



FIGURE 234-1 Filovirus phylogeny/evolution. Bayesian coalescent analysis of representative variants of all known filovirus clades (represented by underlined GenBank accession numbers). The maximal clade credibility tree is shown with the most recent common ancestor (MRCA) at each node. Posterior probability values are shown beneath MRCA estimates in years. Scale is in substitutions/site based on an analysis performed by Dr. Serena Carroll, Centers for Disease Control and Prevention. BDBV, Bundibugyo virus; EBOV, Ebola virus; LLOV, Lloviu virus; MARV, Marburg virus; RAVV, Ravn virus; RESTV, Reston virus; SUDV, Sudan virus; TAFV, Tai Forest virus.

EPIDEMIOLOGY



To date (i.e., as of December 3, 2014), a total of 20,012 human filovirus infections and 8058 fatalities have been recorded (Fig. 234-3). These numbers emphasize both the high degree of lethality (number of deaths per number of sick people; 40.3%) and the overall low mortality (impact on healthy population) of filovirus infections. At least for the moment, natural filovirus infections do not



FIGURE 234-2 Ebola virus particle: the first transmission electron micrograph of an Ebola virion in a culture of Vero cells inoculated with a blood sample from a patient from the 1976 Zaire outbreak of Ebola virus disease. Shown is the typical and unique filamentous and pleomorphic structure of filovirions. (PHIL ID#1833, taken by Dr. Fredrick A. Murphy, Centers for Disease Control and Prevention.)

pose a global threat. Filoviruses pathogenic for humans appear to be exclusively endemic to Equatorial Africa, although this distribution may change if natural or artificial environmental alterations lead to filovirus host migration and increased contacts between nonhuman hosts and humans (Fig. 234-4). The majority of recorded EVD and MVD outbreaks can be traced back to single index cases who transmitted the infection to others. These chains of contacts suggest that only around 50 natural host-to-human spillover events have occurred since the discovery of filoviruses in 1967. Outbreak frequency, case numbers, and overall lethality probably depend on the particular etiologic agent, the geographic location and socioeconomic conditions of the affected country, and local customs. In particular, the availability of personal protective gear and reusable medical equipment, such as syringes and needles, has affected overall case numbers in the past, and outbreaks have been contained when local burial practices, such as ritual washing, have been either prevented or altered by the use of gloves. The incidence of EVD and MVD may have increased over the past two decades (Figs. 234-3 and 234-4), but researchers debate whether the observed change is due to increased filovirus activity, more frequent contact between filovirus hosts and humans, or continuous improvement in surveillance capabilities.

EVD and MVD outbreaks are associated with distinct meteorologic and geographic conditions and are probably associated with distinct hosts or reservoirs. The four ebolaviruses that cause disease in humans are endemic in humid rainforests. EVD outbreaks have often been linked to hunting or contact with bush meat (i.e., meat from apes, other nonhuman primates, duikers, or bush pigs) in forests. Ecologic studies indicate that EBOV may be the etiologic agent of extensive and frequently fatal epizootics among wild chimpanzee and gorilla populations. However, replicating isolates of ebolaviruses from wild nonhuman primates have thus far been obtained only in the case of TAFV, which was isolated from a succumbed western chimpanzee in Côte d'Ivoire in 1994. The marburgviruses MARV and RAVV, on the other hand, seem to infect hosts inhabiting arid woodlands. MVD outbreaks have almost always been epidemiologically linked to visits to or work in natural or artificial caves or mines. A pteropid (fruit) bat, the cave-dwelling Egyptian rousette (*Rousettus aegyptiacus*), serves as a natural and subclinically infected reservoir for both MARV and RAVV. Although bats are suspected to be the hosts for ebolaviruses as