



The Intricacies of Filovirus Emergence: Unravelling Ecological Trends, Reservoirs, Transmission, and Prevention Strategies

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Filoviruses, a group of zoonotic pathogens, have garnered infamy for their potent lethality, with mortality rates during outbreaks soaring to a staggering 90%. The complexities surrounding the host reservoir identification and the intricate cycle of transmission between animal hosts and humans have enshrouded filoviruses in mystery. Over the past decade, filovirus outbreaks have surged, marked by shifting epidemiological patterns. As these outbreaks continue to carry high fatality rates and with no effective antiviral drugs or preventive vaccines available, concerns have escalated, hinting at the looming potential of a global pandemic. The origin of filovirus outbreaks can be traced back to zoonotic events, where spillovers from wildlife reservoirs to humans trigger a chain reaction of human-to-human transmissions. In this context, the pivotal approach to curbing filovirus outbreaks lies in mitigating spillover occurrences and discerning the underlying risk factors.

The Causative Agents: A Closer Look at Filoviruses

Filoviruses belong to the family Filoviridae within the order Mononegavirales, constituting non-segmented negative-stranded RNA viruses. The filovirus family encompasses five genera: Ebolavirus, Marburgvirus, Cuevavirus, Striavirus, and Thamnovirus. The Ebolavirus genus stands out with six species, namely Zaire ebolavirus, Sudan ebolavirus, Tai Forest ebolavirus, Reston ebolavirus, Bundibugyo ebolavirus, and Bombali ebolavirus. Among these, Ebola virus (EBOV) is infamous for its virulence and threat.

The Marburgvirus genus consists of a sole species, Marburg marburgvirus, housing Marburg virus (MARV) and Ravn virus (RAVV). Other genera include Cuevavirus, Striavirus, and Thamnovirus, with their respective species and members. Notably, filovirus infections afflict six of the twelve identified filoviruses, signaling their potential to trigger disease in humans. The recent discovery of the Dianlovirus genus, characterized by Měnglà virus (MLAV) in China, unveils the complexity of filovirus diversity and transmission.

Ecological Trends in Filovirus Outbreaks

An epidemiological bifurcation defines most filovirus disease outbreaks, underscoring their distinct ecological contexts. The first category occurs in secluded forested regions, often linked to bush-meat consumption or wildlife interaction, resulting in a limited number of cases. The second category encompasses outbreaks in densely populated areas, where human-to-human transmission thrives, culminating in substantial case numbers. Forest-based outbreaks predominantly strike regions like Gabon, Uganda, and the Democratic Republic of Congo (DRC), attributed to the dense rainforest environment harbouring filovirus-reservoir animals. The surge in filovirus outbreaks correlates with intensified human-wildlife interaction propelled by deforestation, mining, and hunting activities. This increased contact

accentuates the probability of pathogen spillover from wildlife reservoirs to humans, intensifying the risk landscape.

The practice of consuming bush-meat, notably non-human primates that might be infected by fruit bats, serves as the initial trigger for human infections, followed by human-to-human transmission within communities and healthcare facilities. Informal and illegal wildlife trade magnifies outbreak risk by facilitating disease transmission between animals and humans. Additionally, climate change's impact on wildlife habitats contributes to the frequency of outbreaks, increasing human exposure to reservoir hosts.

Unmasking Reservoirs: A Puzzle of Culprits

Filovirus disease operates as a quintessential zoonotic ailment, often disseminated through direct contact with infected live or deceased animals. While bats play a pivotal role in filovirus transmission, other species like pigs, dogs, duikers, and non-human primates might also be involved. Bats have been identified as vital reservoirs, especially for the transmission of EBOV, yet the extent of their role remains nebulous. The catastrophic outbreaks in gorilla and chimpanzee populations unveil the threat filoviruses pose to great ape conservation.

Nonetheless, the exact reservoir hosts and the means of geographical virus spread remain enigmatic. Cave visits by index cases are frequently associated with the onset of filovirus infections, raising questions about how bats may transmit the virus to humans. Experimental studies demonstrate that filoviruses replicate significantly in various organs of fruit and insectivorous bats, illuminating potential transmission pathways. However, the intricate interplay between bats, humans, and non-human primates warrants further investigation.

Transmission Dynamics: Unravelling the Chain

The origins of human index cases remain elusive, often rooted in wildlife-to-human transmission through contact with reservoir fruit bats and intermediate hosts like monkeys, great apes, and pigs. The consumption of infected animals, especially bats, and the hunting of primates for sustenance perpetuate transmission in rural communities. Instances of human infections following outbreaks in wildlife populations underline the link between animal infections and human spillovers.

Secondary transmission occurs through close contact with infected patients and exposure to their bodily fluids. Unsafe burials, involving direct contact with deceased bodies, and traditional healing practices compound the transmission risk. Prolonged virus survival on surfaces after death further amplifies the potential for infection. Filoviruses have also been detected in a range of bodily fluids, including semen, raising concerns about sexual transmission.

Avenues for Prevention and Control

Effective strategies for tackling filovirus outbreaks entail early recognition, isolation of suspected cases, proper personal protective equipment (PPE) usage by healthcare workers, safe injections, rigorous contact management, culturally sensitive burial practices, and community engagement. Enhanced understanding of disease transmission and its prevention is indispensable.

In the complex realm of filovirus emergence, understanding ecological trends, identifying reservoirs, deciphering transmission dynamics, and implementing comprehensive prevention strategies are vital. By addressing these multifaceted aspects, societies can strive for a better grasp of filovirus outbreaks and work collectively to curtail their impact.

References

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