Ebola and great apes in Central Africa: current status and future needs.

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Zoonotic diseases, pathogens that transcend the “Darwinian divide”, have been in existence for as long as humans and animals have walked the Earth. Through the centuries, diseases such as the bubonic plague, rabies, anthrax, tuberculosis, rift valley fever, and salmonellosis, have crossed from the animal world to the human realm. Recently, zoonosis have captured international attention as SARS and Ebola outbreaks take their toll on human populations around the world. Ebola Hemorrhagic Fever Virus (EHFV) is only one of a hundred infectious agents that humans and great apes share in common.

Ebola has been known to the scientific and medical community since it was first identified in 1976 (1, 7). Since that time it has entered into human populations at least a dozen times in six different countries of Equatorial Africa. The most recent epidemic in Central Africa made headlines as gorilla (Gorilla gorilla), chimpanzee (Pan troglodytes) and human populations were hard hit (11). In a small area in Northwest Republic of Congo, this devastating disease killed over 100 humans and was estimated to have killed approximately 600 great apes from a population of roughly 1200. Entire family groups of gorillas and chimpanzees could not be found during and following the outbreak. This was associated with EHFV, which was confirmed by laboratory testing of samples collected from gorilla carcasses. Some family groups of gorillas survived even after members in the group died of EHFV. Though caused by a different strain of EHFV, this is consistent with observations in chimpanzee mortalities due to EHFV in the Côte-d’Ivoire, where some family group members died and others did not (2).

The worst-case scenario for EHFV in great apes may have been demonstrated in the Minkebe forest region of northeastern Gabon where lowland gorilla and chimpanzee populations have come close to disappearing during the period of the human EHFV outbreaks in 1994 and 1996 (3). Up to tens of thousands of gorillas and chimpanzees may have died due to EHFV. Unfortunately, no one was working in the forested areas during the human outbreak periods to collect either samples or observations on wildlife to determine conclusively if or how EHFV affected the ape populations.

Proceeding the 2002/2003 outbreaks, the Wildlife Conservation Society and ECOFAC had been working together to train national park and protected areas management staff in the Republic of Congo and the Republic of Gabon where lowland gorilla and chimpanzee populations have come close to disappearing during the period of the human EHFV outbreaks in 1994 and 1996 (3). Up to tens of thousands of gorillas and chimpanzees may have died due to EHFV. Unfortunately, no one was working in the forested areas during the human outbreak periods to collect either samples or observations on wildlife to determine conclusively if or how EHFV affected the ape populations.

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At the same time (4), suggesting the possibility of multiple reservoir species or a guild of species. Due to these trained teams being in place in anticipation of the subsequent EHFV epemics or another disease event, and equally essential, established relationships with local villagers and hunters, field teams were able to detect and report great ape mortalities due to EHFV weeks to months before the first human cases (9). In the last decade, assessment of EHFV outbreak index cases in Central Africa have shown a link with the handling of either EHFV infected gorillas or chimpanzees (4). Reducing the frequency of this contact route could reduce the incidence of human outbreaks as well as reduce the impact of hunting on gorilla and chimpanzee populations.

Work is still underway to identify the natural reservoir of EHFV. Laboratory experiments have shown not only that some species of bats (Chiroptera) can survive infection with EHFV, but the virus was observed to replicate in their blood and immune responses, in apparently healthy humans and primates, fragments and mosaics (6). That observation could help determine only the presence of the genetic material but not indicate live or viable virus. Other studies have shown the presence of antibodies, indicative of previous exposure and immune responses, in apparently healthy humans and primates in the Central African region (5, 6).

The scientific evidence to date suggests that EHFV is widespread in Equatorial Africa and persists in nature between observed outbreaks. At this time, the conditions in which the virus passes from its natural host or hosts, where it likely causes minimal disease problems at the population scale, to inadvertent host species which have lower survival rates are unknown. The rate of individual to individual spread of the disease in non-human species is also poorly understood. MORVAN et al. suggest that rather than being a virus of deep forest refugia, EHFV is actually more common in forest peripheries, fragments and mosaics (6). That observation could stem from the preferred habitats of the potential reservoir species or could be descriptive of the type of habitat in which transmission events among the reservoir species and other species are more likely to occur. Changes in climate or vegetation patterns with resultant changes in ecological relationships of animal populations may stimulate the transfer of the virus among species as is seen with other viral diseases. Though a mechanism has not been identified, correlations of EHFV outbreaks in humans with greater than average variance in climate and/or vegetation changes has been reported by PINZON et al. (8).

In order to better understand the disease caused by EHFV and develop methods to prevent its spread both in humans and wildlife (as well as understand and prevent the effects of other diseases on great apes) the following objectives need to be addressed:

1) anticipate EHFV outbreaks and populations at risk in order to provide better support to areas that could be affected by the virus;
2) establish monitoring teams to determine the existence and progression of the EHFV and other serious infectious disease agents in the forest, and their impact on wildlife (affected species, mortality rates and resistance, natural barriers, etc.);
3) establish response plans to alert appropriate people to findings of the presence of EHFV and other diseases;
4) improve knowledge of the EHFV and its ecology (reservoir, mode of transmission inter and intra-specific, strains, immunity, etc.);
5) evaluate ways of reducing the effect of EHFV and other infectious diseases on great apes using techniques such as vaccination programs, separation of reservoir species and affected species in time and space, meta-population management approaches, and other preventive medicine and hygiene practices.
6) using EHFV as an example of disease risks, improve local community education and awareness campaigns to reduce human contact with great apes and reduce hunting of great apes.

Références bibliographiques