Victoria

Viral circulation and sharing in sympatric bat and rodent species living at the interface with humans and potential risks of zoonotic spillover in southern Africa

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EDIFICE
BIOLOGY OF VIRAL INFECTIONS

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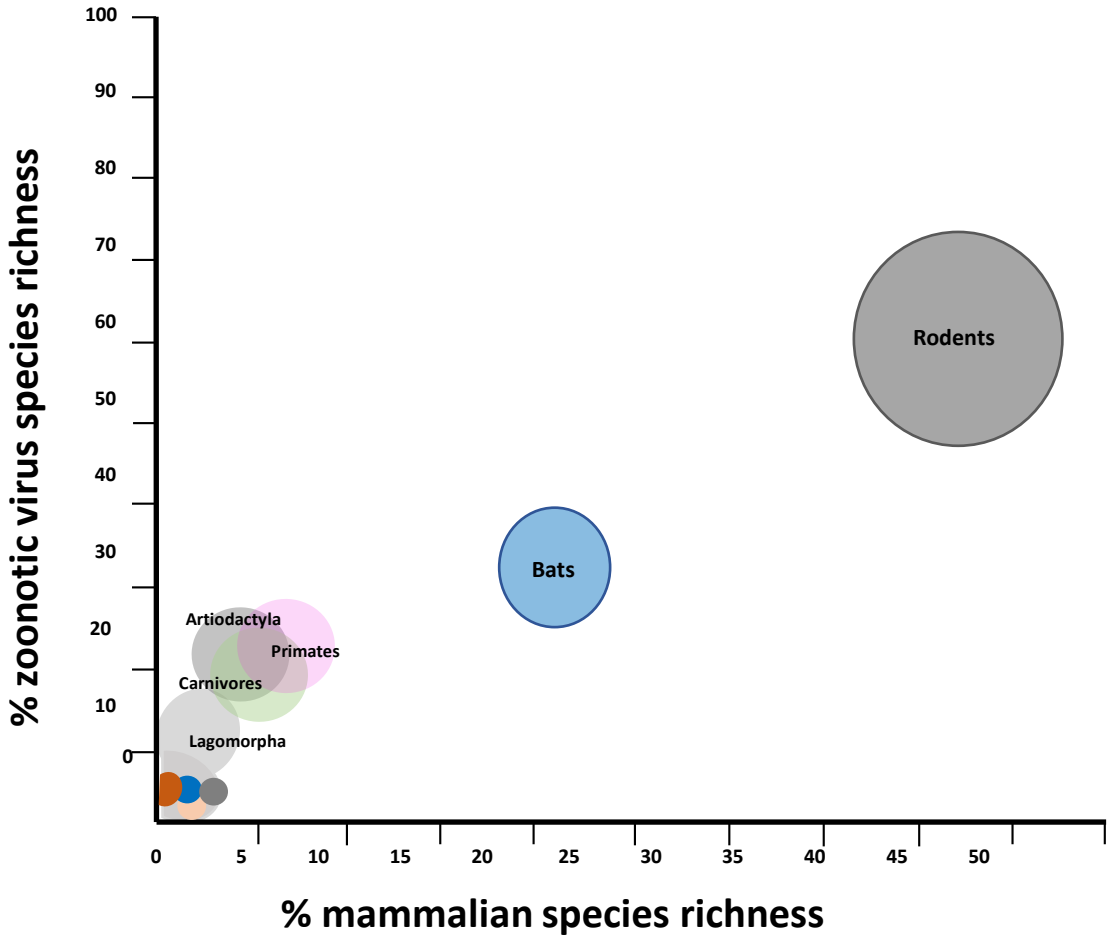
A large number of viral studies on bats and rodents



Erica S. Neves et al 2021

Genetic diversity and expanded host range of astroviruses detected in small mammals

Marina Escalera-Zamudio et al 2015

A Novel Endogenous Betaretrovirus in the Common Vampire Bat (Desmodus rotundus) Suggests Multiple Independent Infection and Cross-Species Transmission Events

A. Berto et al, 2016

Detection of potentially novel paramyxovirus and coronavirus viral RNA in bats and rats in the Mekong Delta region of southern Viet Nam

William Marciel de Souza et al 2018

Discovery of novel anelloviruses in small mammals expands the host range and diversity of the Anelloviridae

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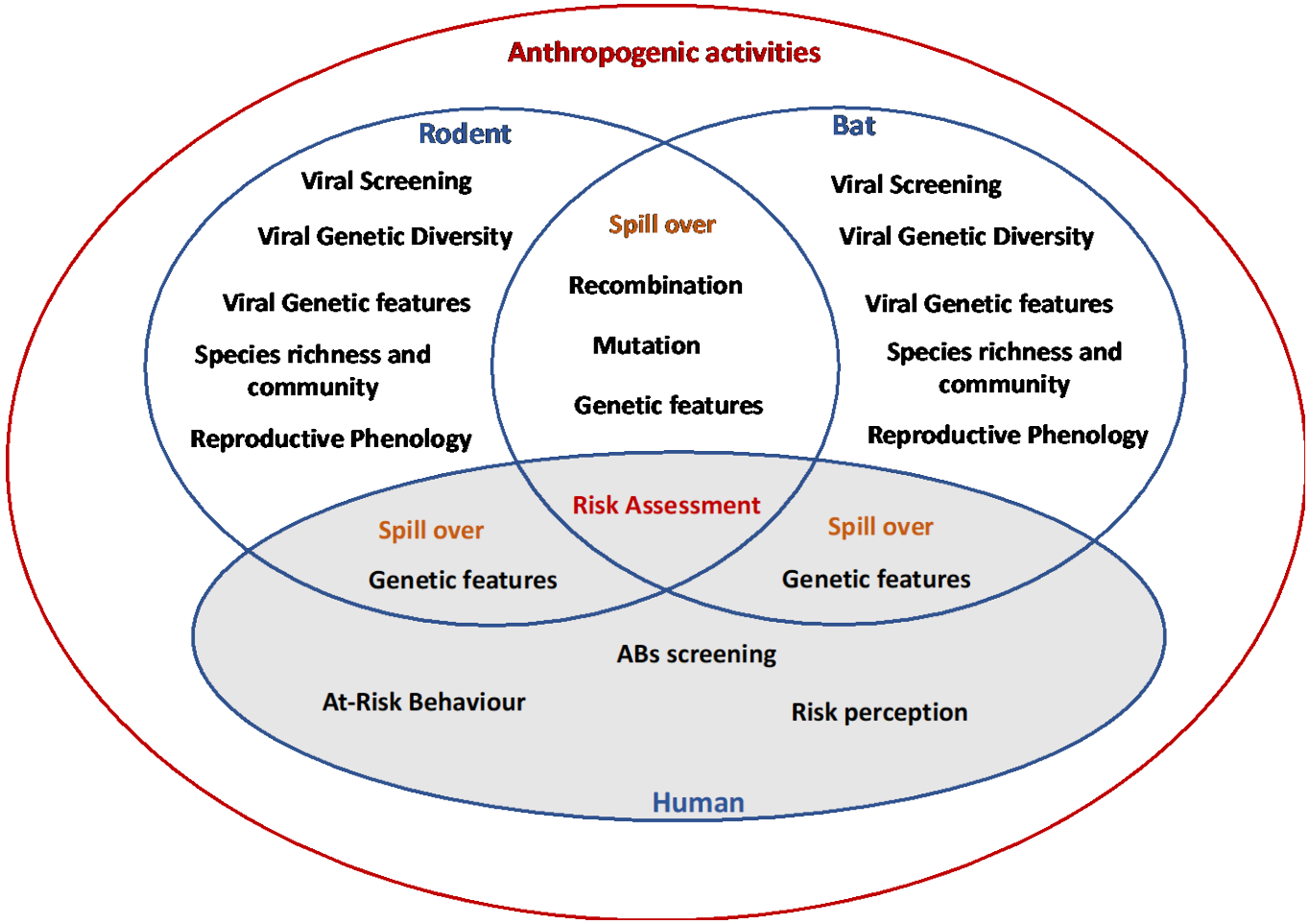
One Health approach



1/ Characterize diversity and prevalence of potentially zoonotic *Corona-*, *Astro-* and *Paramyxovirus* in bat and rodent species sharing the same habitat

2/ Investigate viral sharing and transmission dynamics between these sympatric bats and rodents

3/ Assess exposure of humans, and risks of spillover

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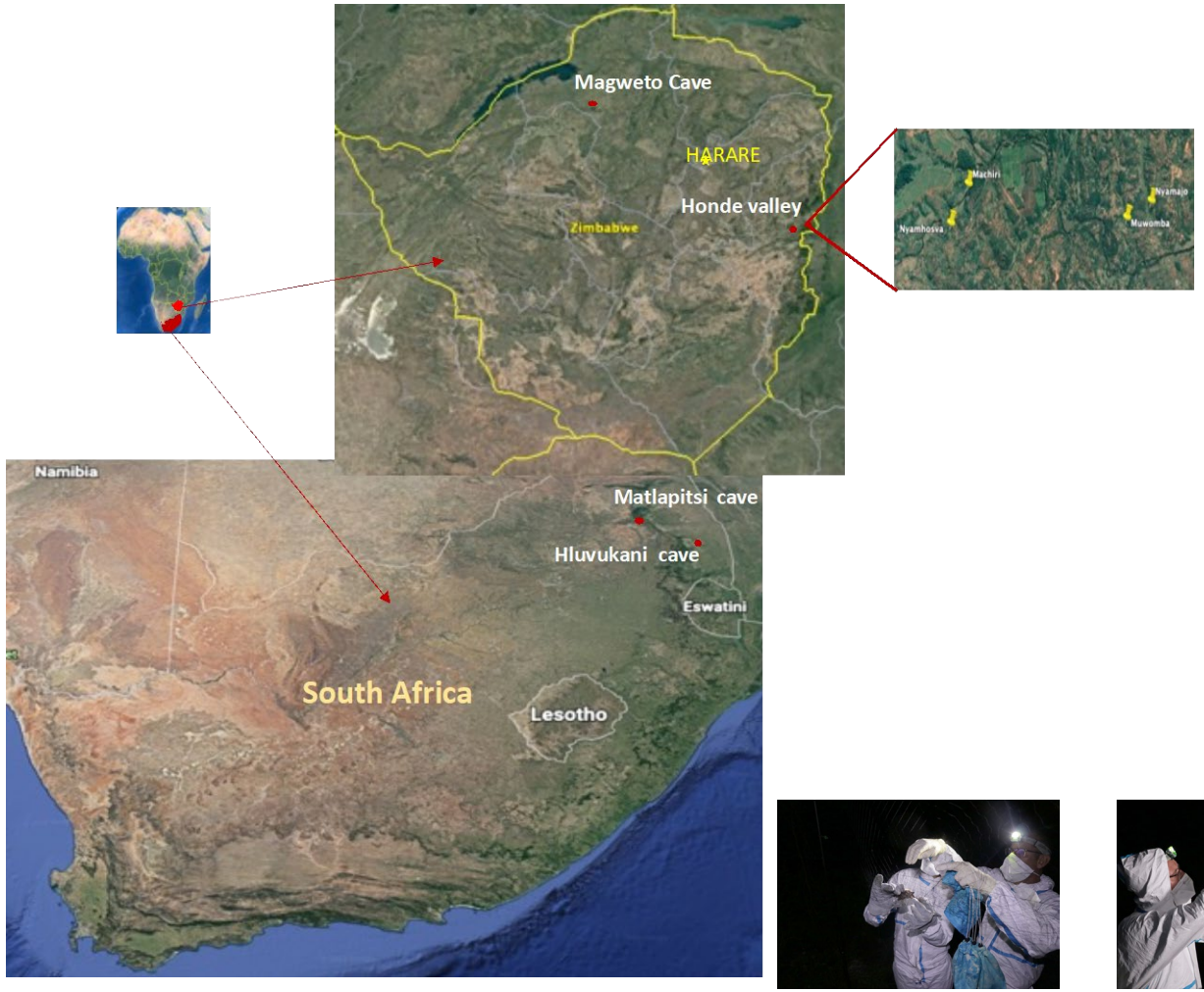
SITES

Bats = 1000 samples/site
Rodents= 600 samples/site



WP-1: Longitudinal monitoring of bat and rodent communities

WP-2: Detection and characterisation of potentially zoonotic viruses in bats and rodents

WP-3: Characterization of human exposure and community perception of zoonotic risks

WP-4: Data analysis and zoonotic spillover risks

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WP-1: Longitudinal monitoring of bat and rodent communities

Data collection and sampling sessions will be carried out every two months on each site for the first two years of the project, hence 12 sessions per site over the study period, in order to cover different seasons of the year.

WP-2: Detection and characterisation of potentially zoonotic viruses in bats and rodents

1/ To identify the different strains of *Corona-*, *Astro-* and *Paramyxoviruses* circulating in rodents and bats,

2/ To estimate prevalence of the main strains for each site and sample session

3/ To determine the genetic features of these viruses and more particularly the binding receptor domains allowing the attachment and fusion of the viral particles to their target cells

4/ To evidence, according to their genetic characteristics and their phylogenetic relationship, the events of species jump between bats and rodents,

5/ To determine and synthetize the antigenic determinants (epitope) or produce recombinant proteins needs for the realization of the WP-3

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WP-3: Characterization of human exposure and community perception of zoonotic risks

1/ To obtain human blood samples for serological analysis

2/ To set up serological assays with the Multiplex Bead Assay method (Luminex),

3/ To determine whether human population has been in contact with zoonotic viruses,

4/ To identify at-risk behaviours for zoonotic transmissions from bats and rodents and assess

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WP-4: Data analysis and zoonotic spillover risks

WP4 will focus on the risk of exposure to transmissions of zoonotic viruses from the small mammal community

1/ To characterize the viral profile of the species composing the small mammal communities in the different study sites and to identify the species with similar or different viral profiles.

2/ To Integrate the species level viral profiles within each site in order to characterize the viral profiles at the small mammal community level and to infer the network of virus transmissions among species.

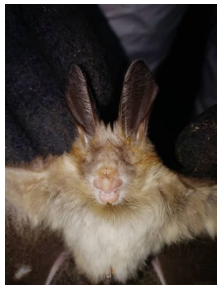
3/ To investigate within year variation in the community viral profile with regard to variation in its composition and to the timing of births (which result in inflows of susceptible individuals in the community).

4/ To identify behavior in humans that can result in transmissions of zoonotic viruses from the studied small mammal communities (especially behavior related with the consumption or manipulation of small mammals, the use of bats' guano as fertilizers, the use of caves) and to identify the viruses that are likely to be transmitted.

5/ **To investigate** variation among individuals in the human community in the risk of exposure to transmissions of zoonotic viruses from the small mammal community and to assess whether such variation result in variation in infections by zoonotic viruses

The final objective of WP4 is to draw predictions regarding the ranking of this risk among the identified zoonotic viruses within each study site as well as among study sites for each identified zoonotic virus.

Longitudinal Survey of Coronavirus Circulation and Diversity in Insectivorous Bat Colonies in Zimbabwe



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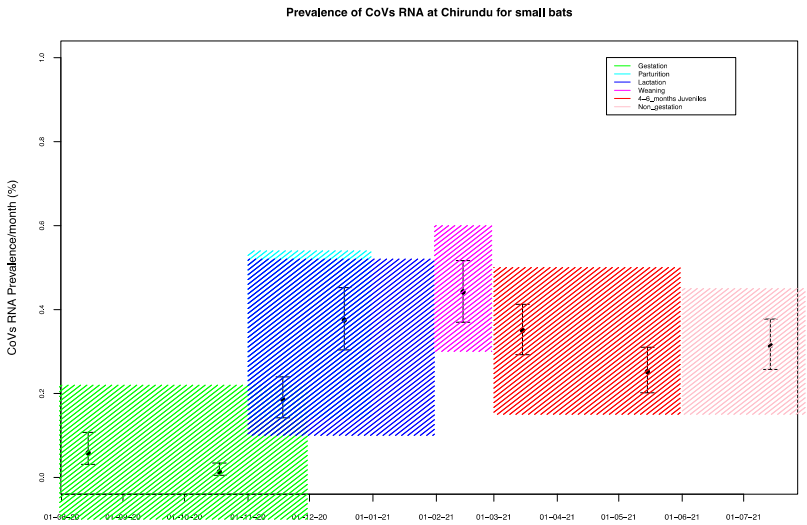

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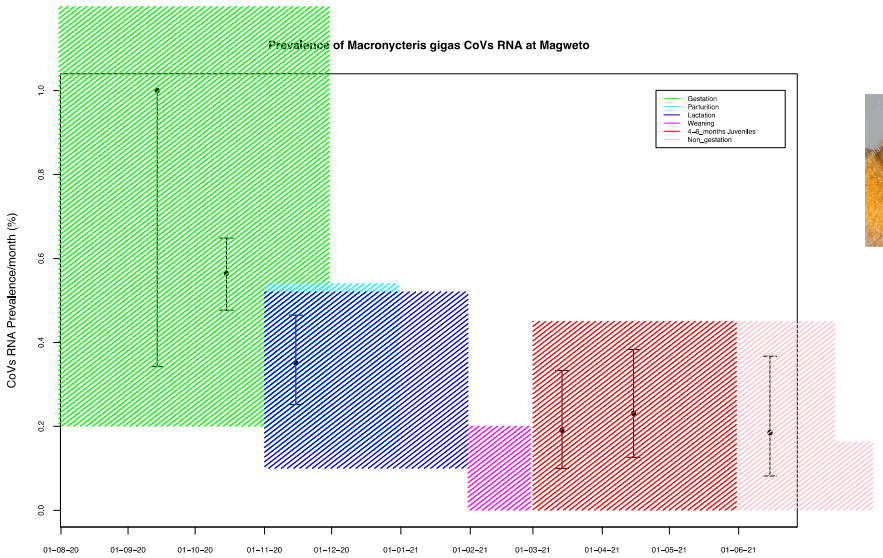

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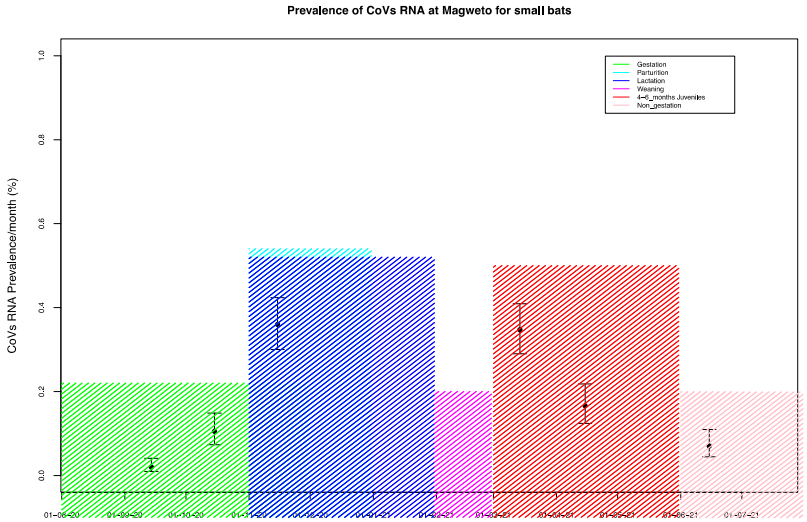


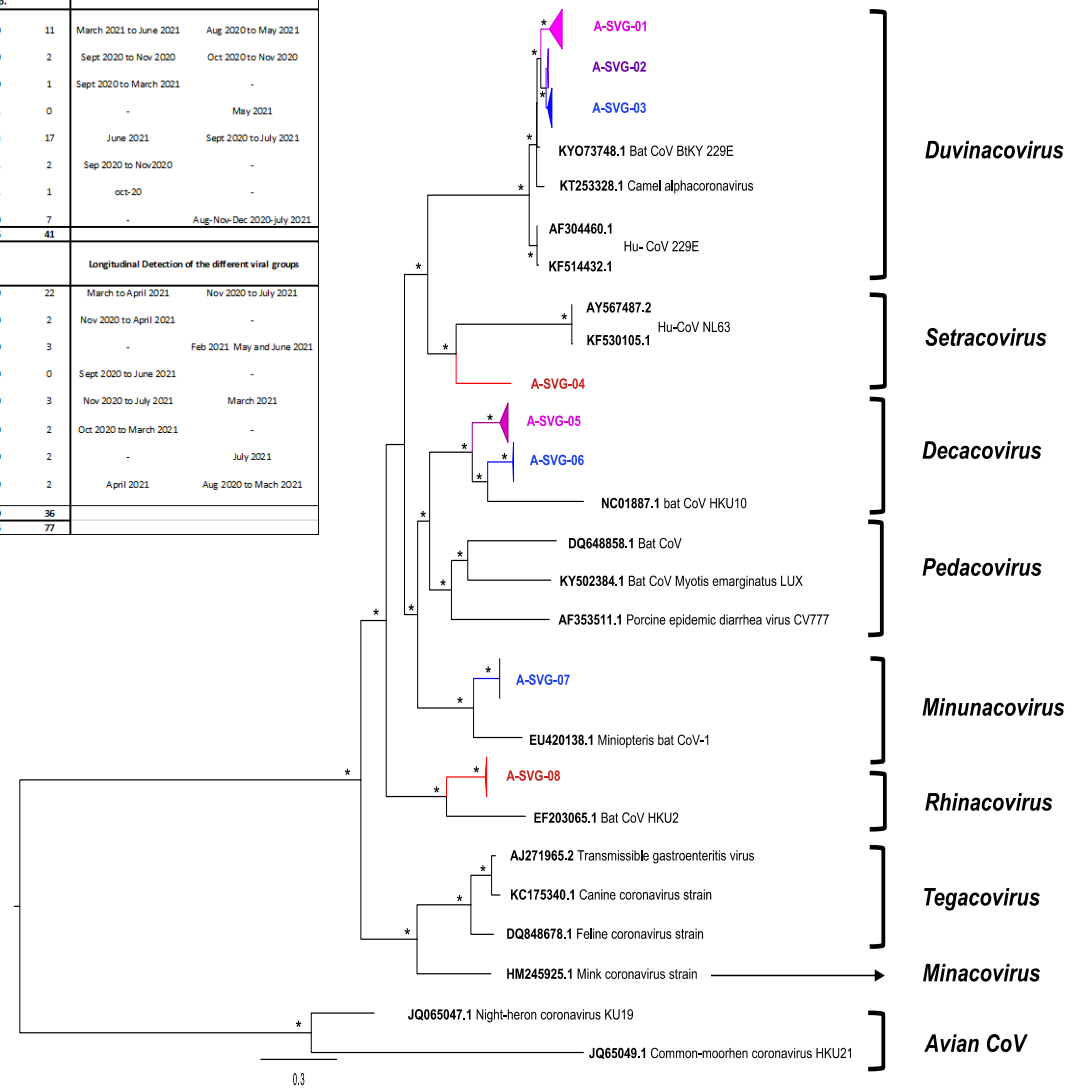
Higher *Coronavirus* prevalence associated with the parturition/lactation period

Chidoti et al, 2022

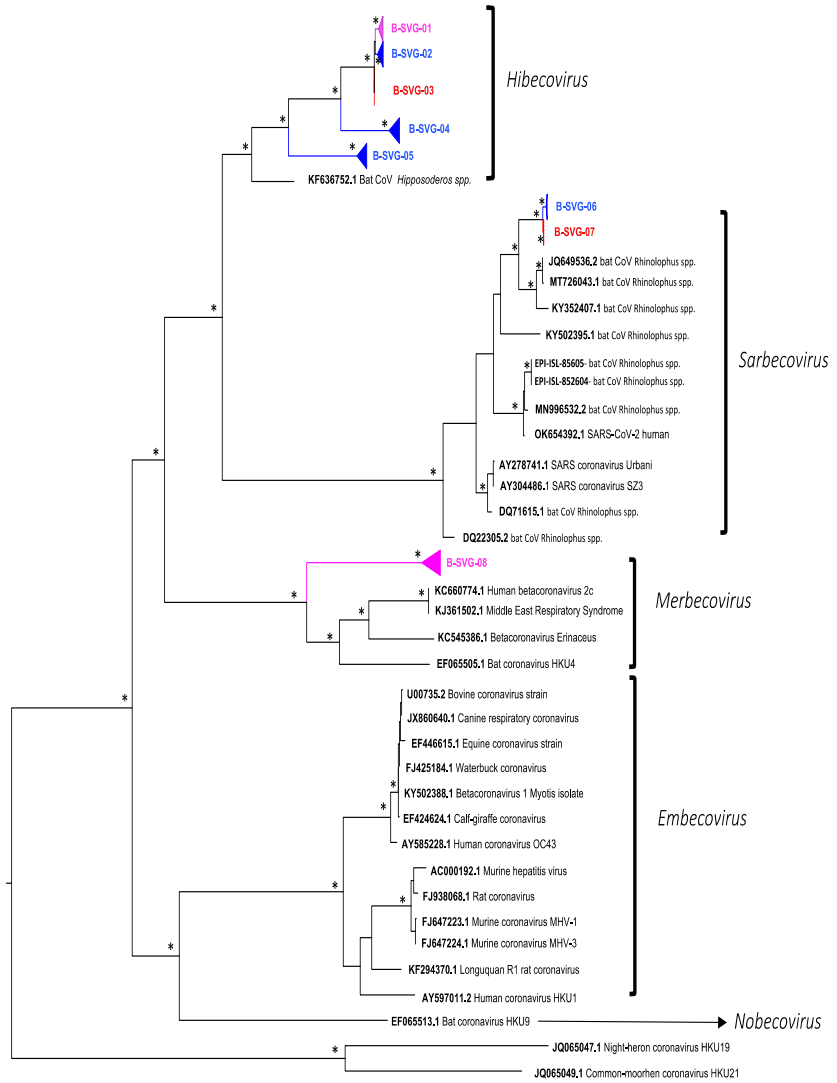
Longitudinal Survey of Coronavirus Circulation and Diversity in Insectivorous Bat Colonies in Zimbabwe

		Number of Sequence per site		Number of sequence per Bat species						Longitudinal Detection of the different viral groups	
Viral Group	total number of sequence	Magweto	Chirundu	Hipposideros spp.	Macronycteris spp.	Rhinolophe spp.	Nycteris spp.	Miniopterus spp.	unknown	Magweto	Chirundu
A-SVG-01	114	8	106	89	4	3	7	0	11	March 2021 to June 2021	Aug 2020 to May 2021
A-SVG-02	45	42	3	0	41	2	0	0	2	Sept 2020 to Nov 2020	Oct 2020 to Nov 2020
A-SVG-03	32	32	0	29	0	2	0	0	1	Sept 2020 to March 2021	-
A-SVG-04	1	0	1	0	0	0	0	1	0	-	May 2021
A-SVG-05	84	6	78	7	4	52	1	3	17	June 2021	Sept 2020 to July 2021
A-SVG-06	13	13	0	1	0	9	0	1	2	Sep 2020 to Nov2020	-
A-SVG-07	2	2	0	0	0	0	0	1	1	oct-20	-
A-SVG-08	16	0	16	0	0	8	1	0	7	-	Aug-Nov-Dec 2020-july 2021
sub Total	307	103	204	126	49	76	9	6	41		
		Number of Sequence per site		Number of sequence per Bat species						Longitudinal Detection of the different viral groups	
B-SVG-01	105	5	100	76	2	4	1	0	22	March to April 2021	Nov 2020 to July 2021
B-SVG-02	21	21	0	19	0	0	0	0	2	Nov 2020 to April 2021	-
B-SVG-03	6	0	6	2	0	1	0	0	3	-	Feb 2021 May and June 2021
B-SVG-04	13	13	0	0	13	0	0	0	0	Sept 2020 to June 2021	-
B-SVG-05	51	51	0	48	0	0	0	0	3	Nov 2020 to July 2021	March 2021
B-SVG-06	8	8	0	0	0	5	1	0	2	Oct 2020 to March 2021	-
B-SVG-07	4	0	4	0	0	2	0	0	2	-	July 2021
B-SVG-08	17	3	14	8	0	1	6	0	2	April 2021	Aug 2020 to Mach 2021
sub Total	225	101	124	153	15	13	8	0	36		
TOTAL	532	204	328	279	64	89	17	6	77		

α-CoV

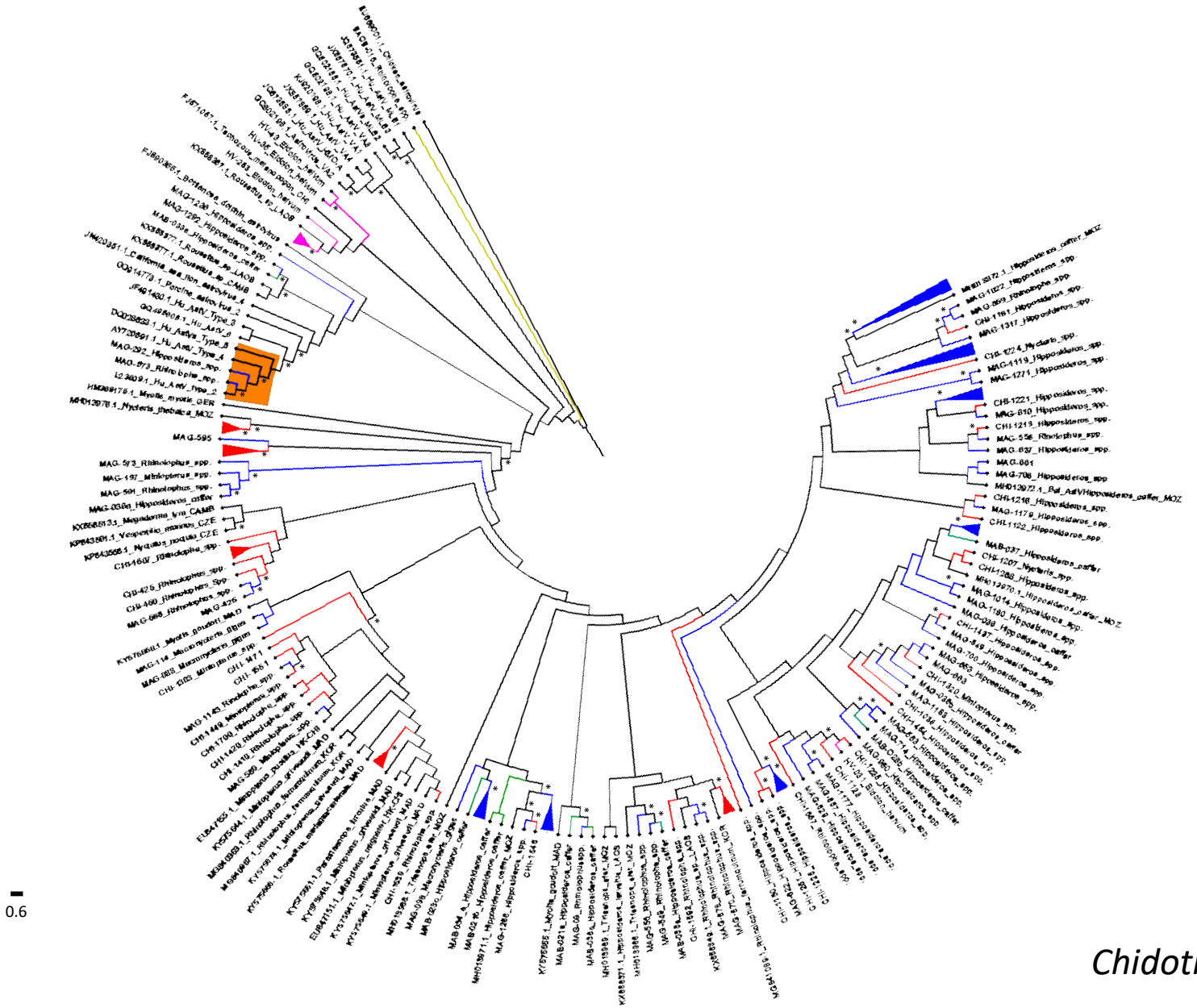


β-CoV



Chidoti et *al, 2022*

Evidence of high Astrovirus diversity in different bat species in Zimbabwe



Chidoti et al, en preparation

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