

# The detection of diverse coronaviruses, including MERS-related coronaviruses, in South African bat populations and their associated ecology in *Neoromicia capensis*


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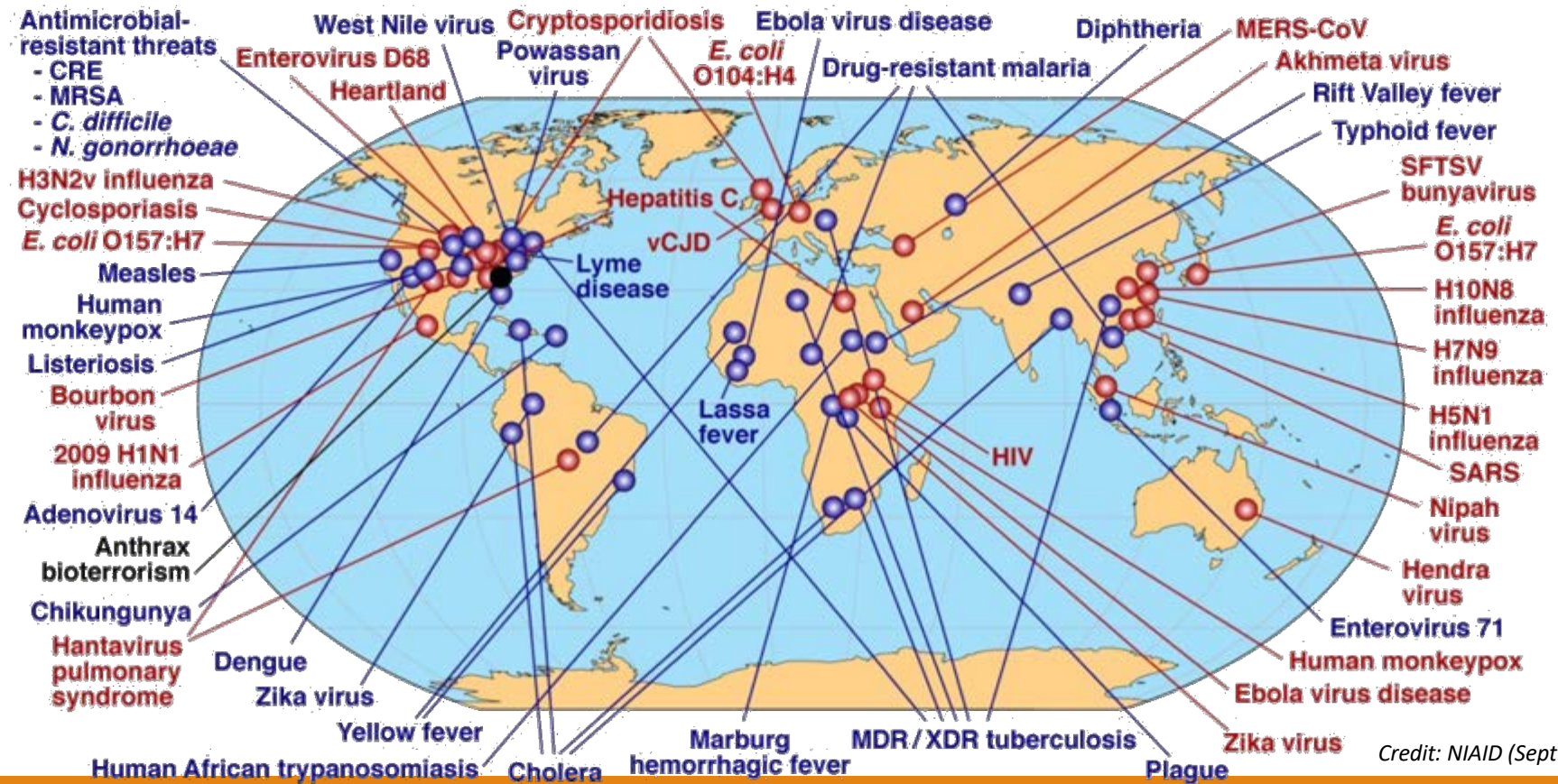
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# EMERGING INFECTIOUS DISEASES

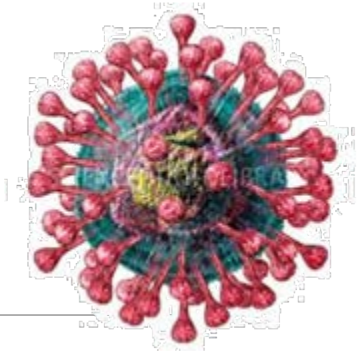
## – WHY ARE THEY IMPORTANT?

Infectious diseases continue to be a **major cause of human suffering and death** around the world.

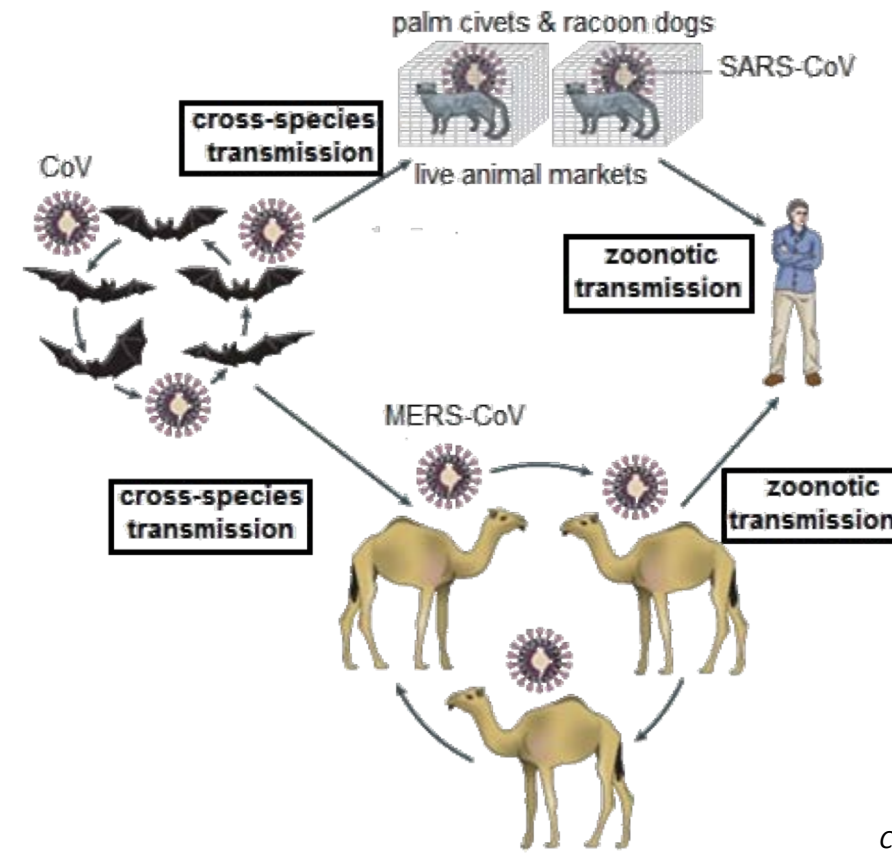


Credit: NIAID (Sept 2017)

# CORONAVIRUSES (CoV)



- ❖ RNA viruses:  $\alpha$ ,  $\beta$ ,  $\gamma$ ,  $\delta$  genera
- ❖ infect wide range of species: **veterinary and public health**
- ❖ in humans:  $\alpha$  &  $\beta$  CoVs commonly cause **mild respiratory illness**:
  - ❖ hCoV-NL63, hCoV-OC43, hCoV-229E
- ❖ **but**: outbreaks of severe respiratory disease in 2002 & 2012: highly pathogenic hCoVs, **SARS-CoV & MERS-CoV**



Credit: de Wit et al. (2016)

# BATS AS RESERVOIR HOSTS OF CORONAVIRUSES

- ❖ bats are considered ancestral hosts for **all mammalian  $\alpha$  &  $\beta$  CoVs**
- ❖ wide diversity of bat CoVs described worldwide
  - ❖ few studies published from South Africa
- ❖ a **MERS-related CoV** was previously detected by our group in a ***Neoromicia capensis* bat**
  - ❖ NeoCoV



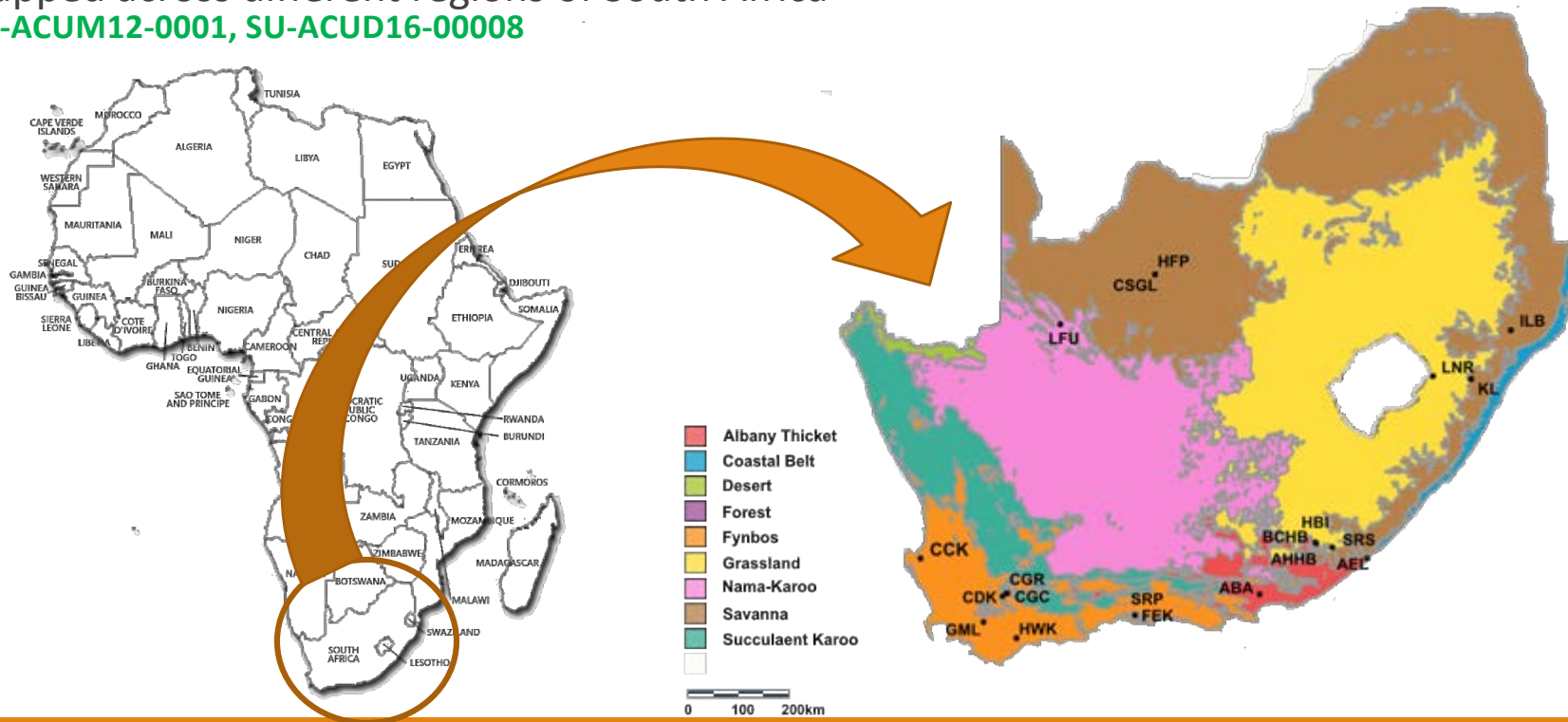
Credit: IUCN Red List (2017)



# METHODS

SAMPLES: **bat faecal pellets** obtained through collaboration with trained zoologists, bats trapped across different regions of South Africa

**SU-ACUM12-0001, SU-ACUD16-00008**



# METHODS

## GENERAL SURVEILLANCE

404 bat faecal pellets collected from  
20 different bat species

- ❖ viral RNA screening by conventional PCR: target = conserved region of RNA dependent RNA polymerase (RdRp)
  - ❖ de Souza Luna et al. 2007, Drexler et al. 2010 (adapted)
- ❖ ecological sampling data collated with *N. capensis* screening results
  - ❖ mixed effects logistic regression analyses
    - ❖ biome, alt., rainfall, sex, rep. state, FMI, weight, temp.

## SPECIES-SPECIFIC SURVEILLANCE

183 faecal pellets collected from  
*Neoromicia capensis* bats



# RESULTS: surveillance studies

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## GENERAL SURVEILLANCE

- ❖ **overall 19 (4.7 %) samples**  
positive
- ❖ **8 different bat species**
- ❖ putative classification:  
**8 different CoV species**

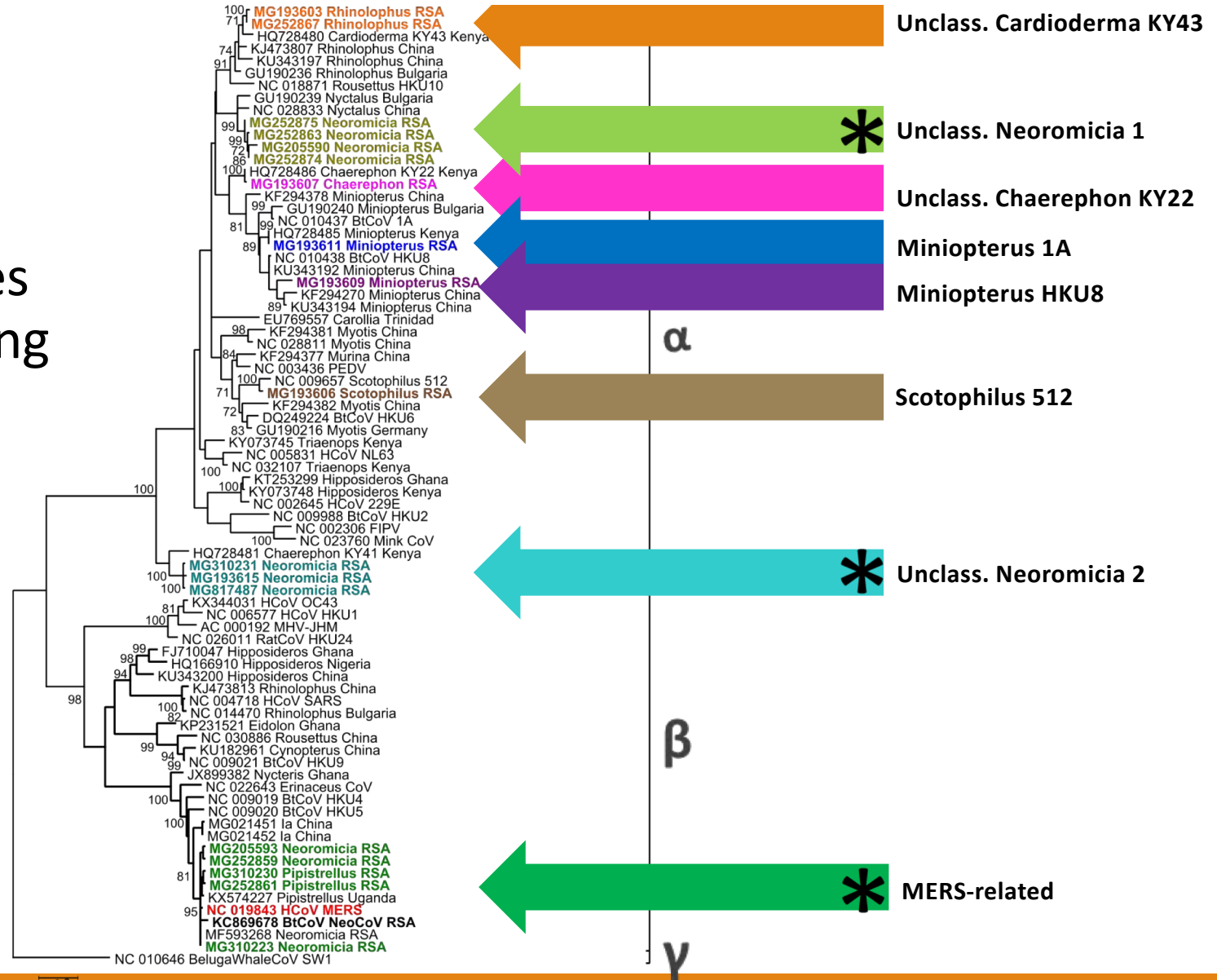
## SPECIES-SPECIFIC SURVEILLANCE

- ❖ **overall 66 (36.1 %) samples**  
positive
- ❖ **14 instances of coinfection:**  
**80 CoV sequences**
- ❖ putative classification:  
**3 different CoV species**

# Coronaviruses detected during this study

Maximum Likelihood  
 (RdRp aa)  
 LG + G + I

\* *N. capensis* surveillance





# RESULTS: logistic regression analyses

- ❖ best model: CoV positive  $\sim 1 + \text{sex} + \text{altitude} + \text{body condition}$
- ❖ significant factors: **sex** (female) **altitude** (low) **body condition** (low FMI)

Predictor	Coeff.	Wald's $\chi^2$	df	p-value	Std error	Confidence interval (95%)		Odds ratio	Confidence interval (95%)	
						Lower limit	Upper limit		Lower limit	Upper limit
sex: female	1.37	3.05	1	<b>&lt;0.01</b>	0.45	-2.25	2.25	<b>3.94</b>	0.11	9.52
altitude	-0.58	-2.60	1	<b>0.01</b>	0.22	-1.02	-0.14	<b>0.56</b>	0.36	0.87
body condition	-0.41	-2.14	1	<b>0.03</b>	0.19	-0.79	-0.04	<b>0.66</b>	0.45	0.97

# CONCLUDING REMARKS

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- ❖ **diverse CoVs are present** in different South African bat species
- ❖ **ongoing circulation of MERS-related CoVs** in our region is likely
- ❖ observed cases of **coinfection indicate potential for recombination**
- ❖ collating ecological data with screening results indicated that **intrinsic and extrinsic factors** may influence coronavirus positivity in *Neoromicia capensis* bats

**These findings could assist the development of improved wildlife surveillance strategies for better detection of novel bat coronaviruses.**

# ACKNOWLEDGEMENTS

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## Sample collection

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- ❖ Prof. Corrie Schoeman
- ❖ Prof. Wolfgang Preiser

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## Technical Services

- ❖ SU CAF: Sequencing electrophoresis

