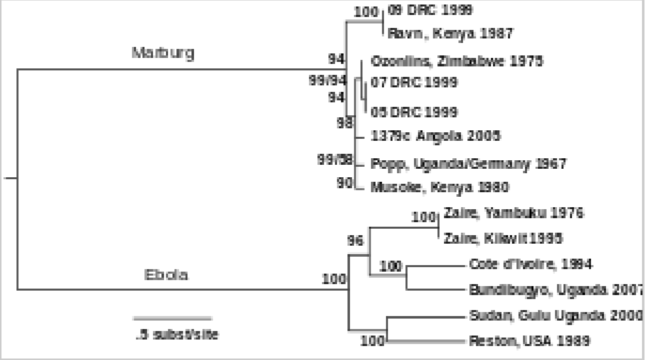


Virus classification

Group:	Group V ((-)ssRNA)
Order:	*Mononegavirales*
Family:	*Filoviridae*
Genus:	*Ebolavirus*
Species:	*Zaire ebolavirus*

Contents

Structure



Phylogenetic tree comparing ebolaviruses and marburgviruses. Numbers indicate percent confidence of branches.

EBOV carries a negative-sense RNA genome in virions that are cylindrical/tubular, and contain viral envelope, matrix, and nucleocapsid components. The overall cylinders are generally approximately 80 nm in diameter, and having a virally encoded glycoprotein (GP) projecting as 7-10 nm long spikes from its lipid bilayer surface.[7] The cylinders are of variable length, typically 800 nm, but sometimes up to 1000 nm long. The outer viral envelope of the virion is derived by budding from domains of host cell membrane into which the GP spikes have been inserted during their biosynthesis. Individual GP molecules appear with spacings of about 10 nm. Viral proteins VP40 and VP24 are located between the envelope and the nucleocapsid (see following), in the *matrix space*.[8] At the center of the virion structure is the nucleocapsid, which is composed of a series of viral proteins attached to a 18–19 kb linear, negative-sense RNA without 3′-polyadenylation or 5′-capping (see following); the RNA is helically wound and complexed with the NP, VP35, VP30, and L proteins;[9] this helix has a diameter of 80 nm and contains a central channel of 20–30 nm in diameter.

The overall shape of the virions after purification and visualization (e.g., by ultracentrifugation and electron microscopy, respectively) varies considerably; simple cylinders are far less prevalent than structures showing reversed direction, branches, and loops (e.g., U-, shepherd's crook-, 9- or eye bolt-shapes, or other or circular/coiled appearances), the origin of which may be in the laboratory techniques applied.[10] The characteristic "threadlike" structure is, however, a more general morphologic characteristic of filoviruses (alongside their GP-decorated viral envelope, RNA nucleocapsid, etc.).[10]

Genome

Each virion contains one molecule of linear, single-stranded, negative-sense RNA, 18,959 to 18,961 nucleotides in length. The 3′ terminus is not polyadenylated and the 5′ end is not capped. This viral genome codes for seven structural proteins and one non-structural protein. The gene order is 3′ – leader – NP – VP35 – VP40 – GP/sGP – VP30 – VP24 – L – trailer – 5′; with the leader and trailer being non-transcribed