

Feeding preference of Rift Valley fever mosquitoes at a wildlife-livestock interface in South Africa

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Introduction

- Rift Valley fever (RVF) is an epizootic disease caused by RVFV virus (Family Phenuiviridae, genus *Phlebovirus*) and mainly transmitted by mosquitoes of the *Aedes* and *Culex* genera.
- RVF causes severe illness, newborn deaths and abortion in ruminants including domestic and wild animals.
- The first epizootic described in South Africa was between 1950-1951. Another two major epidemics were reported in 1973-1976 and 2010-2011, affecting even wildlife species in the Kruger National Park (KNP) such as the African buffalo (*Syncerus caffer*) [1,2].

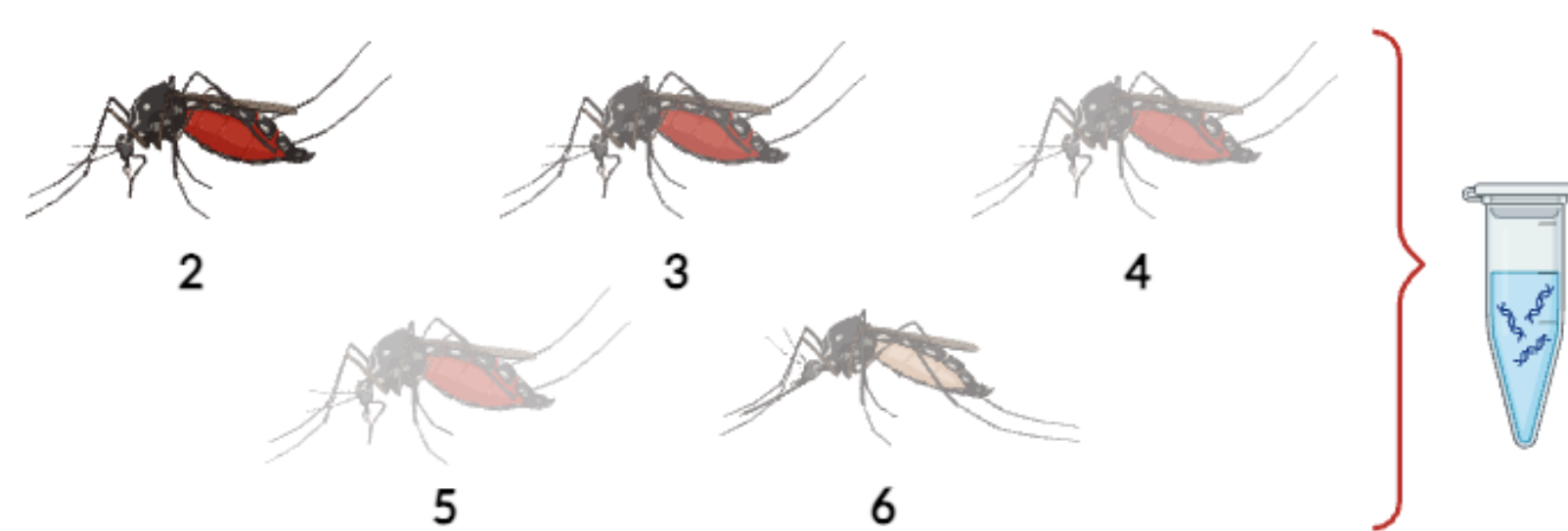
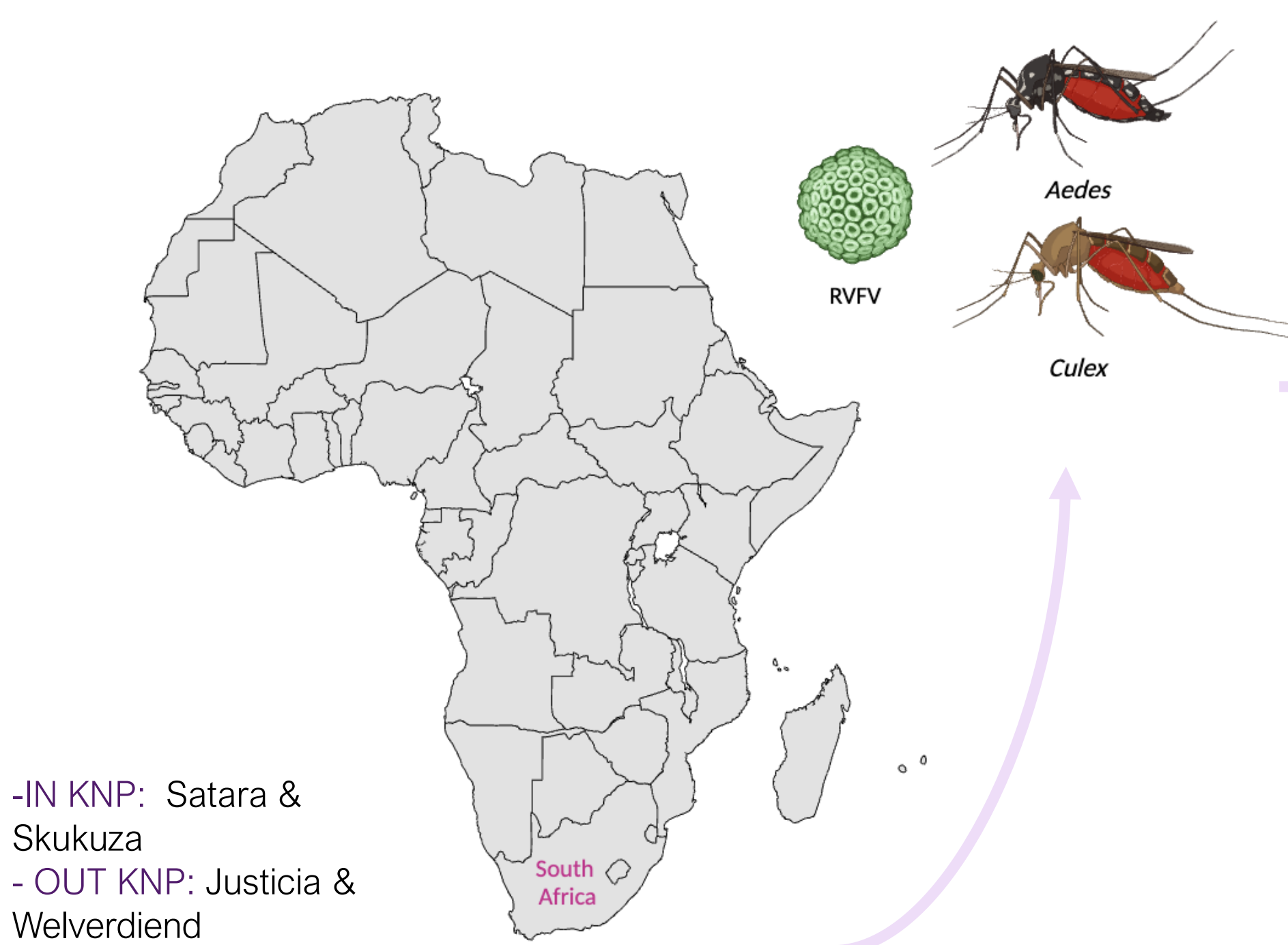
Objectives

Identify the feeding behaviour of mosquitoes collected both inside and outside the Kruger National Park during March, October and November of 2023.

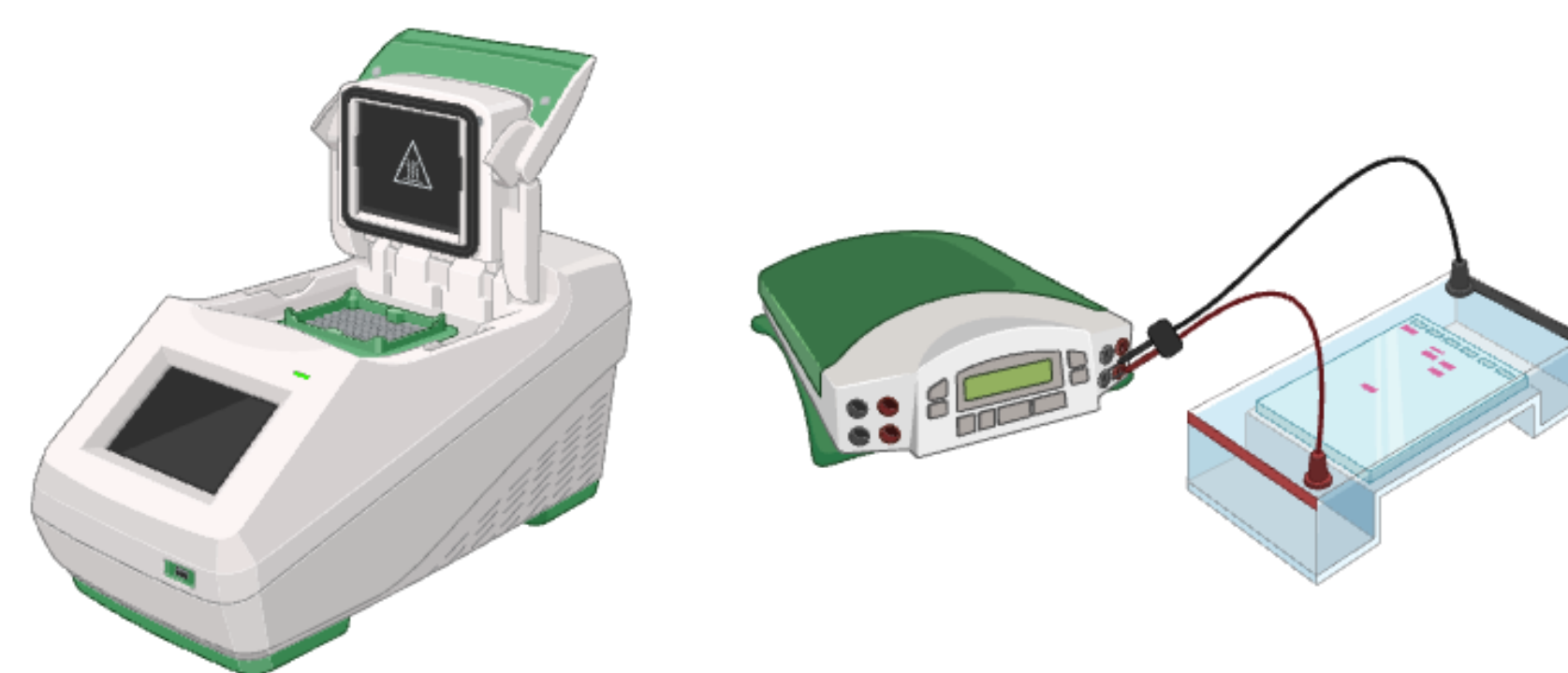
Analyse the impact of the degree of blood digestion in the molecular determination of the blood sources using two target genes cytochrome c oxidase I (COI) and cytochrome B (CytB).

Methods

RVF Mosquito vectors collection + Taxonomic identification (CDC, BG trapping / Keys *Jupp, 1996)



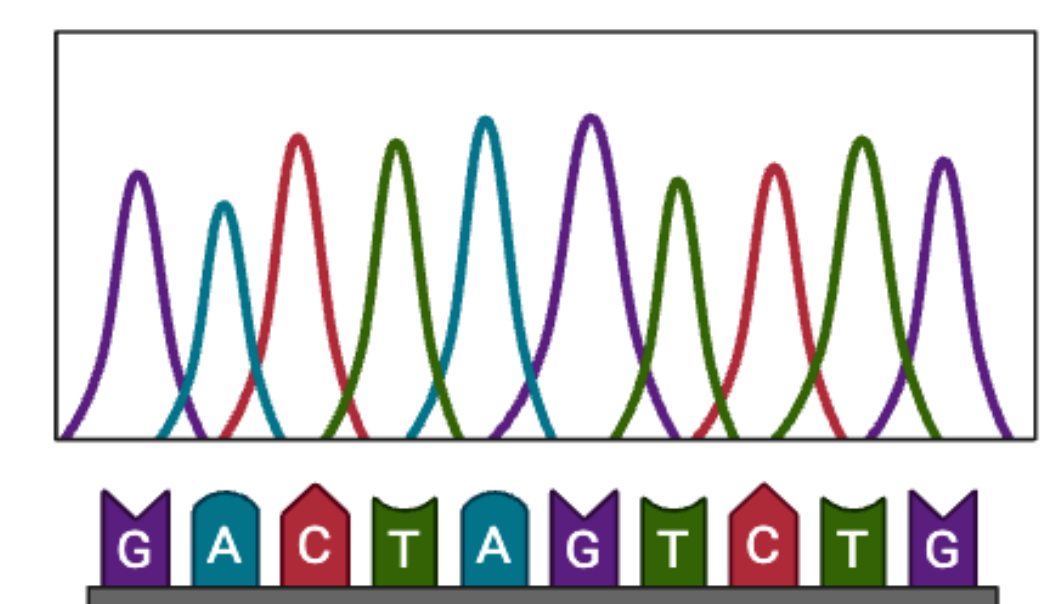
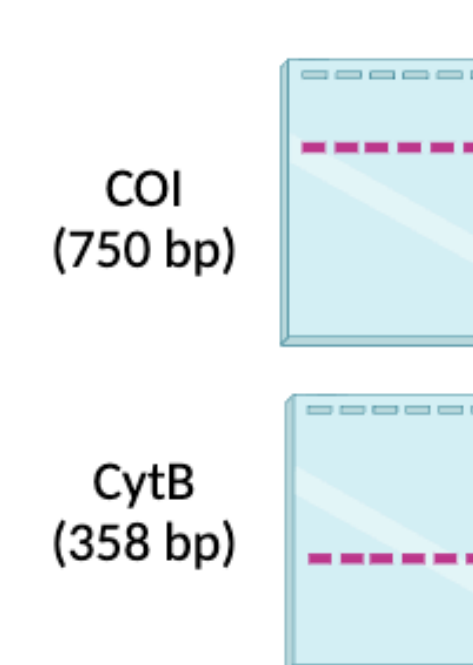
Sella Scale classification + Individual DNA extraction (EZNA Tissue DNA Kit Omega BioTek)



PCR for COI and CytB + Gel Electrophoresis (BioRad T100/BioRad PowerPac)



DNA Quantification (Qubit 4.0)



Sequences edit + comparison (4Peaks / Basic Local Alignment Search Tool - BLAST)

Results

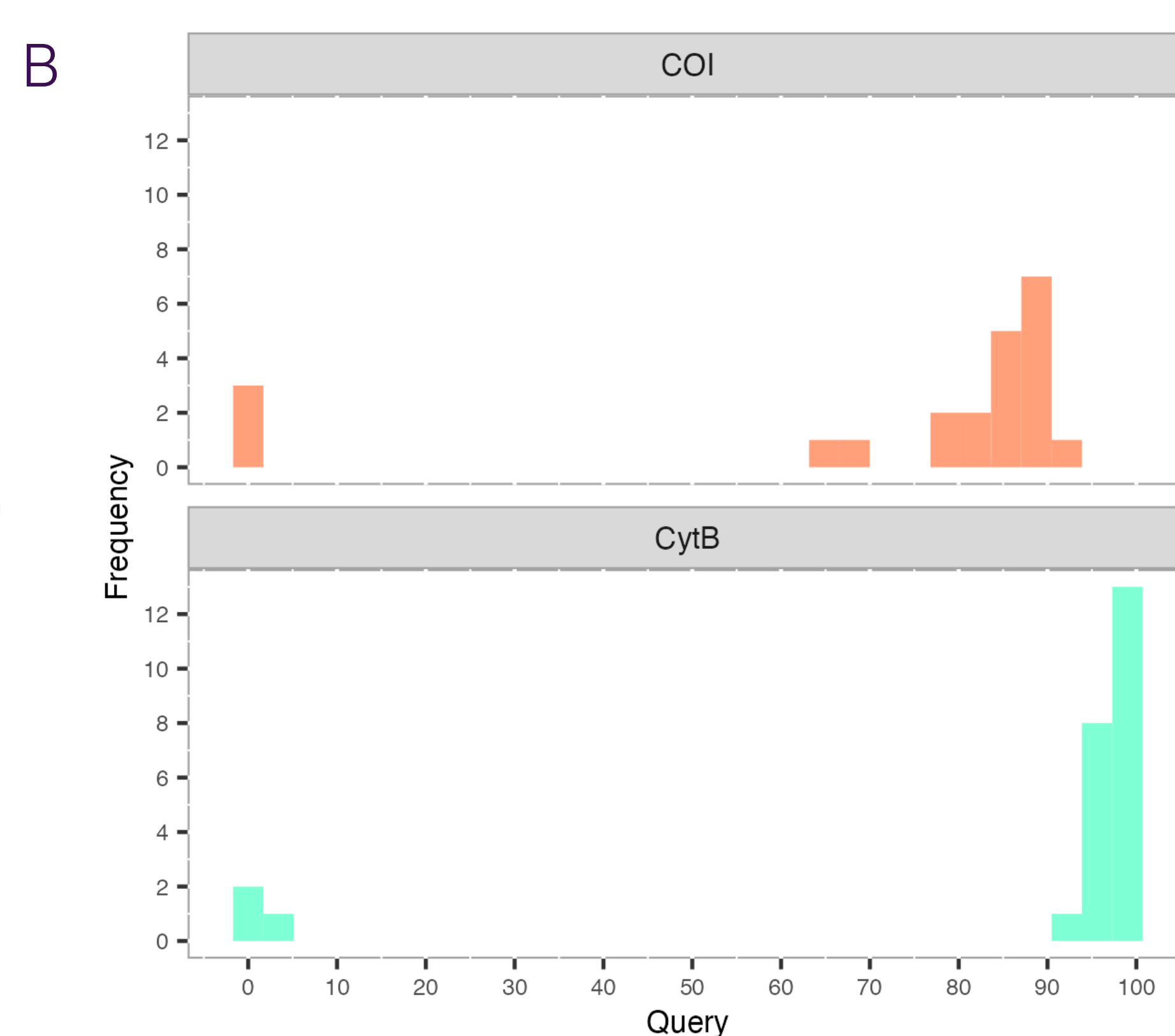
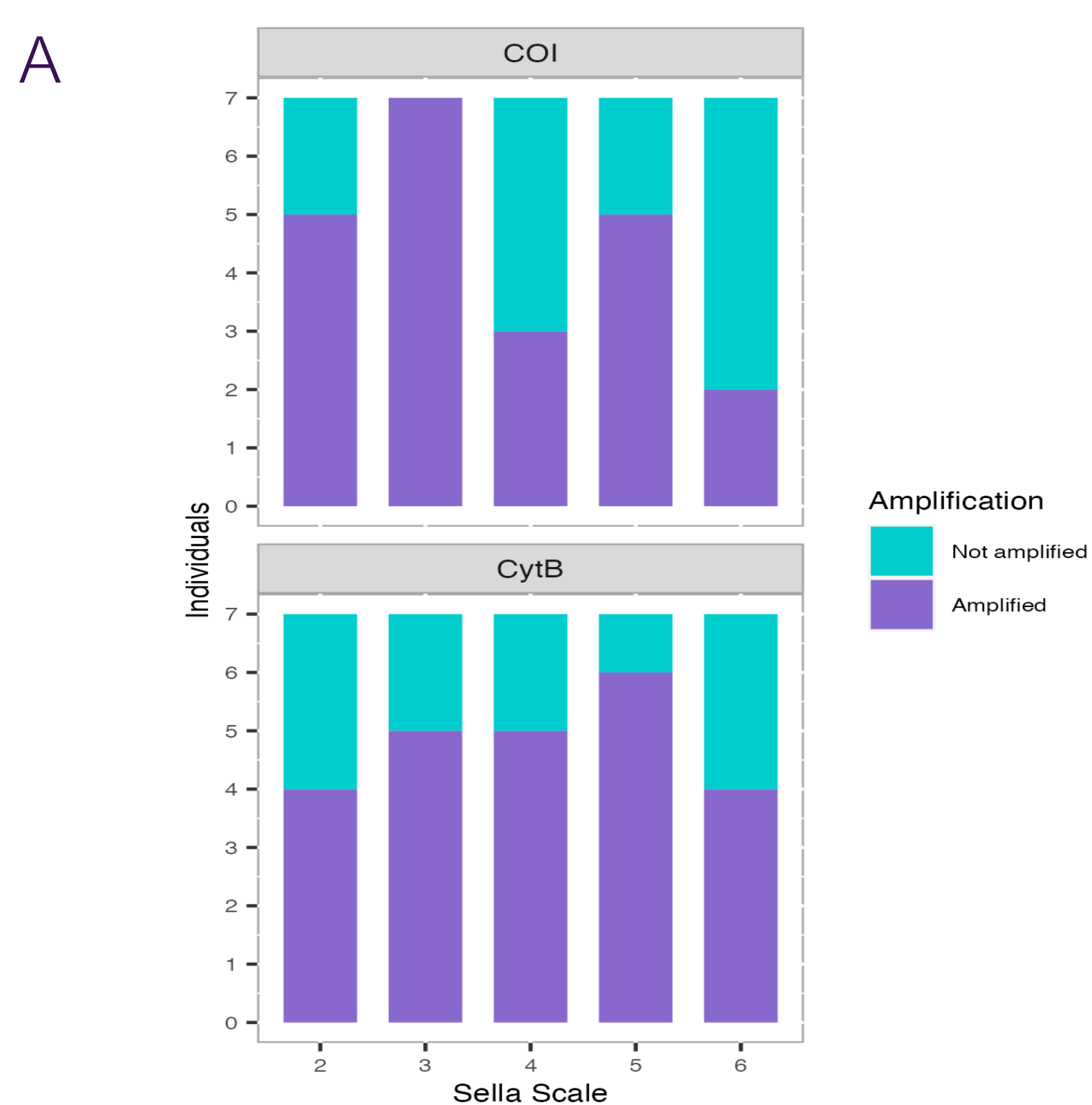
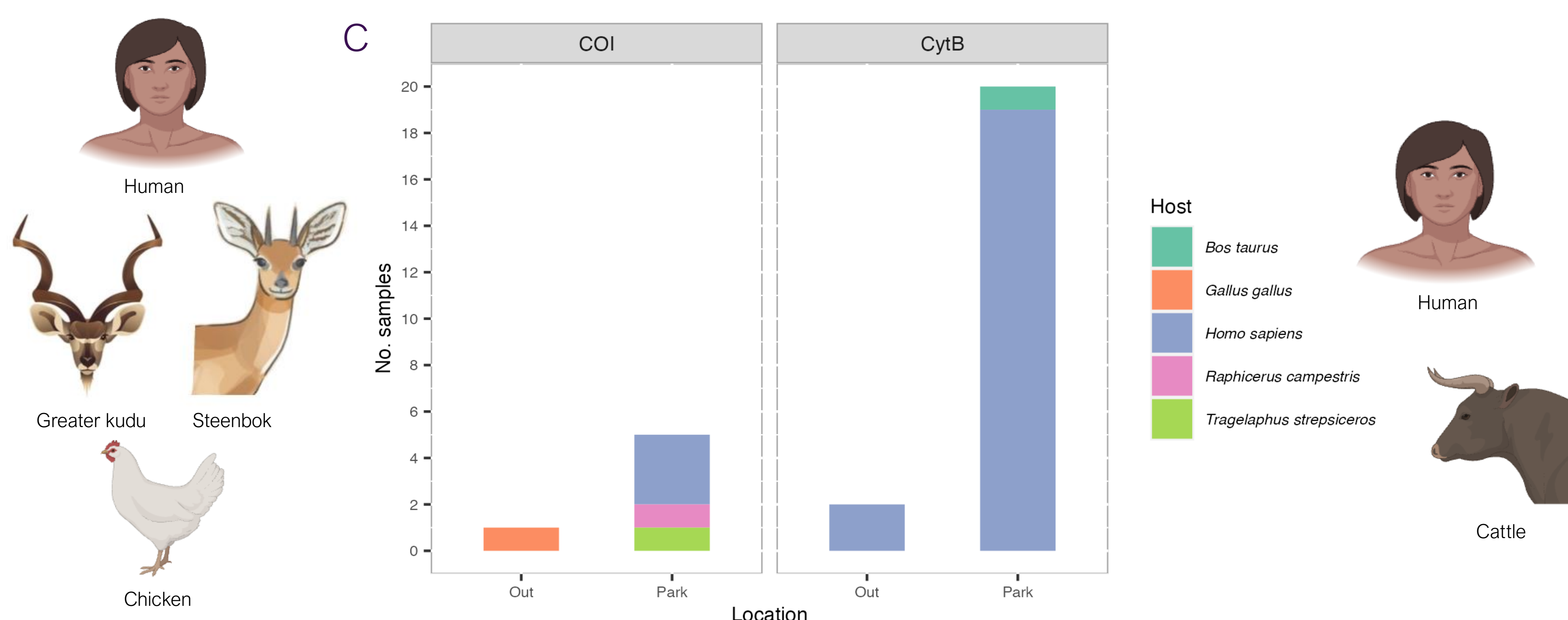


Table 1. Amount of samples and percentage of expected product size, acceptable query cover (cut-off COI>80, CytB >90) and acceptable match in the sequences alignment (>90 % identity) per Sella scale.

Gene	Sella Scale	Engorged females	Expected product size (%)	Acceptable query (%)	Acceptable match (%)
COI	2	7	4 (80)	3 (75)	1 (33)
	3	7	7 (100)	4 (57)	0 (0)
	4	7	3 (100)	2 (67)	2 (100)
	5	7	4 (80)	4 (100)	2 (50)
	6	7	2 (100)	2 (100)	1 (50)
CytB	2	7	3 (75)	3 (100)	3 (100)
	3	7	5 (100)	5 (100)	5 (100)
	4	7	5 (100)	5 (100)	5 (100)
	5	7	6 (100)	6 (100)	6 (100)
	6	7	3 (75)	3 (100)	3 (100)



CytB

- Blood meals of 22 out of 35 samples were successfully characterized.
- 95% of these were human.
- More trustable -> identify the feeding behaviour of the mosquitoes even in more blood digested stages of the Sella scale.

COI

- Just 5 samples were successfully characterized.
- Apparently more sensitive to identify wildlife species such as greater kudu and steenbok present in the KNP. Further analyses are needed to corroborate this.

Figure 1. A. Number of samples amplified or not according to location COI or CytB genes per Sella Scale (n=35). B. Histogram of Query cover of samples according to COI or CytB genes. C. Host preference per Location and per genes.

References

- Jupp, P. (1996). Mosquitoes of Southern Africa: Culicinae and Toxorhynchitinae. Ekogilde Pubs.
- Grobbelaar, A. A., Weyer, J., Leman, P. A., Kemp, A., Paweska, J. T., & Swanepoel, R. (2011). Molecular epidemiology of Rift Valley fever virus. Emerging infectious diseases, 17(12), 2270.
- Pienaar, N. J., & Thompson, P. N. (2013). Temporal and spatial history of Rift Valley fever in South Africa: 1950 to 2011. Onderstepoort Journal of Veterinary Research, 80(1), 1-13.
- Images: Created with BioRender.com