

Henipaviruses at the interface between bats, livestock and human population in af...

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Disease emergence results from the dynamic interactions between pathogen, animal and/or human hosts and the perpetually changing environment. These interactions are at the core of disease emergence, therefore understanding these drivers and impacts will allow an evidence-based risk assessment and the development of mitigation strategies that will enable an effective and timely response to new disease outbreaks (Wang et al. 2014).

The frugivorous bat species *Eidolon helvum*, is highly abundant particularly across the Sub-Saharan region and also present on some off-shore and isolated islands (Thomas and Henry, 2013). Fruit bat colonies undergo annual transcontinental migration following the rainfall gradient to suitable feeding grounds or the seasonal changes in food availability and was observed that migration of *E. helvum* was driven by abundance of food supply. Besides, with reports of individual bats covering more than 2500km yearly (Thomas. 1983, Richter and Cumming. 2006, Richter and Cumming. 2008, Ossa et al. 2012, Fahr et al. 2015). Generally, they roost in urban settlements and feed in close proximity to human and livestock populations thereby increasing the possibility of disease agents such as henipaviruses to cross species barriers and infect new hosts, resulting in putatively harmful or even fatal disease outbreaks (Peel et al. 2013).

In addition, husbandry practices/ management in developing nations in Africa allow close contact between bats and livestock populations since animals are mostly kept free-ranging. There is a high probability for bats to

contaminate their food, pasture and water with secretions and excretory products thus culminating to infection (Peel et al. 2013, Olufemi et al. 2015).

Moreover, deforestation causes degradation and severely impacts natural habitats of bats, forcing them to further migrate towards urban centers and thereby increasing the possibility of contact with domestic animals and humans potentially leading to cross-species transmission of viral agents (Weiss and McMichael, 2004, Wolfe, 2005, Lloyd-Smith et al. 2009, Murray and Daszak, 2013). In addition, bat migration towards urban centres could alter their feeding habits which might subsequently affect their immune responses by limiting their ability to combat or clear the viruses they harbor and possibly increase the probability of virus spillover to other species (Plowright et al. 2015, Plowright et al. 2017, Giles et al. 2018, Paez et al. 2018).

Indeed, socio-economic and cultural activities like bat hunting, sale, handling, butchering and consumption as bushmeat is one of the primordial risk factors associated with henipavirus spillover to human populations in Africa (Weiss et al. 2012, Pernet et al. 2014), and humans may also be infected through environmental contamination when they inhale virus particles from bats' secretion and excretion upon intrusion into bats' roost areas (Weiss et al. 2012). Although no specific disease symptoms have been associated with henipavirus infections in bats, pigs and humans in Africa (Hayman et al. 2008, Drexler et al. 2009, Pernet et al. 2014), there is a possibility of underreporting of clinical cases connected with such infections. This is especially the case since febrile flu-like infections in humans that may

also develop into encephalitis which occur frequently in Sub-Saharan Africa without further investigation into the infectious source. It is therefore important to continue the screening for such infections and to associate these virological results with clinical data of the sampled individuals.