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Distribution and Seasonality of Potential Ebola Bat Reservoirs

Identification of the natural Ebola virus (EBOV) reservoir has remained elusive. Thirty-five mammalian species in Africa and Asia, including wild primates, rodents, carnivores, and ungulates, have tested positive via PCR or serology for at least one of the five different viral strains of Ebola virus (Bundibugyo, Cote d'Ivoire/Tai Forest, Reston, Sudan, Zaire)¹. Bats likely play a key role in EBOV ecology, with 23 species found positive or seropositive. Ten of these species occur in Africa (Table 1), where all human EBOV cases have originated.

To better understand spatial risk of EBOV spillover, the PREDICT-2 Modeling & Analytics team used ecological niche models to predict the spatial occurrence of these ten African bat species. In addition, to examine seasonal changes in spillover risk, we conducted a thorough literature review for these species to better understand the role of life history traits (Table 1) and reproductive seasonality (Table 2) in Ebola disease dynamics.

Table 1: Life-history traits of the ten potential African Ebola bat hosts.

			birth		
group	species	diet	periods	strain	source
Megachiroptera	Eidolon helvum	fruits	one	Reston, Sudan, Zaire	2,3
	Epomops franqueti	fruits	two	Zaire	4,5
	Epomorphus gambianus	fruits	two	Reston, Zaire	6
	Hypsignathus monstrosus	fruits	two	Zaire	4,5
	Micropteropus pusillus	fruits	two	Zaire	4
	Myonycteris torquata	fruits	two	Zaire	4,5
	Rousettus aegyptiacus	fruits	two	Zaire	4
	Nanonycteris veldkampii	fruits	two	Reston/Zaire	6
Microchiroptera	Mops condylurus	insects	two	Zaire	4
	Hipposideros gigas	insects	one	Zaire	4

GEOGRAPHY OF EBOV SPILLOVER RISK

An aggregate ecological niche model (ENM) for the ten potential bat EBOV reservoir species is shown in Figure 1. Pigott et al. (2014) modeled the zoonotic niche of EBOV using occurrence















data of three EBOV reservoirs: *E. franqueti, H. monstrosus*, and *M. torquata* as one component. We expanded this to include all known African EBOV-positive bat species and used an ensemble approach to minimize model uncertainty.

Gatherer (2014) proposed that the ranges of *H. monstrosus* and *M. torquata* overlapped Meliandou village in the Guéckédou Region of Guinea (location of the index for the 2014 Ebola outbreak)⁸. Thirteen species of bats have been captured in southeastern Guinea near this village, including four known EBOV hosts: *E. helvum*, *N. veldkampii*, *M. condylurus*, and *M. torquata*⁹. Our ENMs confirm the presence of three of these species, *E. helvum*, *N. veldkampii*, *M. torquata*, and suggested that *H. gigas* likely occurs there (Fig. 2).

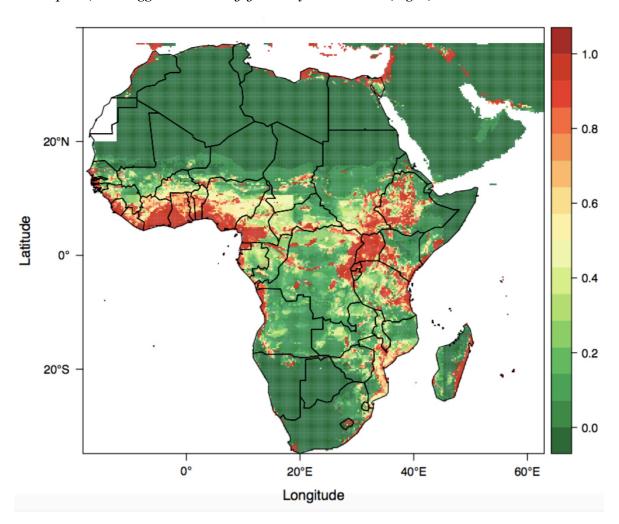


Figure 1. Stacked ecological niche models for the ten African bat species that potentially harbor the Ebola virus.

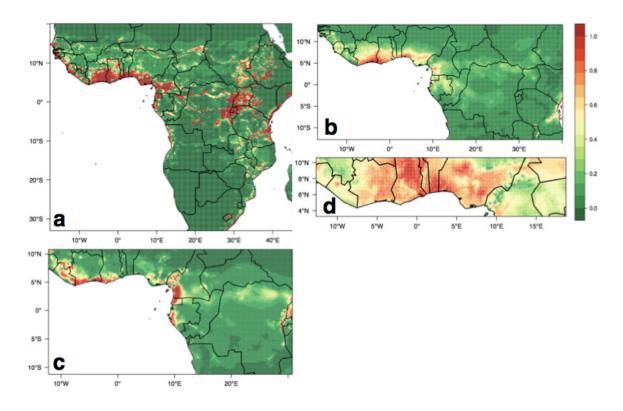


Figure 2. Ecological niche models for the four bats (a. E. helvum, b. H. gigas, c. M. torquata, d. N. veldkampii) whose suitable range include Meliandou village in Guinea, the index case of the 2014 EBOV outbreak.

POTENTIAL FOR SEASONALITY OF EBOV SPILLOVER RISK

Previous work has shown seasonal pulses of human Marburg virus cases, and of viral prevalence within the bat R. aegyptiacus. It is therefore logical that EBOV may also exhibit seasonal pulses within its bat reservoir hosts, tied to their life history traits. Bats have highly synchronous mating strategies, with the most energetically costly periods (late pregnancy and early lactation) occurring during the wet season, when food sources are most abundant 10. This provides two potential drivers for EBOV spillover: 1) population pulses of recently emerged susceptible juveniles may increase risk of viral transmission¹¹; and 2) abundant fruit in the wet season may increase the potential interface between humans and bats. Analysis of the literature for all likely EBOV bat reservoirs show that the reproductive cycles of West African bats exhibit birth periods from February-to-April and August-to-October, at the onset of the wet seasons (Table 2). Weaning and first flight of juvenile bats is most often during peak rainfall of May – June. These patterns suggest that there is a reasonable likelihood that seasonal patterns of EBOV spillover risk occur, perhaps with two peaks per year, at the time when maternal antibodies wane in juvenile bats, a few weeks after birth. PREDICT surveillance plans will need to include multiple field visits each year to analyze the change in viral spillover risk over time and identify peak seasonal risk.

CONCLUSIONS

- 1. Ensemble Ecological Niche Modeling of all 10 likely EBOV bat reservoirs suggests widespread risk of future EBOV spillover across West and Central Africa, and provides fine scale risk maps to target surveillance.
- Analysis of life history traits for all likely EBOV bat reservoirs reveals evidence of seasonality that could drive seasonal spikes of EBOV spillover risk, perhaps with two peaks each year. Surveillance of EBOV in bats will therefore need to be planned to examine these seasonal fluctuations.

Table 2: Reproductive cycles of the West African bats that have demonstrated evidence of EBOV exposure. *Key*: G, gestation; P, parturition; L, lactation; W, weaning. Blue fill shows the wet seasons for West Africa.

Species	Jan	Feb	Mar	Apr	May	Jun	July	Aug	Sep	Oct	Nov	Dec
E. helvum ¹²	G	G	GP	PL	L	W			G	G	G	G
$E.\ gambianus^{13,14}$	G	G	GL	PL	PL	GW	GW	G	G	PL	G	G
H. gigas¹5	L	L	L	L	LW	W	G	G	G	GP	L	L
H. monstrosus ¹⁶	G	GP	PL	L	W	G	G	GP	PL	L	W	G
$M.\ pusillus^{13}$	G	P	PL	L	GL	GW	G	P	PL	L	GL	G
$M.\ torquata^{17}$	G	P	PL	L	GW	GW	G	P	PL	L	GW	GW
N. veldkampii ^{14,18}	GL	G	G	G	P	PL	L	G	G	G	GP	PL

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