

Re-examining the Origins of Ebola virus Emergence

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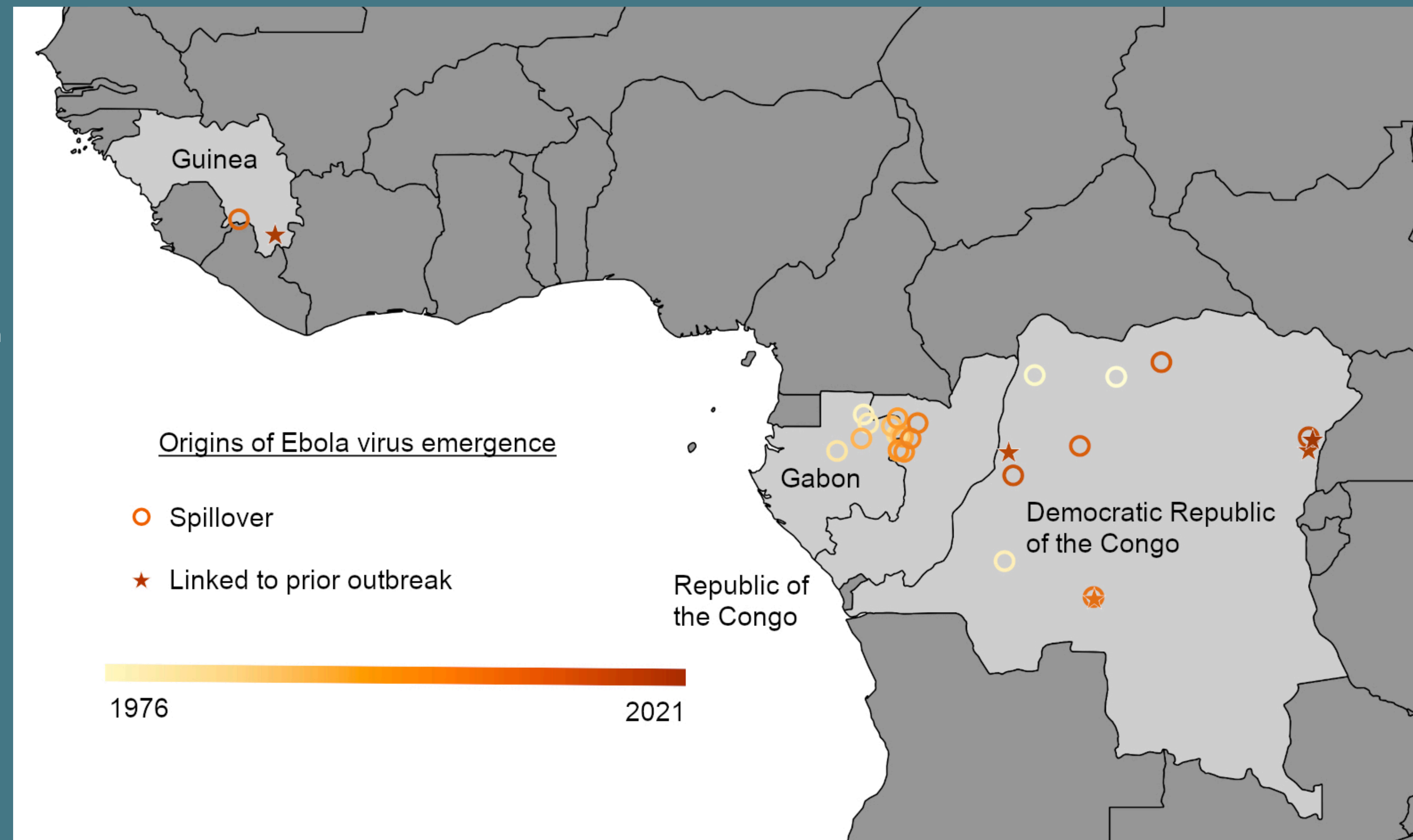
Introduction

Ebola virus (EBOV) is one of four ebolaviruses known to cause Ebola virus disease (EVD). It was originally thought that all EVD outbreaks originate from spillover of ebolaviruses from wildlife into humans.¹ However, phylogenetic analysis of EBOV sequences from recent EVD cases reveal genetic similarity to EBOV from prior outbreaks.² It is thought that these new EVD outbreaks have originated from delayed sexual transmission, reactivation of latent infection, or unrecognized chains of transmission among humans instead of spillover. Given this new knowledge, the aim of this study is to re-examine the origins and contexts of EVD outbreaks.

Methods

All known EVD outbreaks and EBOV emergence events from 1976-2022 were analyzed via literature review. The suspected primary and index cases for each outbreak were compared based on demographics and suspected sources of transmission. The diagnostic testing and treatment locations for each EVD index case were also investigated. Phylogenetic and epidemiologic relationships were examined to characterize whether outbreaks likely originated from separate spillover events or human-to-human transmission.

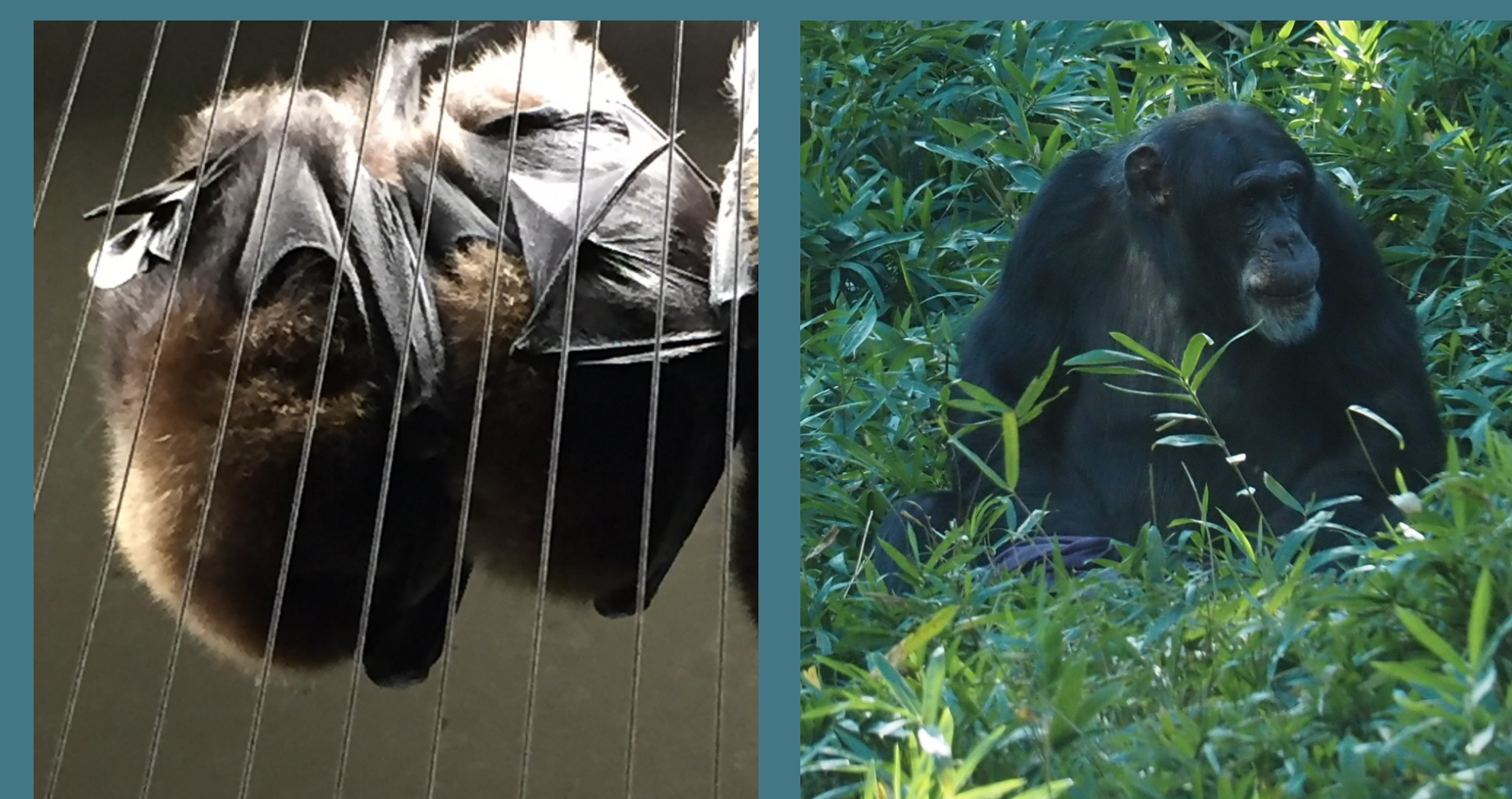
Results



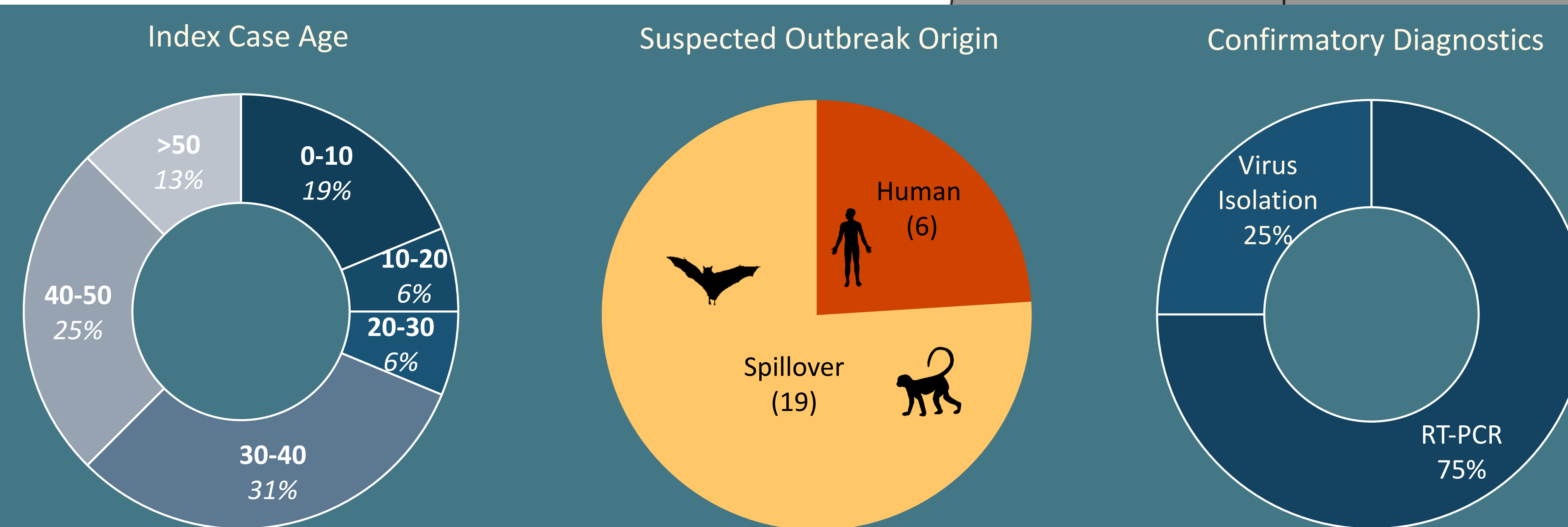
Origins of Ebola virus Disease Outbreaks 1976-2022*				
Year	Nation	Location	Suspected Origin	Cases (CFR %)
1976	DRC	Yambuku	spillover (antelope, monkey)	318 (88)
1977	DRC	Bonduni	spillover	1 (100)
1994	Gabon	Mékouka	spillover	52 (60)
1995	DRC	Kikwit	spillover	315 (81)
1996	Gabon	Mayibout	spillover	37 (57)
1996	Gabon	Booué	spillover (chimpanzee)	60 (75)
2001	Gabon	Mendemba	spillover (gorilla, duiker)	65 (82)
2001	ROC	Olooba	spillover (gorilla)	59 (75)
2003	ROC	Yembelangoye Mvoula	spillover (gorilla)	143 (90)
2003	ROC	Mbandza	spillover (monkey)	35 (83)
2005	ROC	Parc d'Odzala	spillover (gorilla, duiker)	12 (83)
2007	DRC	Luebo	spillover (bat)	264 (71)
2008	DRC	Luebo	2007 human vs spillover	32 (47)
2013	Guinea	Meliandou	spillover (bat)	28610 (40)
2014	DRC	Ikanamongo	spillover (monkey)	69 (71)
2017	DRC	Likati	spillover	8 (50)
2018	DRC	Ikoko-Impenge	spillover	54 (61)
2018	DRC	Mangina	spillover	3470 (66)
2020	DRC	Mbandaka	spillover and 2018 human	130 (42)
2021	DRC	Butembo	2018-2020 human	12 (50)
2021	Guinea	Gouéké	2013-2016 human	23 (52)
2021	DRC	Butsili	2018-2020 human	11 (55)
2022	DRC	Mbandaka	spillover	5 (100)
2022	DRC	Beni	2018-2020 human	TBD



Western Lowland Gorilla Duiker



Multiple bat species Chimpanzee



Conclusions

1. EVD outbreaks have been largely associated with wildlife spillover, however 5 of 6 outbreaks since 2020 have originated from human transmission from previous outbreaks.
2. Multiple recent EVD outbreaks with high case numbers have created the potential for future resurgence among humans.
3. We need to carefully re-evaluate the origins of EVD outbreaks through epidemiological and phylogenetic analyses to evaluate risk factors while also preventing stigma among survivors.

Wildlife associated with Ebola virus spillover
Photographs by Seth Judson, MD

References

1. Judson SD, et al. (2016) Ecological Contexts of Index Cases and Spillover Events of Different Ebolaviruses. PLoS Pathog 12(8): e1005780
2. Keita AK et al. (2021) Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. Nature 597(7877):539-543

